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OM nucleic - nucleic search, using sw model

Run on: April 22, 2005, 10:47:36 ; Search time 5329.58 seconds
(without alignments)
10646.432 Million cell updates/sec

Title: US-10-689-861-1

Perfect score: 1171
Sequence: 1 atgaagtcgctcctacgcg.....acatgagatccagctgtga 1171

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%

Listing first 45 summaries

Database :

GenBankl: *
1: gb_ba: *
2: gb_hcg: *
3: gb_in: *
4: gb_om: *
5: gb_ov: *
6: gb_pat: *
7: gb_ph: *
8: gb_pl: *
9: gb_pr: *
10: gb_ro: *
11: gb_sts: *
12: gb_sy: *
13: gb_un: *
14: gb_vl: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	979	83.6	1488	6	AR075987 Sequence
2	979	83.6	1488	6	AR371655 Sequence
3	979	83.6	2970	9	BC040968 Homo sapi
4	847	72.3	1216	6	AR270911 Sequence
5	847	72.3	1216	6	HSU31332 Human DP pr
6	847	72.3	156808	2	AC012407 Homo sapi
7	847	72.3	187947	9	CNS05TF6 AL365475 Human chr
8	847	72.3	197817	9	CNS05TCS AL358833 Human chr
9	556	47.5	1315	10	RNU92289 U92289 Rattus nov
10	554.4	47.3	1074	10	AF120101 Rattus nov
11	554.4	47.3	1240	6	E10040 Base sequen
12	552.8	47.2	1071	6	E10039 Base sequen
13	544.8	46.5	895	10	D29764S1 D29764 Mus musculi
14	541.6	46.3	67632	2	AC095991_1 Continuation (4 of
15	541.6	46.3	110000	2	AC112324_0 Rattus no
16	541.6	46.3	110000	2	AC112324_1 Continuation (2 of
17	541.6	46.3	110000	2	AC115635_2 Continuation (3 of
18	541.6	46.3	299134	2	AC128783 Rattus no
19	541.6	46.3	349877	2	AC115218 Rattus no

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C	23	538.4	46.0	110000	2	AC099237_4	Continuation (5 of
C	24	538.4	46.0	110000	2	AC115635_1	Continuation (2 of
C	25	538.4	46.0	254094	2	AC120220	AC120220 Rattus no
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C	27	360	30.7	205345	2	AC128247	AC128247 Rattus no
C	28	360	30.7	232703	2	AC098748	AC098748 Rattus no
C	29	335	28.6	485	6	AX549001	AX549001 Sequence
C	30	335	28.6	485	9	HSU31039	U31039 Human DP pr
C	31	228.8	19.5	2935	4	AY166779	AY166779 Oryctolag
C	32	217.8	18.6	1428	4	BT293039	293039 B.taurus pr
C	33	211	18.0	1077	9	AY275471	AY275471 Homo sapi
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C	35	211	18.0	2286	6	I88011	I88011 Sequence 3
C	36	211	18.0	2286	6	AR372105	AR372105 Sequence
C	37	211	18.0	2373	6	CQ720365	CQ720365 Sequence
C	38	210.8	18.0	2550	4	AF075602	AF075602 Canis fam
C	39	210.2	18.0	161100	2	AC025659	AC025659 Homo sapi
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C	42	209.4	17.9	2372	6	AX549005	AX549005 Sequence
C	43	209.4	17.9	2372	9	HSU19487	U19487 Human prot
C	44	209.4	17.9	6446	6	AR208580	AR208580 Sequence
C	45	208.6	17.8	3875	9	HSPYGER2G1	AF134201 Homo sapi

ALIGNMENTS

RESULT 1	AR075987	1488 bp	DNA	linear	PAT 30-AUG-2000
LOCUS	AR075987				
DEFINITION	Sequence 4 from patent US 5958723.				
ACCESSION	AR075987				
VERSION	AR075987.1	GI:10002733			
KEYWORDS	Unknown.				
SOURCE	Unknown.				
ORGANISM	Unclassified.				
REFERENCE	1 (bases 1 to 1488)				
AUTHORS	Abrahamovitz, M., Boile, Y., Metters, K., Sawyer, N. and Slipeitz, D.M.				
TITLE	DNA encoding prostaglandin receptor DP				
JOURNAL	Patent: US 5958723-A 4 28-SEP-1999;				
FEATURES	Location/Qualifiers				
source	1..1488				
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	/mol_type="unassigned DNA"				

ORIGIN

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QY	1	ATGAAGTCGCGCTTACCGCTGCCAGAACACACCTGTGTGAAAAGCACTGGCG	60	
DB	350	ATGAAGTCGCGCTTACCGCTGCCAGAACACACCTGTGTGAAAAGCACTGGCG	409	
QY	61	GTGATGAGGCGGAGTCTTACAGACCGGCTCTCTGGGAACCTGTGGCCCTGGGCTG	120	
DB	410	GTGATGAGGCGGAGTCTTACAGACCGGCTCTCTGGGAACCTGTGGCCCTGGGCTG	469	
QY	121	CTGGCGCGCTCGGAGCTGGAGTGTCTGCGGCGTTCACCTGCGCCCTGCTGCTG	180	
DB	470	CTGGCGCGCTCGGAGCTGGAGTGTCTGCGGCGTTCACCTGCGCCCTGCTGCTG	529	
QY	181	TTCTACATGCTGTGTGTGCTGAGGCTACCGACTTGTCTGGGCAAGTCCCTAAG	240	
DB	530	TTCTACATGCTGTGTGTGCTGAGGCTACCGACTTGTCTGGGCAAGTCCCTAAG	589	
QY	241	CCGGTGTGCTGGCTGCTACGCTGCAACCGGAGTCTGCGGCTGCTGCGCCGCTTG	300	

LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM
AR371655	Sequence 4 from patent US 6395499.	AR371655	AR371655.1	GI:34608648	Unknown.	Unknown.
LOCUS	AR371655	1488 bp	DNA	linear	PAT 12-SEP-2003	
DEFINITION	Sequence 4 from patent US 6395499.					
ACCESSION	AR371655					
VERSION	AR371655.1	GI:34608648				
KEYWORDS						
SOURCE	Unknown.					
ORGANISM	Unknown.					
	Unclassified.					

REFERENCE	(bases 1 to 1488)
AUTHORS	Abrahamovitz, M., Melter, K., Bole, Y., Sawyer, N. and Slipetz, D.M.
TITLE	Methods of identifying modulators of a D β prostaglandin receptor
JOURNAL	Patent: US 6395499-A 4 28-MAY-2002;
FEATURES	Location/Qualifiers
source	1..1488
	/organism="unknown"
ORIGIN	/mol_type="genomic DNA"
Query Match	83.6%; Score 979; DB 6; Length 1488;
Best Local Similarity	92.2%; Pred. No. 8e-177;
Matches 1080; Conservative	0; Mismatches 0; Indels 91; Gaps 1;
OY	1 ATGAAGTGCCTTTACTACCGCTGCCAGAACCACTTCGTGGAAAAAGGCAATCCGGC 60
DB	350 ATGAAGTGCCTTTACTACCGCTGCCAGAACCACTTCGTGGAAAAAGGCAATCCGGC 409
OY	61 GTGANTGGCGGGGGGAGCTTTCAGAACCGGCTCTCTGGGCAACCTGAGCCCTGAGGGCTG 120
DB	410 GTGANTGGCGGGGGGAGCTTTCAGAACCGGCTCTCTGGGCAACCTGAGCCCTGAGGGCTG 469
OY	121 CTGGCGGCGCTGGGGGCTGGGGTGCTCGCGGAGTCCAATGACCCTGCTCCCTCGGTC 180
DB	470 CTGGCGGCGCTGGGGGCTGGGGTGCTCGCGGAGTCCAATGACCCTGCTCCCTCGGTC 529
OY	181 TTCTACATGCTGTGTGTGTGGCTTAGACGGTCAACCGCATTTGCTGGCAAGTGCCTCTAAGC 240
DB	530 TTCTACATGCTGTGTGTGTGGCTTAGACGGTCAACCGCATTTGCTGGCAAGTGCCTCTAAGC 589
OY	241 CCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 300
DB	590 CCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 649
OY	301 GACAACCTGTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 360
DB	650 GACAACCTGTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 709
OY	361 CTGCAACTCTCCGAGCATAGGCACTGGAAGTGTGAGCTTCTCCAGAGGCAACCTTTCTTAC 420
DB	710 CTGCAACTCTCCGAGCATAGGCACTGGAAGTGTGAGCTTCTCCAGAGGCAACCTTTCTTAC 769
OY	421 CGAGGGCAATCACCTTCGCGCTTGGGGGCACTGGTGGCCCCGGTGTGTGTGTGTGTGTGTGT 480
DB	770 CGAGGGCAATCACCTTCGCGCTTGGGGGCACTGGTGGCCCCGGTGTGTGTGTGTGTGTGTGT 829
OY	481 CTGGCTTTCTGCGGGCTACCTTTATGAGGGCTTCGAGAAATTGCGACAGTAATGACCCCGGC 540
DB	830 CTGGCTTTCTGCGGGCTACCTTTATGAGGGCTTCGAGAAATTGCGACAGTAATGACCCCGGC 889
OY	541 AACTGTGCTTTATTCAGATGGTCCACGAGGAGGAGCTTCGCTGCTGAGGGTACTCT 600
DB	890 AACTGTGCTTTATTCAGATGGTCCACGAGGAGGAGCTTCGCTGCTGAGGGTACTCT 949
OY	601 GTGCTCTACTCAAGCTATGAGCGTGTGTCTTCCGCAACCGTGTGTGTGTGTGTGTGTGT 660
DB	950 GTGCTCTACTCAAGCTATGAGCGTGTGTCTTCCGCAACCGTGTGTGTGTGTGTGTGTGT 1009
OY	661 GCCATGGGCACCTCTATNGGATGACACCGGGGGGCGAGAGGAGCAACCGCGCTCCMGAC 720
DB	1010 GCCATGGGCACCTCTATNGGATGACACCGGGGGGCGAGAGGAGCAACCGCGCTCCMGAC 1069
OY	721 AGGACTGTGCGGAGCGCGCGCGAGACGGAGGAGAAGTCCCTCAACCCCTGAGAGAG 780
DB	1070 AGGACTGTGCGGAGCGCGCGCGAGACGGAGGAGAAGTCCCTCAACCCCTGAGAGAG 1129
OY	781 CTGATATCATCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 840
DB	1130 CTGATATCATCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1189
OY	841 GTAATTGCAATTGTCTTCTGAGAGTCCCAGCAAGACCTGGGAGTGTGTGTGTGTGTGTGT 900
DB	1190 GTAATT-----1195

QY 421 CGACGGACATACCCCTGGCCCTGGGGGCACTGTGTGCCCCGGTGTGAGCCCTTCTCC 480
DB 523 CGACGGACATACCCCTGGCCCTGGGGGCACTGTGTGCCCCGGTGTGAGCCCTTCTCC 582
QY 481 CTGGCTTTCTGGGGGCTTACCTTTTCAAGGGCTTGAGGAAGTTGTGTGAGTACGCCCCGGG 540
DB 583 CTGGCTTTCTGGGGGCTTACCTTTTCAAGGGCTTGAGGAAGTTGTGTGAGTACGCCCCGGG 642
QY 541 ACCTGGTGTCTTATTCAGATGTGTCAAGAGAGGGCTGCTGTGGTGTGGGTATCTCT 600
DB 643 ACCTGGTGTCTTATTCAGATGTGTCAAGAGAGGGCTGCTGTGGTGTGGGTATCTCT 702
QY 601 GTGCTTACTTCCAGCTCATGAGGCTGTGTGTCTTCTGCCACCGTGTGTGCAACTGTGGC 660
DB 703 GTGCTTACTTCCAGCTCATGAGGCTGTGTGTCTTCTGCCACCGTGTGTGCAACTGTGGC 762
QY 661 GGCATGCGCAACTCTATGAGATGCAACGGGGCTGCAAGCGGAGCCGGGCTCTGTGACCC 720
DB 763 GGCATGCGCAACTCTATGAGATGCAACGGGGCTGCAAGCGGAGCCGGGCTCTGTGACCC 822
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DB 943 GTAATT----- 948
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DB 949 -----TATCGGCTTACTATGAGCAATT 971
QY 961 TAAGATGTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
DB 972 TAAGATGTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1031
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DB 1032 ATTTCTATCTGTGATTTTCAATGTGTGACCTTGTGATTTTATGATTTTCAATGTGTGAG 1091
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RESULT 4
LOCUS AR270911 1216 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 1474 from patent US 6500938.
ACCESSION AR270911
VERSION AR270911.1 GI:29702145
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1216)
AUTHORS Au-Young,J. and Seilhamer,J.J.
TITLE Composition for the detection of signaling pathway gene expression
JOURNAL Patent: US 6500938-A 1474 31-DEC-2002;
FEATURES
source Location/Qualifiers
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Query Match 72.3%; Score 847; DB 6; Length 1216;
Best Local Similarity 100.0%; Pred.No. 1,3e-151;
Matches 847; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGAAGTGGCCGCTTTCACCGCTGCCAGAACACACACTCTGTGTGAAAAAAGCAACTGGCG 60
DB 350 ATGAAGTGGCCGCTTTCACCGCTGCCAGAACACACACTCTGTGTGAAAAAAGCAACTGGCG 409
QY 61 GTGATGGGGGGGGGTGTCTTTACAGACCGGCTCTGTGGCAACCTGTGGCCCTGGGGCTG 120
DB 410 GTGATGGGGGGGGGTGTCTTTACAGACCGGCTCTGTGGCAACCTGTGGCCCTGGGGCTG 469
QY 121 CTGGCGCGCTCGGGGCTGGGGGTGTGTCTGCGGCGCTTCCACTGCGCCCTGTGCGGTG 180
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DB 530 TTCTATCATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 589
QY 241 CCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 300
DB 590 CCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 649
QY 301 GACAACTCGTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 360
DB 650 GACAACTCGTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 709
QY 361 CTGCAACTCTGTGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 420
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DB 1130 CTGGATCACTCTCTGCTGTGCGCTGAGTGAACCGTGTCTTCACTATGTGTCTTGTGCC 1189
QY 841 GTAATTG 847
DB 1190 GTAATTG 1196
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DEFINITION Human DP prostanoind receptor (PTGR) gene, 5' region and partial cds.
ACCESSION U31332
VERSION U31332.1 GI:940378
KEYWORDS

SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 1216)
 AUTHORS Boie,Y., Sawyer,N., Slietz,D.M., Metters,K.M. and Abramovitz,M.
 TITLE Molecular cloning and characterization of the human prostanoid DP
 receptor
 JOURNAL J. Biol. Chem. 270 (32), 18910-18916 (1995)
 MEDLINE 95370201
 PUBMED 7642548
 REFERENCE 2 (bases 1 to 1216)
 AUTHORS Abramovitz,M. and Boie,Y.
 TITLE Direct Submission
 JOURNAL Submitted (10-JUL-1995) Mark Abramovitz, Biochemistry and Molecular
 Biology, Merck Frost Center for Therapeutic Research, P.O. Box
 1005, Pointe Claire Dorval, Quebec H9R 4P8, Canada
 FEATURES
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 ORIGIN
 Intron
 Query Match 72.3%; Score 847; DB 9; Length 1216;
 Best Local Similarity 100.0%; Pred. No. 1.3e-151;
 Matches 847; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ATGAAGTCCGCGCTTCAACCGCTGCCAGAACCACTCTGTGAAAAAGCACTGGCG 60
 DB 350 ATGAAGTCCGCGCTTCAACCGCTGCCAGAACCACTCTGTGAAAAAGCACTGGCG 409
 QY 61 GTGATGGGCGGGGTGCTCTTCAGACCGGCTCTGGGCAACCTGTGGCGGCTG 120
 DB 410 GTGATGGGCGGGGTGCTCTTCAGACCGGCTCTGGGCAACCTGTGGCGGCTG 469
 QY 121 GTGGCGCGCTGGGGGTGGTGTCTCGCGCGTCACTGCGCGCGCTCGCTG 180
 DB 470 GTGGCGCGCTGGGGGTGGTGTCTCGCGCGTCACTGCGCGCGCTCGCTG 529
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 QY 301 GACAACTGCTGTGCTCAAGCTTGTGCTTCTTATGCTCTTGTGGCTCTCTGACA 360
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QY 421 CGACGGCAATCAACCTGCGCTGGGCGCATGCTGTGCCCCGGTGTGAGCGCTTCTCC 480
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 QY 661 GCATGCGCAACTCTATGAGATGACACCGGCGCTGACAGGCAACCGGCTCTGTGACC 720
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 DB 1070 AGGACCTGTCGAGCGCGCGCGGAGCGGAGAGGAGCGTCCCTCAGCCCTGAGAGAG 1129
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 QY 841 GTATTG 847
 DB 1190 GTATTG 1196

RESULT 6
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 LOCUS Homo sapiens chromosome 14 clone RP11-221N7 map 14, WORKING DRAFT
 DEFINITION SEQUENCE, 26 unordered pieces.
 AC012407
 AC012407.4 GI:8569158
 HTG; HTGS_PHASE1; HTGS_DRAFT.
 KEYWORDS Homo sapiens (human)
 SOURCE Homo sapiens
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 156808)
 AUTHORS Birren,B., Linton,L., Nusbaum,C. and Lander,E.
 TITLE Homo sapiens chromosome 14, clone RP11-221N7
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 156808)
 AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.,
 Baldwin,J., Barna,N., Beckert,R., Boguslavsky,L., Bouhassira,B.,
 Brown,A., Castle,A., Colangelo,M., Collins,S., Collymore,A.,
 Cooke,P., Dearellano,K., Dewar,K., Domingo,M., Donelan,L., Doyle,M.,
 Ferreira,P., Fitzhugh,W., Forrest,C., Funke,R., Gage,D.,
 Galagan,J., Gardyna,S., Grant,G., Hagos,B., Heathford,A., Horton,L.,
 Howland,J.C., Johnson,R., Jones,C., Kann,L., Karates,A., Klein,J.,
 Lehoczy,J., Lien,C., Locke,K., MacDonald,P., Margulis,N.,
 McEwan,P., McGuirk,A., McKernan,K., McLaughlin,J., Meldrum,J.,
 Morrow,J., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,
 Peterson,K., Pollara,V., Riley,R., Roy,A., Santos,R., Severy,P.,
 Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
 Testaye,S., Turrell,A., Vassiliev,H., Vo,A., Wheeler,J., Wu,X.,
 Wyman,D., Ye,W.J., Zimmer,A. and Zody,M.
 TITLE Direct Submission
 JOURNAL Submitted (27-OCT-1999) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 REFERENCE 3 (bases 1 to 156808)
 AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
 Anderson,S., Baldwin,J., Barna,N., Baerlein,V., Bede,F.,
 Boguslavsky,L., Bouhassira,B., Brown,N., Burkett,G.,
 Campoliano,A., Castle,A., Choepel,Y., Colangelo,M., Collins,S.,
 Collymore,A., Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S.,

STS
 RHdb: RH9028
 dbSTS: STS22645
 Identified using the e-PCR software (G. Schuler)
 96853...97026
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 RHdb: RH71220
 dbSTS: STS50986
 Identified using the e-PCR software (G. Schuler)
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 RHdb: RH92017
 dbSTS: STS65021
 Identified using the e-PCR software (G. Schuler)"

ORIGIN

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 Best Local Similarity 100.0%; Pred. No. 1e-151;
 Matches 847; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAAGTCCCGCTTCTACCGCTGCGCAACACCACTCTGTGGAAAAAGCACTCGCG 60
 DB 103968 ATGAAGTCCCGCTTCTACCGCTGCGCAACACCACTCTGTGGAAAAAGCACTCGCG 103969
 QY 61 GTGATGGCGGGGTGCTTTCAAGACCGGCTCTCTGGGCAACTGCTGGCCTGGGGCTG 120
 DB 103908 GTGATGGCGGGGTGCTTTCAAGACCGGCTCTCTGGGCAACTGCTGGCCTGGGGCTG 103849
 QY 121 CTGGCGCGCTCGGGGGGTGGGTGCTGCGCGGCTCACTGCGCGCGCTCGCGTGC 180
 DB 103848 CTGGCGCGCTCGGGGGGTGGGTGCTGCGCGGCTCACTGCGCGCGCTCGCGTGC 103789
 QY 181 TTCTACATCTGGTGTGTGGGCTGACGGTCAACCGACTTGTGGGCAAGTGCCTCTTAAC 240
 DB 103788 TTCTACATCTGGTGTGTGGGCTGACGGTCAACCGACTTGTGGGCAAGTGCCTCTTAAC 103729
 QY 241 CCGGTGTGCTGCTGCTTACCTCAAGACCGGACTGTGGGTGCTTGGCGCGCATG 300
 DB 103728 CCGGTGTGCTGCTGCTTACCTCAAGACCGGACTGTGGGTGCTTGGCGCGCATG 103669
 QY 301 GACAACTCGTGGGCAAGGCTTGGCTTTCATGCTCTTGGGGCTCTCTCGACA 360
 DB 103668 GACAACTCGTGGGCAAGGCTTGGCTTTCATGCTCTTGGGGCTCTCTCGACA 103609
 QY 361 CTGCAACTCTGGGCACTGAGCTGAGTGTGCTCTCCCTAGAGGCACTTCTTCTAC 420
 DB 103608 CTGCAACTCTGGGCACTGAGCTGAGTGTGCTCTCCCTAGAGGCACTTCTTCTAC 103549
 QY 421 CGACGGCAATCACTCTGGGCTGGGCGCACTGTGGCCCCGGTGTGAGCGCTTCTTC 480
 DB 103548 CGACGGCAATCACTCTGGGCTGGGCGCACTGTGGCCCCGGTGTGAGCGCTTCTTC 103489
 QY 481 CTGGCTTTCTGGGCGGCTTACCTTTCATGGGCTTGGGAAAGTGTGAGACTGCCCCGG 540
 DB 103488 CTGGCTTTCTGGGCGGCTTACCTTTCATGGGCTTGGGAAAGTGTGAGACTGCCCCGG 103429
 QY 541 ACCTGGTCTTTATCCAGATGTCTCAAGAGAGGCTGCTGTGCGTGTGGGTACTCT 600
 DB 103428 ACCTGGTCTTTATCCAGATGTCTCAAGAGAGGCTGCTGTGCGTGTGGGTACTCT 103369
 QY 601 GTGCTTACTCCAGCTCATGGGCTGTGTGTCTTGGCCACGCTGTGCAACTCTCGG 660
 DB 103368 GTGCTTACTCCAGCTCATGGGCTGTGTGTCTTGGCCACGCTGTGCAACTCTCGG 103309
 QY 661 GGCATGCGCACTCTATGCGATGCAACGGGCGCTGCAAGGGAACCGGCTCTCGAC 720
 DB 103308 GGCATGCGCACTCTATGCGATGCAACGGGCGCTGCAAGGGAACCGGCTCTCGAC 103249
 QY 721 AAGGACTGTGCGAGCGCGCGCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 780
 DB 103248 AAGGACTGTGCGAGCGCGCGCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 103189
 QY 781 CTGATCACTCTCTGCTGCTGGCGCTGATGACCTGTCTTCAATGTGTTCTTGGCC 840

DB 103188 CTGATCACTCTCTGCTGCTGGCGCTGATGACCGCTTCTTCAATGTGTTCTTGGCC 103129

QY 841 GTAATTG 847

DB 103128 GTAATTG 103122

RESULT 8
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 LOCUS
 DEFINITION
 Human chromosome 14 DNA sequence BAC R-262M8 of library RCI-11
 from chromosome 14 of Homo sapiens (human), complete sequence.
 ACCESSION
 AL355833
 VERSION
 AL355833.4 GI:13990340
 KEYWORDS
 HTG.
 SOURCE
 Homo sapiens (human)
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 197817)
 Heilig, R., Petit, J.L., Vico, V., Dasilva, C., Robert, C., Winkler, P.,
 Brotier, P., Catolico, L., Barbe, V., Pelletier, E., Artiguenave, F.,
 Levy, M., Eckenberg, R., Bruls, T., deBardins, V., Cruaud, C.,
 Gyapay, G., Saurin, M. and Weissenbach, J.
 Sequencing of the human chromosome 14
 Unpublished
 2 (bases 1 to 197817)
 Genoscope.
 Direct Submission
 Submitted (02-MAY-2001) Genoscope - Centre National de Sequencage :
 BP 191 91006 Evry cedex - FRANCE (E-mail : sequef@genoscope.cns.fr
 - Web : www.genoscope.cns.fr)
 On May 7, 2001 this sequence version replaced gi:13897294.
 ----- Genome Center
 Center: Genoscope / Centre National de Sequencage
 Web site: http://www.genoscope.cns.fr/
 Contact: sequef@genoscope.cns.fr

COMMENT
 The following BAC sequence is oriented from the T7 to the SP6 end.
 Upstream BAC (overlapping the T7 end) : R-452D12
 Downstream BAC (overlapping the SP6 end) : R-933I1 (AC=AL157971)
 ----- Summary Statistics
 Assembly program: Phrap, version 2.0
 Quality coverage: 8.90x in Q20 bases; sum-of-contigs

 Overall quality chart :
 Range : bases
 0 2
 1 - 9 : 4
 10 - 19 : 41
 20 - 29 : 112
 30 - 39 : 876
 40 - 49 : 4041
 50 - 59 : 8035
 60 - 69 : 5759
 70 - 79 : 10473
 80 - 89 : 37260
 90 - 99 : 131214

Percentage of bases with a quality value >= 40 : 99 %.

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 RHdb: RH9028

dbSTS:STS22645
Identified using the e-PCR software (G. Schuler)"
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RHD:RH92017
dbSTS:STS65021
Identified using the e-PCR software (G. Schuler)"

ORIGIN

Query Match 72.3%; Score 847; DB 9; Length 197817;
Best Local Similarity 100.0%; Pred. No. 1e-151; Indels 0; Gaps 0;
Matches 847; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 160450 GTGATGGGGGGGTCTTTCAGACCGGCTCTCTGGGCAACTGCTGGGGCTG 160391
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DB 160390 CTGGCGCGCTCGGGGGGTGGTGTGGGGCTTCACTGGCGCGCTCGCTGGGTC 160331
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DB 160330 TTCTACATGCTGTGTGTGGCTGACGGTCAACGACTTGTGGGCAAGTCTCTAAC 160271
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DB 160270 CCGGTGTGTGGCTGCTCTACGCTCAGAACCGAGTCTGGGGTCTTGGCGCGCAT 160211
QY 301 GACAACTCGTGTGCAAGGCTTGGCTTCTTGTGCTTCTTGGGCTCTCTGACA 360
DB 160210 GACAACTCGTGTGCAAGGCTTGGCTTCTTGTGCTTCTTGGGCTCTCTGACA 160151
QY 361 CTGCACTCTCGGCACTGAGCTGTGCTCTCTCTAGGAGCACTTCTCTTAC 420
DB 160150 CTGCACTCTCGGCACTGAGCTGTGCTCTCTCTAGGAGCACTTCTCTTAC 160091
QY 421 CGACGGCACTACCTCTGGGCTGGGGCTGAGTGGCGCGGTGTGAGCGCTTCTCC 480
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DB 160030 CTGGCTTCTGGCGGCTACCTTCTATGGGCTTGGGAAAGTTCGTGACATGCCCCGCG 159971
QY 541 ACCTGTGCTTATTCAGATGTCACAGAGAGGCTCGTGTGCTGGGTACTCT 600
DB 159970 ACCTGTGCTTATTCAGATGTCACAGAGAGGCTCGTGTGCTGGGTACTCT 159911
QY 601 GTGCTTACTCCAGCTCATGGGCTGTGTCTTCCCAACGCTGTGTCACACTCGAG 660
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DB 159790 AAGGACTGTGCGCGCGCGCGGAGAGGAGAGGCTCCCTGAGAGAGAG 159731
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QY 841 GTAAATG 847
DB 159670 GTAAATG 159664

RESULT 9
LOCUS RNU92289 1315 bp mRNA linear ROD 08-MAR-1999
DEFINITION Rattus norvegicus prostaglandin D2 receptor mRNA, complete cds.
ACCESSION U92289
VERSION U92289.1 GI:2459674
KEYWORDS
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE 1 (bases 1 to 1315)
AUTHORS Geraschenko,D., Beuckmann,C.T., Kanaoka,Y., Eguchi,N.,
Gordon,W.C., Urade,Y., Bazan,N.G. and Hayashi,O.
TITLE Dominant expression of rat prostanoïd DP receptor mRNA in
epithelium, inner segments of photoreceptor cells, Irtis
JOURNAL J. Neurochem. 71 (3), 937-945 (1998)
MEDLINE 98387174
PUBMED 9721719

REFERENCE 2 (bases 1 to 1315)
AUTHORS Geraschenko,D., Kanaoka,Y., Beuckmann,C. and Urade,Y.
TITLE Direct Submition
JOURNAL Submitted (07-MAR-1997) Molecular Behavioral Biology, Osaka
Bioscience Institute, 6-2-4 Furendai, Suita, Osaka 565, Japan

FEATURES
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ORIGIN

Query Match 47.5%; Score 556; DB 10; Length 1315;
Best Local Similarity 71.2%; Pred. No. 4.9e-96;
Matches 830; Conservative 0; Mismatches 230; Indels 106; Gaps 3;

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DB 129 TGTGCTTCAAGTCAAGAGCTGTGGCAATCTCTGGGCTGGGTCTGTGGCGGATC 188
QY 132 GGGGCTGGGGGTGTCTCGCGGCTCACTGGCGCGCTGGCTCTTACATGCT 191
DB 189 CGGGGCTGGGGGTCTGTGGCGGCAAGGCACTGCATCGCGCGCTCTTTATGTGCT 248
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DB 369 ATGTGAAGCTTGGCTTCTTCAATGCTTCTTGGGCTCTCCTGCACTGCAATCTCT 428
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DB 429 GGCTATGAGCACTGAGTGTGCTCTCTGAGACACCTTTCTTACCAAGGACAT 488
QY 432 CACCTGCGCTGGGCGCACTGTGAGCCCGGTGTGAGCGCTTCTCTGCTTCTG 491
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DB 904 -----TATGCTGCTTACTATGAGCACTTTAACTGT-- 935
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RESULT 10
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LOCUS AF120101
DEFINITION Rattus norvegicus prostaglandin D2 receptor mRNA, complete cds.
ACCESSION AF120101
VERSION AF120101.1 GI:4567037
KEYWORDS
SOURCE Rattus norvegicus (Norway rat)

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ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 1074)
AUTHORS Wright,D.H., Nanel,F., Metters,K.M. and Ford-Hutchinson,A.W.
TITLE A novel biological role for prostaglandin D2 is suggested by
distribution studies of the rat DP prostanooid receptor
JOURNAL Eur. J. Pharmacol. 377 (1), 101-115 (1999)
MEDLINE 99376163
PUBMED 10448933
REFERENCE 2 (bases 1 to 1074)
AUTHORS Wright,D.H. and Abramowitz,M.
TITLE Direct Submision
JOURNAL Submitted (13-JAN-1999) Biochemistry and Molecular Biology, Merck
Frost Centre for Therapeutic Research, P.O. Box 1005, Pointe
Claire - Dorval, Quebec H9R 4P6, Canada
FEATURES
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ORIGIN

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Query Match 47.3%; Score 554.4; DB 10; Length 1074;
Best Local Similarity 71.1%; Pred. No. 1e-95;
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DB 9 GTCTTATCCCTCTCAAGGACGACCACTGAGTGAAGCGGCGCTCTCAGCAATAGGTGG 68
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DB 69 TGTGCTTCAATGAGAGAGCTGTGGCAACTCTGCGCTGTGTGTGTGTGTGTGTGT 128
QY 132 GGGGCTGGGGTGTGCTCGCGCGTTCACATGCGCGCGCTGCGCTGCTTCAATGCT 191
DB 129 CGGGCTGGGGTGTGCTCGCGCGCAAGGCACTGATCGCGCGCTGCTTTTATGCTGT 188
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DB 189 AGTGTGCGGCTTGAACAGTCAACGACTTGTGTGGCAAGTCTCTTCAAGCCGCTGT 248
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DB 249 GGCTGCTTACGCGCAAAATCGAGAGCTTAAAGAACTGTGCTGCTCCTCAGGACCACT 308
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DB 369 GGCTATGAGCACTGAGTGTGCTCTCTGAGACACCTTTCTTACCAAGGACAT 428
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 E10040
 VERSION E10040.1 GI:22026662
 KEYWORDS JP 1995258295-A/2.
 SOURCE Mus sp.
 ORGANISM Mus sp.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (baeas 1 to 1240)
 Ichikawa, A., Nakao, I. and Narumiya, S.
 PROSTAGLANDIN D RECEPTOR, ITS PRODUCTION, DNA ENCODING THE SAME
 RECEPTOR, VECTOR COMPRISING THE SAME DNA AND HOST TRANSFORMED WITH
 THE SAME VECTOR
 Patent: JP 1995258295-A 2 09-OCT-1995;
 JOURNAL ONO PHARMACEUT CO LTD
 COMMENT OS Mus sp. (mouse)
 PN JP 1995258295-A/2
 PF 22-MAR-1994 JP 1994075382

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 C12R1:91);
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 CC topology: Linear;
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 FT /product="Prostaglandin D receptor".
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 ORIGIN
 Query Match 47.3%; Score 554.4; DB 6; Length 1240;
 Best Local Similarity 71.1%; Pred. No. 1e-95;
 Matches 829; Conservative 0; Mismatches 231; Indels 106; Gaps 3;
 QY 12 GTTCTACCGCTGCGACAGACCACTCTGTGAAAAAGCAACTCGCGGTGATGCGCG 71
 DB 45 GTCTATGCTGTGTCAGACATCCACTGTGGGTGAGAAAGGGCTCTCGGACGATGGGCGC 104
 QY 72 GGTGCTCTTACAGACCGGCTCTGTGGCAACTGTGCGCTTGGGGCTGTGGCGGCTC 131
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 DB 285 GGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 344
 QY 312 GTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 371
 DB 345 ATGCGAAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 404
 QY 372 GGCATGAGCATGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 431
 DB 405 GGTATGAGGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 464
 QY 432 CACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 491
 DB 465 CACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 524
 QY 492 CGGCTACCTTTTATGAGGCTTGTGGGAAGTGTGTGACGATCTGCCCGGACCTGTGCTT 551
 DB 525 TGGGCTCCCTTTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 584
 QY 552 TATCCAGATGATCCAGAGAGGCTCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 611
 DB 585 CATCCAGATGATCCAGAGAGGCTCATTTCTGGTAAATAGGCTTCTCTGTGCTTACTC 644
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 DB 645 CAGCTCATGGGCTGTGTGCTCTCGGACCGGTGTGTGACCTCGGCGCCATGCGCAA 704
 QY 672 CCTCTATGAGTGAACCGGCGGCTGTGAGGAGACCGGCTCTGTGACAGGAGCTGTGCT 731
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Db 825 TGTGCTGCTGCGCTGATGACCGTGTCTTCACTATGTGTCTGTCCGTAATGCAAT 879
Qy 852 TGTTCCTGAGTCCCGCCAGACACCTGAGAGTGAAGTGAAGGCAATTTTCA 911
Db 880 ----- 879
Qy 912 GTGCTGCTCTCTCTCTTCTTCTCCCAAGTATCGCGCTTACTATGAGACATTTAAGATGTCA 971
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Qy 972 AGAGAGAAAAACAGACCTCTGAGAGAGACAGACCTCCGAGCTTGCGATTTCTATCTG 1031
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Qy 1092 TTTTTCACAGATTTTTCATTTAGCTTTCAGTACGAGACCGGTGACGAATTC--- 1147
Db 1025 TATTTTCACAGATTTTTCATTTAGCTTTCAGTACGAGAACTGGAGACGAATTCGACG 1084
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Db 1085 AAGTAACTGGATCACTTGTGA 1110

RESULT 12
E10039 1071 bp RNA linear PAT 29-SEP-1997
LOCUS Base sequence of the open leading frame of prostaglandin D
DEFINITION receptor.
E10039

ACCESSION E10039.1 GI:22026661
VERSION JP 1995258295-A/1.
KEYWORDS unidentified
SOURCE unidentified
ORGANISM unidentified.

REFERENCE 1 (bases 1 to 1071)
AUTHORS Ichikawa,A., Nakao,I. and Narumiya,S.
TITLE PROSTAGLANDIN D RECEPTOR, ITS PRODUCTION, DNA ENCODING THE SAME
RECEPTOR, VECTOR COMPRISING THE SAME DNA AND HOST TRANSFORMED WITH
THE SAME VECTOR
JOURNAL Patent: JP 1995258295-A 1 09-OCT-1995;
ONO PHARMACEUT CO LTD

COMMENT OS Mus.sp (mouse)
PN JP 1995258295-A/1
PD 09-OCT-1995
PE 22-MAR-1994 JP 1994075382
PI ICHIKAWA ATSUSHI, NAKAO ICHIKAZU, NARUMIYA SHU PC
C07K14.7/05, C12N5/10, C12N15/09, C12P21/02//A61K8/00, C12P21/02, PC
C12R1(91);
CC strandedness: Single;
CC topology: Linear;
FH Key Location/Qualifiers

FEATURES
source 1..1071
FT /organism='Mus sp.'
FT /tissue='Lung'.
FT Location/Qualifiers
1..1071
/organism='unidentified'
/mol_type='genomic RNA'
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ORIGIN

Query Match 47.2%; Score 552.8; DB 6; Length 1071;
Best Local Similarity 71.2%; Pred. No. 2e-95;
Matches 809; Conservative 0; Mismatches 227; Indels 100; Gaps 2;

Qy 12 GTTCTACCGCTCCAGAACACCACCTGTGTGAAAAAGGCAACTCGCGGTGATGGGCGG 71
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Qy 72 GGTGCTCTTACAGACCGGCTCTTGTGGCAACTGCTGAGCCCTGGGGCTGTGGCGGCTC 131
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Qy 132 GGGGCTGGGGGTGGGTGGTGGCGGCGTGCACCTGGCGCCGCTCGCTGTCTTACATAGCT 191
Db 129 GGAATGGGGTCTTGTGGCGGCGCAGGGGCACTTACACCGCGCGCTTGTATGTGCT 188
Qy 192 GGTGTGTGGCTGACGCTGACCGACTTGTGTGGGCAAGTGCCTTAAAGCCGGGTGCT 251
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Qy 312 GTGCCAAGCCTTGGCTTGTATGTCTTGTGGGCTGTCTGTGACACTGCAACTGCT 371
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Qy 432 CACCTGCGCTGGGGGCGCACTGTGTGCCCCGGTGTGAGCGCTTCTCCCTGGCTTCTG 491
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Qy 492 CGCGCTACCTTTCATGGGCTTGGGAGTGTGTGTGAGTACTGCCCGGCACTGTGCTT 551
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Qy 552 TATCCAGATGTCTCAGAGAGAGGCTCGCTGTGTGTGTGTGTGTGTGTGTGTGTGT 611
Db 549 CATCCAGATGTCTCAGAGAGAGGCTCGCTGTGTGTGTGTGTGTGTGTGTGTGTGT 608
Qy 612 CAGCTCATGCGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 671
Db 609 CAGCTCATGCGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 668
Qy 672 CCTATGAGATGACCGGCGGCTGAGGCGGCACTGTGTGTGTGTGTGTGTGTGTGTGT 731
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Db 844 ----- 843
Qy 912 GTGCTGCTCTCTCTCTTCTCCCAAGTATCGCGCTTACTATGAGACATTTAAGATGTCA 971
Db 844 -----TATCGTGGACTATGAGAGCTTTAAACCTTG--- 874
Qy 972 AGAGAGAAAAACAGACCTCTGAGAGAGACAGAAAGCTCCGAGCTTGGCATTTCTATCTG 1031
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RESULT 13
LOCUS D29764S1 895 bp DNA linear ROD 12-OCT-2002
DEFINITION Mus musculus gene for prostaglandin D receptor, exon 1.
ACCESSION D29764
VERSION D29764.1 GI:577718
KEYWORDS 1 of 2
SEGMENT Mus musculus (house mouse)
SOURCE
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 895)
Hirata, M., Kakizuka, A., Aizawa, M., Ushikubi, F. and Narumiya, S.
Molecular characterization of a mouse prostaglandin D receptor and
functional expression of the cloned gene
Proc. Natl. Acad. Sci. U.S.A. 91 (23), 11192-11196 (1994)
JOURNAL 95062232
MEDLINE 7972033
REFERENCE 2 (bases 1 to 895)
HIRATA, M.
AUTHORS Hirata, M.
TITLE Direct Submission
SUBMITTED (01-APR-1994) Masakazu Hirata, Faculty of Medicine, Kyoto
University, Department of Pharmacology, Yoshida-Koae, Sakyo-Ku,
Kyoto, Kyoto 606, Japan (Tel:81-75-753-4392, Fax:81-75-753-4693)
LOCATION/Qualifiers
1. 895
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/mol_type="genomic DNA"
/strain="129Sv"
/db_xref="taxon:10090"
/clone="lambdaDP16"
1. 879
/product="prostaglandin D receptor"
/note="CDS is reported in Acc# D29765."
/number=1

FEATURES
source
1. 895
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="129Sv"
/db_xref="taxon:10090"
/clone="lambdaDP16"
1. 879
/product="prostaglandin D receptor"
/note="CDS is reported in Acc# D29765."
/number=1

ORIGIN
Query Match 46.5%; Score 544.8; DB 10; Length 895;
Best Local Similarity 78.2%; Pred. No. 6.9e-94;
Matches 654; Conservative 0; Mismatches 182; Indels 0; Gaps 0;
Qy 12 GTTTCACCGCTGCAGAACCACTCTGTGAAAAAGGCACTCGCGGTGATGGCGG 71
Db 45 GTCTATCGCTGTCAAGCAATCCACTGGGTGAAAGGGCTCTCGCGCAAGATGGCGG 104
Qy 72 GGTGCTCTTACAGACCGGCTCTGTGGCAACTGTGGCCCTGGGGCTGTGGCGGCTC 131
Db 105 TGTGCTCTTACAGACCGGCTCTGTGGCAACTGTGGCCCTGTGGCTGTGGCGGCTC 164
Qy 132 GGGGCTGGGGTGTGCTCGCGGCTCACTGCGCGCGCTCGCTTCTTCAATGCT 191
Db 165 GGAACCTGGGGTGTGCTCGCGGCTCACTGCGCGCGCTCGCTTCTTATGCT 224
Qy 192 GGTGTGTGCTGACCGGTCAACCACTGTGGCAAGTGCCTTAAGCCCGGTGTGCT 251
Db 225 CGTGTGTGCTTACCGGTCAACCACTGTGGCAAGTGTGTATAGCCCGATGCT 284
Qy 252 GGTGTGTGCTGACCGGTCAACCACTGTGGCAAGTGTGTGTGTGGCCGCAATGGACAATCTGCT 311
Db 285 GGTGTGTGCTGACCGGTCAACCACTGTGGCAAGTGTGTGTGTGTGGCCGCAATGGACAATCTGCT 344
Qy 312 GTGGCAAGCTTGTGCTTCTTCAATGCTCTTGTGGCTCTCTGCAACTGCAATCTCT 371
Db 345 ATGCGAAAGCTTGTGCTTCTTCAATGCTCTTGTGGCTCTCTGCAACTGCAATCTCT 404
Qy 372 GGCATGGAAGTGTGCTTCTCTTGTGGCAAGCTTGTGTCTTACCGAGCGGCAAT 431

Db 405 GGTATGAGGAGTGTGCTGTGTCTGTGGACACCCCTTCTTACCAAGGACGT 464
Qy 432 CACCTGCGCTGGGCGCACTGGTGGCCCGGTGTAGAGGCTTCTCCCTGCTTCTG 491
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Db 525 TGGGCTCCCTTGTGTGTGTGTGGAAAGTGTGTGAGTGTGCCCCGCACTGTGCTT 584
Qy 552 TATTCAGATGTGTCAAGAGAGGCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGT 611
Db 585 CATTCAGATGTGTCAAGAGAGGCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGT 644
Qy 612 CAGCTCATGAGGCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 671
Db 645 CAGCTCATGAGGCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 704
Qy 672 CCTTATGAGATGACACCGCGCTGTGAGCGGACCCGCGCTCTGTGACCAAGGACTGTGC 731
Db 705 CCTTATGAGATGACACCGCGCTGTGAGCGGACCCGCGCTCTGTGACCAAGGACTGTGC 764
Qy 732 CGAGCCGCGCGGAGACGGAAGGAGCTTCTTCAAGCCCTGTGAGAGTGTGATCACT 791
Db 765 CGAGTACGCTCAGATCAAGGACCGGCTCTGTGATCTTGTGAGAGCTGTGACCACT 824
Qy 792 CCGCTGCTGGGCGCTGATGACCGTGTCTTCACTATGTGTCTTCCCGTATATG 847
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RESULT 14
AC095991.3
WPCOMMENT
Sequence split into 4 fragments LOCUS AC095991 Accession AC095991
Fragment Name Begin End
AC095991.0 1 110000
AC095991.1 100001 210000
AC095991.2 200001 310000
AC095991.3 300001 367632
Continuation (4 of 4) of AC095991 From Base 300001 (AC095991 Rattus norvegicus clone CH2:
Query Match 46.3%; Score 541.6; DB 2; Length 67632;
Best Local Similarity 78.0%; Pred. No. 2.3e-93;
Matches 652; Conservative 0; Mismatches 184; Indels 0; Gaps 0;
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Qy 192 GGTGTGTGCTGACCGGTCAACCACTGTGGCAAGTGCCTTCAAGCCCGGTGTGCT 251
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Qy 252 GGTGTGTGCTGACCGGTCAACCACTGTGGCAAGTGTGTGTGTGTGGCCGCAATGGACAATCTGCT 311
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Qy 312 GTGGCAAGCTTGTGCTTCTTCAATGCTCTTGTGGCTCTCTGCAACTGCAATCTCT 371
Db 63444 ATGCGAAAGCTTGTGCTTCTTCAATGCTCTTGTGGCTCTCTGCAACTGCAATCTCT 404
Qy 372 GGCATGGAAGTGTGCTTCTCTTGTGGCAAGCTTGTGTCTTACCGAGCGGCAAT 431
Db 63504 GGTATGAGGAGTGTGCTGTGTCTGTGGACACCCCTTCTTACCAAGGACAT 63563

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QY 432 CACCTGCGCCCTGCGGCGCACTGCTGCGCCCGGCTGTGAGCGCCTTCTCCCTGCTTCTG 491
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QY 492 CCGGCTACCTTTTCATGCGGCTTGGGAAAGTTGCTGCACTGCTCCCGGCGCACTGCTGCTT 551
DB 63624 TCGGCTCCCTTGTGCTGCTTGTGGGAAAGTTGCTGCACTGCTCCCGGCGCACTGCTGCTT 63683
QY 552 TATTCAGATGCTCAGAGAGAGGCTCGCTGTGCGTGTGCGGCTGCTGCTGCTGCTGCTGCTGCT 611
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DB 63744 CAGCCTCATGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 63803
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RESULT 15

AC112324_0/c

WPCOMMENT

Sequence split into 4 fragments LOCUS AC112324 Accession AC112324

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AC112324_1 100001 210000

AC112324_2 200001 310000

AC112324_3 300001 357027

LOCUS AC112324 357027 bp DNA linear HTG 26-SEP-2002

DEFINITION Rattus norvegicus clone CH230-75L12, *** SEQUENCING IN PROGRESS

AC112324

AC112324.3 GI:23321735

HTG: HTGS PHASE1: HTGS DEAPT: HTGS_ENRICHED.

KEYWORDS Rattus norvegicus (Norway rat)

SOURCE

ORGANISM

Rattus norvegicus

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

Rattus.

1 (bases 1 to 357027)

Muzny, D. Marie, Metzker, M. Lee, Abramson, S., Adams, C., Alder, J.,

Allen, C., Allen, H., Albrooks, S., Amin, A., Anguiano, D.,

Anyalebech, V., Aoyagi, A., Ayodeji, M., Baca, B., Baden, H.,

Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benhmed, F.,

Biswal, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M.,

Bryant, N., Burch, C., Burch, P., Burrell, K., Calderon, E.,

Cardenas, V., Carter, K., Cavazos, I., Caesar, H., Center, A.,

Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J.,

Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L.,

Davila, M. L., Davis, C., Davy-Carroll, L., De Anda, C., Delecluch, D.,

Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Diya, K.,

Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K.,

Egan, A., Escotto, M., Eugene, C., Evans, C. A., Falls, T., Fan, G.,

Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P.,

Frazer, C. M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M.,

Gebregergis, E., Geer, K., Gilly, R., Grady, M., Guerra, W., Guevara, W.,

Gunaratne, P., Haaland, W., Hamill, C., Hamilton, C., Hamilton, K.,

Harvey, Y., Haylak, P., Hawes, A., Henderson, N., Hernandez, J.,

Hernandez, R., Hines, S., Hladun, S. L., Hodgson, A., Hognes, M.,

Hollins, B., Howells, S., Hulyk, S., Hume, J., Idlebird, D., Jackson, A.,

Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A.,

Karpathy, S., Kelly, S., Kelly, S., Khan, Z., Kling, L., Kovar, C.,

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

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JOURNAL

Kowis, C., Kraft, C. L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J., Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J., Lorenshew, L., Louised, H., Lozano, R. J., Lu, X., Ma, J., Maheshwari, M., Mahindaratne, M., Mahmoud, M., Malloy, K., Mangum, A., Mangum, B., Mapua, P., McNeill, T. Z., Meenan, E., Mawhinney, S., McLeod, M. P., McNeill, T. Z., Meenan, E., Mawhinney, S., Minner, G., Minja, E., Montemayor, J., Moore, S., Morgan, M., Morris, K., Morris, S., Munda, M., Murphy, M., Naif, L., Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Nwankweli, O., Okunolu, G., Olarnunsgoon, A., Pal, S., Parks, K., Pasternak, S., Paul, H., Perez, A., Perez, L., Pfankuch, C., Plopper, F., Ponder, A., Popovic, D., Primm, E., Pu, L., Pu, L., Puzo, M., Quiroz, J., Rachlin, E., Reeves, K., Regier, M. A., Reigh, R., Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F., Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S. J., Sanders, M., Savary, G., Scherer, S., Scott, G., Shatman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sison, I., Sitter, C. D., Smaj, D., Sneed, A., Sodergren, E., Song, X., Z., Sorrell, R., Sosa, D., Steimle, M., Strong, N., Sutton, A., Svatek, A., Taber, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usmani, K., Valas, R., Vera, V., Villasana, D., Waldron, L., Walker, B., Wang, J., Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, F., Williams, G., Willson, R., Wlezyk, R., Wooden, H., Wright, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, Y., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von Niederhausern, A., Weiss, R., Smith, D. R., Holt, R. A., Smith, H. O., Weinstock, G. and Gibbs, R. A.

Unpublished

Direct Submission

2 (bases 1 to 357027)

Worley, K. C.

Direct Submission

Submitted (21-FEB-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 357027)

Rat Genome Sequencing Consortium.

Direct Submission

Submitted (26-SEP-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On Sep 26, 2002 this sequence version replaced gi:11737250.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (<http://www.hgsc.bcm.tmc.edu/projects/rat/>). As a result, the sequence may extend beyond the ends of the clone and there may be contigs that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

Genome Center

Center: Baylor College of Medicine

Center code: BCM

Web site: <http://www.hgsc.bcm.tmc.edu/>Contact: hgsc-help@bcm.tmc.edu

Project Information

Center project name: G00G

Center clone name: CH230-75L12

Summary Statistics

Assembly program: Phrap; version 0.990329

Consensus quality: 294995 bases at least Q40

Consensus quality: 299994 bases at least Q30

Consensus quality: 302651 bases at least Q20

Estimated insert size: 390689; sum-of-contigs estimation

Quality coverage: 3x in Q20 bases; sum-of-contigs estimation

NOTE: Estimated insert size may differ from sequence length

NOTE: (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draai_data.html)

NOTE: This sequence may represent more than one clone.

NOTE: This is a 'working draft' sequence. It currently

consists of 11 contigs. The true order of the pieces

is not known and their order in this sequence record is

arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 7987: contig of 7987 bp in length
* 7988 8087: gap of unknown length
* 8088 15583: contig of 7496 bp in length
* 15584 15683: gap of unknown length
* 15684 133212: contig of 117529 bp in length
* 133213 133312: gap of unknown length
* 133313 261674: contig of 128362 bp in length
* 261675 261774: gap of unknown length
* 261775 274519: contig of 12745 bp in length
* 274520 285073: contig of 10454 bp in length
* 285074 285173: gap of unknown length
* 285174 327168: contig of 41995 bp in length
* 327169 327268: gap of unknown length
* 327269 331337: contig of 4069 bp in length
* 331338 331437: gap of unknown length
* 331438 344641: contig of 13204 bp in length
* 344642 351023: gap of unknown length
* 351024 351123: gap of 6282 bp in length
* 351124 357027: contig of 5904 bp in length.
Location/Qualifiers

1. 357027
/organism="Rattus norvegicus"

/mol_type="genomic DNA"

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/clone="CH230-75L12"

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/note="wgs contig"

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8088. 10145
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261775. 263469
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/note="wgs contig"

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/note="wgs contig"

274620. 279177
/note="wgs contig"

283699. 285073
/note="wgs contig"

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/note="wgs contig"

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/note="wgs contig"

333452. 334831
/note="wgs contig"

342450. 344641
/note="wgs contig"

ORIGIN

Query Match 46.3%; Score 541.6; DB 2; Length 110000;
Best Local Similarity 78.0%; Pred. No. 2.2e-93;
Matches 652; Conservative 0; Mismatches 184; Indels 0; Gaps 0;

QY 12 GTTCTACCGCTGCACAAACCACTCTGTGAAAAAGCAACTCGCGGTGATGAGCGG 71
DB 108350 GTTCTATCCCTGTCAGACGACCACTGTGTGAAACGCGGCTCTCAAGCACAATGGGTGG 108291
QY 72 GGTGCTCTTCAGACCGGCTCTCTGGGCAACTGTGCGCTGGGCTGCGCGCTC 131
DB 108290 TGTGCTCTTCAGTGAAGACTGTGTGGCAACTCTCTGGCGCTGTGTGCTGCGCGACT 108231
QY 132 GGGGCTGGGGGTGTGTCTCGCGGCTCACTGCGCGCGCTGCGCTCTTCAATGCT 191
DB 108230 CGGGCTGGGGGTCTCGCGGCTCACTGCGCGCGCTGCGCTCTTCAATGCT 108171

QY 192 GGTGTGCGCTGACAGGTACACGACTTGTGCGCAAGTGTGCTTAAGCCCGGTGTCT 251
DB 108170 AGTGTGCGCTTACAGTACACGACTTGTGCGCAAGTGTGTATACGCCCAATGTCT 108111
QY 252 GGTGCTTACGCTCAGAACCGAGTGTGCGGCTGTGCGCGCAATGGACAATCTGTT 311
DB 108110 GGTGCTTACGCGCAAAATCGAGCTTAAGGAATGTGTGCTGCTCAAGGCAACGTT 108051
QY 312 GTTCCAAAGCTTGTGCTTCTTCAATGTCTTCTTGTGGGCTCTCTCGACACTGAACTCT 371
DB 108050 ATGTGAAGCTTGTGCTTCTTCAATGTCTTCTTGTGGGCTCTCTCGACACTGAACTCT 107991
QY 372 GGCATGACACTGAGAGTGTGCTTCTTCTTGTGGGCACTTCTTCTTACGAGCAAT 431
DB 107990 GGTATGACACTGAGAGTGTGCTTCTTCTTGTGGGCACTTCTTCTTACGAGCAAT 107931
QY 432 CACCTGCGCTGTGGGCGCACTGTGTGCGCGCGCTGTGTGAGCGCTTCTTCTTGTCT 491
DB 107930 CACCTGCGCGCGGAGGTGTGTGTGCAACAGTGTGCGCGCGCTTCTTCTTGTCT 107871
QY 492 CGGCTACCTTTTATAGGCTTGTGTGGAAGTGTGTGCAAGTGTGTGCAAGTGTGTG 551
DB 107870 TGTGCTTCTTGTGTGTGTGTGTGGAAGTGTGTGCAAGTGTGTGCAAGTGTGTG 107811
QY 552 TATCCAGATGTTCACAGAGAGGCTGCTGTGTGCGGCTTCTTGTGTCTTACTC 611
DB 107810 CATCCAGATGTTCACAGAGAGGCTTCTTGTGTGCAAGTGTGTGCAAGTGTGTG 107751
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DB 107690 CCTTATGTGATGACACCGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 107631
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DB 107630 CGAGCGCGCGCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 107571
QY 792 CTTGCTGTGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 847
DB 107570 TTTTCTGTGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 107515

Search completed: April 22, 2005, 15:32:10
Job time : 5338.58 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 22, 2005, 09:24:18 ; Search time 707.49 Seconds
(without alignments)
9798.042 Million cell updates/sec

Title: US-10-689-861-1
Perfect score: 1171
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: geneseqn1980s:*
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5: geneseqn2001as:*
6: geneseqn2002as:*
7: geneseqn2002as:*
8: geneseqn2003as:*
9: geneseqn2003as:*
10: geneseqn2003as:*
11: geneseqn2003as:*
12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	992.8	84.8	1505	10	AD07082	Ad07082 Novel cod
2	979	83.6	1253	4	ABA09244	AbA09244 Human pro
3	979	83.6	1253	4	AAK53126	AAk53126 Human pol
4	979	83.6	1253	10	AD08862	Ad08862 Novel DNA
5	979	83.6	1303	4	AAK52142	AAk52142 Human pol
6	979	83.6	1488	2	AAT37402	AAt37402 Prostagla
7	976	83.3	1077	12	AD030026	Ad030026 Human GPC
8	950.6	81.2	1264	3	AAA27056	AAa27056 Human cel
9	848.4	72.5	14607	3	AAA35113	AAa35113 Human ade
10	848.4	72.5	14607	3	AAFP21235	AAf21235 Human low
11	848.4	72.5	14607	10	ABZ96929	ABz96929 Human nuc
12	848.4	72.5	14607	11	ABD20778	ABd20778 Human pul
13	847	72.3	1216	3	AAA35105	AAa35105 Human ade
14	847	72.3	1216	3	AAFP21227	AAf21227 Human low
15	847	72.3	1216	10	ABZ96921	ABz96921 Human nuc
16	847	72.3	1216	10	ACA56876	ACa56876 Human sig
17	847	72.3	1216	11	ABD20770	ABd20770 Human pul
18	847	72.3	1216	12	AD156672	ADi56672 Human pol
19	830	70.9	964	12	ACH90941	ACH90941 Human gen
20	590	50.4	597	12	ACH76886	ACH76886 Human gen

21	556	47.5	1074	12	AD030316	Ad030316 Mouse GPC
22	556	47.5	1315	10	ADB58427	ADb58427 Toxicity-
23	554.4	47.3	1240	2	AAT05172	AAt05172 Prostagla
24	552.8	47.2	1071	2	AAT05171	AAt05171 Prostagla
25	371	31.7	371	12	ACH90586	ACH90586 Human gen
26	335	28.6	495	3	AAA35104	AAa35104 Human ade
27	335	28.6	495	3	AAFP21226	AAf21226 Human low
28	335	28.6	495	8	ABZ42748	ABz42748 Human pro
29	335	28.6	495	8	ABZ96920	ABz96920 Human nuc
30	335	28.6	495	11	ABD20769	ABd20769 Human pul
31	335	28.6	495	13	ADP55148	ADp55148 Human PRO
32	211	18.0	1077	3	AAA34921	AAa34921 Human ade
33	211	18.0	1077	3	AAFP21043	AAf21043 Human low
34	211	18.0	1077	10	ABZ96737	ABz96737 Human nuc
35	211	18.0	1077	11	ABD20586	ABd20586 Human pul
36	211	18.0	2296	2	AAV12457	AAv12457 Human HP4
37	211	18.0	2286	6	ABK88459	ABk88459 Human CDN
38	211	18.0	2395	12	AD005737	ADo05737 Human pro
39	211	18.0	9060	3	AAA34925	AAa34925 Human pro
40	211	18.0	9060	3	AAFP21047	AAf21047 Human low
41	211	18.0	9060	10	ABZ96741	ABz96741 Human nuc
42	211	18.0	9060	11	ABD20590	ABd20590 Human pul
43	210.2	18.0	36509	13	ACH37241	ACH37241 Human per
44	209.4	17.9	1077	12	AD030028	ADo30028 Human GPC
45	209.4	17.9	2372	3	AAA34919	AAa34919 Human ade

ALIGNMENTS

RESULT 1	
AD07082	
ID	AD07082 standard; DNA; 1505 BP.
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AC	AD07082;
XX	
DT	29-JAN-2004 (first entry)
XX	
DE	Novel coding sequence (useful for identifying genetic disorders) #148.
XX	
KW	novel gene; novel protein; tissue marker; molecular weight marker;
KW	chromosome marker; genetic disorder; gene; ds.
XX	
OS	Unidentified.
XX	
PN	MO2003054152-A2.
XX	
PD	03-JUL-2003.
XX	
PF	10-DEC-2002; 2002WC-US039555.
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PR	10-DEC-2001; 2001US-0339739P.
PR	11-DEC-2001; 2001US-0339453P.
PR	14-MAR-2002; 2002US-0365091P.
PR	14-MAR-2002; 2002US-0365384P.
PR	12-APR-2002; 2002US-0372381P.
PR	12-APR-2002; 2002US-0372615P.
PR	22-APR-2002; 2002US-00128558.
PR	24-APR-2002; 2002US-0376045P.
XX	
PA	(HYSE-) HYSEQ INC.
XX	
PI	Tang YT, Asundi V, Goodrich RW, Ren F, Zhang J, Zhao QA, Wang J;
PI	Ghosh M, Xue AJ, Weinman T, Weng G, Zhou P, Drmanac RT, Wang Z;
PI	Ma Y, Wang D, Chen R, Xu C, Boyle BJ;
XX	
DR	WPI; 2003-569235/53.
XX	
PT	P-PSDB; AD070993.
XX	
PT	New polynucleotides, useful for expressing recombinant proteins for
PT	analysis, characterization or therapeutic use, or as markers for tissues
PT	in which the corresponding protein is preferentially expressed.
XX	

PS Claim 1; SEQ ID NO 148; 1177bp; English.
 CC The invention comprises the amino acid and coding sequences of novel
 CC proteins. The DNA and protein sequences of the invention are useful as:
 CC markers for tissues in which the corresponding protein is preferentially
 CC expressed; as molecular weight markers on gels; as chromosome markers or
 CC tags; to identify chromosomes or to map related gene positions; and to
 CC compare with endogenous DNA sequences in patients to identify potential
 CC genetic disorders. The present DNA sequence represents a gene of the
 CC invention.
 XX
 SQ Sequence 1505 BP; 265 A; 434 C; 441 G; 365 T; 0 U; 0 Other:
 Query Match 84.8%; Score 992.8; DB 10; Length 1505;
 Best Local Similarity 92.3%; Pred. No. 1.1e-225;
 Matches 1069; Conservative 0; Mismatches 57; Indels 32; Gaps 1;
 QY 1 ATGAAGTCGCGCTTCTAAGCGCTGCGAAGACCACTCTGTGAAAAAGCAACTGGCG 60
 DB 231 ATGAAGTCGCGCTTCTAAGCGCTGCGAAGACCACTCTGTGAAAAAGCAACTGGCG 290
 QY 61 GATGATGGGCGGGGATGCTCTTACAGACCGGCTCTGTGGCAACCTGTGGCGCTGGGGCTG 120
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 QY 121 CTGGCGCGCTCGGGGCTGGGGGATGCTCGAGCGCTCAGCTGCGCCGCTGCGCTCGCTC 180
 DB 351 CTGGCGCGCTCGGGGCTGGGGGATGCTCGAGCGCTCAGCTGCGCCGCTGCGCTCGCTC 410
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 QY 301 GACAACTGCTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
 DB 531 GACAACTGCTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 590
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 DB 591 CTGCAACTCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 650
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 DB 651 CGAGCGCAATCAACCTGCGGCTGCGGCGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 710
 QY 481 CTGGCTTTTCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
 DB 711 CTGGCTTTTCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 770
 QY 541 ACCTGCTGCTTTATCCAGATGCTTCAAGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
 DB 771 ACCTGCTGCTTTATCCAGATGCTTCAAGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 830
 QY 601 GTCCTCACTCCAGGCTCATGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
 DB 831 GTCCTCACTCCAGGCTCATGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 890
 QY 661 GCCATGCGCAACCTTATGCGATGCAACCGGCTGCGAGGAGACCGGCTGCTGCTGCTGCTG 720
 DB 891 GCCATGCGCAACCTTATGCGATGCAACCGGCTGCGAGGAGACCGGCTGCTGCTGCTGCTG 950
 QY 721 AGGAGCTGTGCGAGCGCGCGCGGAGCGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAG 780
 DB 951 AGGAGCTGTGCGAGCGCGCGCGGAGCGAGAGGAGAGGAGAGGAGAGGAGAGGAGAGGAGAG 1010
 QY 781 CTGAGTCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840
 DB 1011 CTGAGTCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1070

QY 841 GTAATTG-----CAATTGTTCTGAGATCCCG 868
 DB 1071 GTAATTGATGTCCTCGGCGCCCGAGGACAGAGGCACTGATGTCCTCGGCGCGGATG 1130
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 DB 1131 CCGGGCGGAGAGGATGAGCGGATGCGGATGAGCGGCGGCGGAGGAGGAGGAGGAGGAGG 1190
 QY 929 TCTCCCAATATCGCCTTACTATGAGAGATTTAAGATGTCAGAGAGAGAGAGAGAGAG 988
 DB 1191 GCCAGAGATATGCGGCTTACTATGAGAGATTTAAGATGTCAGAGAGAGAGAGAGAGAG 1250
 QY 989 TCTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1048
 DB 1251 TCTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1310
 QY 1049 CCTTGATTTTATATGATTTTCAATGATGATGATGATGATGATGATGATGATGATGATG 1108
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 QY 1109 ATTAGACTCTTAAAGTAC 1126
 DB 1371 ATTAGACTCTTAAAGTAC 1388

RESULT 2
 ABA09244
 ID ABA09244 standard; cDNA; 1253 BP.
 XX
 AC ABA09244;
 XX
 DT 11-JAN-2002 (first entry)
 XX
 DE Human prostaglandin DP receptor homologue cDNA, SEQ ID NO:1020.
 XX
 KW Human; cytokine; cell proliferation; cell differentiation; growth factor;
 KW haematopoiesis regulation; tissue growth; immunomodulator; activin;
 KW inhibin; chemokinesis; chemokinesis; oncogenesis;
 KW proliferation; metastasis; cancer; tumour; haematopoietic disorder;
 KW myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;
 KW chronic inflammatory condition; proliferative retinopathy;
 KW atherosclerosis; coronary heart disease; arterial ischemia;
 KW bone disorder; osteoporosis; vascular growth disorder;
 KW tissue regeneration; wound healing; infection; immune disorder;
 KW cell culture; drug screening; gene therapy; antiinflammatory;
 KW antistatic; antiarthritic; haemostatic; antiarteriosclerotic;
 KW cyostatic; osteopathic; vasotropic; cardiac; virucide; antibacterial;
 KW antifungal; vulnery; antidiarr; ss.
 XX
 OS Homo sapiens.
 XX
 PN MO200157188-A2.
 XX
 PD 09-AUG-2001.
 XX
 PF 05-FEB-2001; 2001MO-US003800.
 XX
 PR 03-FEB-2000; 2000US-00496914.
 PR 27-APR-2000; 2000US-00560875.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Tang YT, Liu C, Drmanac RT;
 XX
 DR WPI: 2001-457740/49.
 DR P-PDB; ABB12000.
 XX
 PT Human proteins and DNA encoding sequences useful for preventing, treating
 PT or ameliorating a medical condition in a mammalian subject e.g. arthritis
 PT and cancer.
 XX
 PS Claim 1; Page 860-861; 1963pp; English.
 XX

PF 05-FEB-2001; 2001MO-US004098.
 XX 03-FEB-2000; 2000US-00496914.
 PR 27-APR-2000; 2000US-00560875.
 PR 20-JUN-2000; 2000US-00598075.
 PR 19-JUL-2000; 2000US-00620325.
 PR 01-SEP-2000; 2000US-00654936.
 PR 15-SEP-2000; 2000US-00663561.
 PR 20-OCT-2000; 2000US-00693325.
 PR 30-NOV-2000; 2000US-00728422.
 XX (HYSE-) HYSEQ INC.
 PA Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y;
 PI Ma Y, Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
 PI Xue AJ, Yang Y, Wejhtman T, Goodrich R;
 DR WPI, 2001-476283/51.
 XX P-SDB; AAM79993.
 PT Nucleic acids encoding polypeptides with cytokine-like activities, useful
 in diagnosis and gene therapy.
 PS Claim 1; Page 4907; 6221pp; English.
 XX The invention relates to polynucleotides (AAK51456-AAK53435) and the
 CC encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to
 CC cytokine, cell proliferation or cell differentiation or which may induce
 CC production of other cytokines in other cell populations. The
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,
 CC e.g. stem cell growth factor activity, haematopoiesis regulating
 CC activity, tissue growth factor activity, immunomodulatory activity and
 CC activity/inhibin activity and may be useful in the diagnosis and/or
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
 CC inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111
 CC (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the
 CC sequence listing were missing at the time of publication
 XX
 XX
 SQ Sequence 1253 BP; 190 A; 405 C; 358 G; 300 T; 0 U; 0 Other;
 Query Match 83.6%; Score 979; DB 4; Length 1253;
 Best Local Similarity 92.2%; Pred. No. 2e-222;
 Matches 1080; Conservative 0; Mismatches 0; Indels 91; Gaps 1;
 QY 1 ATGAAGTCGCGCTTCTACGCTGCGTGCAGAACCACTCTGTGAAAAAGCACTCGGCG 60
 DB 122 ATGAAGTCGCGCTTCTACGCTGCGTGCAGAACCACTCTGTGAAAAAGCACTCGGCG 181
 QY 61 GTGATGGGCGGGGTGCTCTTCAAGACCGGCTCTGTGGCAACCTGTGGGCTG 120
 DB 182 GTGATGGGCGGGGTGCTCTTCAAGACCGGCTCTGTGGCAACCTGTGGGCTG 241
 QY 121 CTGGCGCGCTGCGGCGTGGGCTGTGCTCGCGGCTCACTGTGCGCCGCTCGGCTG 180
 DB 242 CTGGCGCGCTGCGGCGTGGGCTGTGCTCGCGGCTCACTGTGCGCCGCTCGGCTG 301
 QY 181 TTCTACATGCTGGGTGTGCTGAGCGGTACCGACTTGTGTGGCAAGTGCCTCTAAGC 240
 DB 302 TTCTACATGCTGGGTGTGCTGAGCGGTACCGACTTGTGTGGCAAGTGCCTCTAAGC 361
 QY 241 CCGGTGGTGTGCTGCTGCTACGCTCAGAACCGAGTGTGGGCTGTGGCGCCGCAATG 300
 DB 362 CCGGTGGTGTGCTGCTGCTACGCTCAGAACCGAGTGTGGGCTGTGGCGCCGCAATG 421
 QY 301 GACAACTCTGTGGCGCAAGCTTGTGCTTCTCATGCTCTTTTGGGCTCTCTGACA 360
 DB 422 GACAACTCTGTGGCGCAAGCTTGTGCTTCTCATGCTCTTTTGGGCTCTCTGACA 481
 QY 361 CTGCAACTCTGTGGCGCAAGCTGAGTGTGCTGCTTCTCTAAGGCACTCTTCTTCTAC 420
 DB 482 CTGCAACTCTGTGGCGCAAGCTGAGTGTGCTGCTTCTCTAAGGCACTCTTCTTCTAC 541

QY 421 CGAGGCAATCACTCGGCGCTGGGCGCACTGTGTGCCCCGGGTGTGAGCCCTTCTCC 480
 DB 542 CGAGGCAATCACTCGGCGCTGGGCGCACTGTGTGCCCCGGGTGTGAGCCCTTCTCC 601
 QY 481 CTGGCTTCTGTGGCGGCTTCTTCAATGAGCTTGTGGAGTGTGTGCAACTGCCCCGGC 540
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 QY 541 ACCTGTGTCTTATTCAGATGTGCAAGAGAGGCTGTGTGCTGTGGGCTTCTTCT 600
 DB 662 ACCTGTGTCTTATTCAGATGTGCAAGAGAGGCTGTGTGCTGTGGGCTTCTTCT 721
 QY 601 GTGTCTTCTTCAAGCTTCAATGAGCTGTGTGTCTGTGCAAGCTGTGCAACTGCGC 660
 DB 722 GTGTCTTCTTCAAGCTTCAATGAGCTGTGTGTCTGTGCAAGCTGTGCAACTGCGC 781
 QY 661 GCCATGCGCAACTCTTATGAGTGAACCGGCGGCTGCAAGGCACTGCGCTCTGACAC 720
 DB 782 GCCATGCGCAACTCTTATGAGTGAACCGGCGGCTGCAAGGCACTGCGCTCTGACAC 841
 QY 721 AGGAGCTGTGCGAGCGCGCGCGGAGAGGAGGAGCTGCTTCAAGCTGAGGAG 780
 DB 842 AGGAGCTGTGCGAGCGCGCGCGGAGAGGAGGAGGAGCTGCTTCAAGCTGAGGAG 901
 QY 781 CTGATCACTCTCTGCTGCTGCGCTGATGACCGCTCTTCACTATGTGTCTCTGCC 840
 DB 902 CTGATCACTCTCTGCTGCTGCGCTGATGACCGCTCTTCACTATGTGTCTCTGCC 961
 QY 841 GTATTTGATTTTGTCTGTGAGTCCCCCGGCAAGACCTGGGAGTGTGAGGCTTGAAG 900
 DB 962 GTATTT----- 967
 QY 901 AAACATTTTCAGTGCTGCTCTCTCTTCTTCCAGATTCGCGCTTACTATGAGCAAT 960
 DB 968 -----TATCGGCTTACTATGAGCAAT 990
 QY 961 TAAAGATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
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 QY 1021 ATTCTATCTGTGATTTCAATTTGTGAGAGCTTGTATTTATCATTTTCAATTTCTCAGT 1080
 DB 1051 ATTCTATCTGTGATTTCAATTTGTGAGAGCTTGTATTTATCATTTTCAATTTCTCAGT 1110
 QY 1081 ATTCTATTTTTCACAGATTTTCAATTTGTGAGAGCTTGTATTTATCATTTTCAATTTCTCAGT 1140
 DB 1111 ATTCTATTTTTCACAGATTTTCAATTTGTGAGAGCTTGTATTTATCATTTTCAATTTCTCAGT 1170
 QY 1141 CAATTCACCTTAACATGGAATTCAGTCTGTGA 1171
 DB 1171 CAATTCACCTTAACATGGAATTCAGTCTGTGA 1201
 RESULT 4
 ADE08862
 ID ADE08862 standard; DNA; 1253 BP.
 XX
 XX ADE08862;
 XX
 XX 29-JAN-2004 (first entry)
 XX
 XX Novel DNA-related contig nucleotide sequence #106.
 XX
 XX novel gene; novel protein; tissue marker; molecular weight marker;
 KW chromosome marker; genetic disorder; contig; ds.
 OS Unidentified.
 XX
 XX W02003054152-A2.
 XX
 XX
 XX
 XX
 XX 03-JUL-2003.
 XX
 XX 10-DEC-2002; 2002MO-US039555.
 PF


```

XX 10-DEC-2001; 2001US-0339739P.
PR 11-DEC-2001; 2001US-0339453P.
PR 14-MAR-2002; 2002US-0365091P.
PR 14-MAR-2002; 2002US-0365384P.
PR 12-APR-2002; 2002US-0372819P.
PR 12-APR-2002; 2002US-0372615P.
PR 22-APR-2002; 2002US-00128558.
PR 24-APR-2002; 2002US-0376045P.
XX
PA (HYSE-) HYSEO INC.
XX
PI Tang YT, Asundi V, Goodrich RW, Ren F, Zhang J, Zhao QA, Wang J;
PI Ghosh M, Xue AJ, Weinman T, Weng G, Zhou P, Drmanac RT, Wang Z;
PI Ma Y, Wang D, Chen R, Xu C, Boyle BJ,
XX WPI; 2003-569235/53.
XX
PT New polynucleotides, useful for expressing recombinant proteins for
PT analysis, characterization or therapeutic use, or as markers for tissues
PT in which the corresponding protein is preferentially expressed.
XX
PS Disclosure, SEQ ID NO 1928; 1177bp; English.
XX
CC The invention comprises the amino acid and coding sequences of novel
CC proteins. The DNA and protein sequences of the invention are useful as:
CC markers for tissues in which the corresponding protein is preferentially
CC expressed; as molecular weight markers on gels; as chromosome markers or
CC tags; to identify chromosomes or to map related gene positions; and to
CC compare with endogenous DNA sequences in patients to identify potential
CC genetic disorders. The present DNA sequence was used in the
CC exemplification of the invention.
XX
SQ Sequence 1253 BP; 190 A; 405 C; 358 G; 300 T; 0 U; 0 Other;
Query Match 83.6%; Score 979; DB 10; Length 1253;
Best Local Similarity 92.2%; Pred. No. 2e-222;
Matches 1080; Conservative 0; Mismatches 0; Indels 91; Gaps 1;
QY 1 ATGAAATCGCGCTTACCGCTCCAGAACACCACTCTGTGAAAAAGCAACTCGGCG 60
DB 122 ATGAAATCGCGCTTACCGCTCCAGAACACCACTCTGTGAAAAAGCAACTCGGCG 181
QY 61 GTGATGGGCGGGGTGCTCTTACAGACCGGCTCTGTGGCAACCTGTGGCCCTGGGGCTG 120
DB 182 GTGATGGGCGGGGTGCTCTTACAGACCGGCTCTGTGGCAACCTGTGGCCCTGGGGCTG 241
QY 121 CTGGCGCGCTCGGGGCTGGGGTGTGCTCGCGGCTCACTGCGCCCGCTCGCTCGGTC 180
DB 242 CTGGCGCGCTCGGGGCTGGGGTGTGCTCGCGGCTCACTGCGCCCGCTCGCTCGGTC 301
QY 181 TTCTACATGCTGTGTGTGTGCTGACGCGTCAACGCACTTGTGGGCAAGTCTCTCAAGC 240
DB 302 TTCTACATGCTGTGTGTGTGCTGACGCGTCAACGCACTTGTGGGCAAGTCTCTCAAGC 361
QY 241 CCGGTGGTGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
DB 362 CCGGTGGTGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 421
QY 301 GACAACTCGTGTGCAAGGCTTGCCTTCTTCAATGCTCTTCTTGGGCTCTCTCGACA 360
DB 422 GACAACTCGTGTGCAAGGCTTGCCTTCTTCAATGCTCTTCTTGGGCTCTCTCGACA 481
QY 361 CTGCAACTCTGGGCTGATGCACTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420
DB 482 CTGCAACTCTGGGCTGATGCACTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 541
QY 421 CGACGGGCAATCACTCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
DB 542 CGACGGGCAATCACTCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 601
QY 481 CTGCGCTTCTGCGCGCTACCTTTCTATGAGGCTTGGGAAAGTTCTGCAATGCTCCCGG 540

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DB 602 CTGCGCTTCTGCGCGCTACCTTTCTATGAGGCTTGGGAAAGTTCTGCAATGCTCCCGG 661
QY 541 ACCGTGCTTTATTCAGATGATGTCAGAGAGAGGCTCGCTGTGCTGCTGCTGCTGCTG 600
DB 662 ACCGTGCTTTATTCAGATGATGTCAGAGAGAGGCTCGCTGTGCTGCTGCTGCTGCTG 721
QY 601 GTGCTTACTTCAGACCTCATGAGGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTG 660
DB 722 GTGCTTACTTCAGACCTCATGAGGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTG 781
QY 661 GCCATGCGCAACTCTATGAGATGACACCGGCTGTGAGGCAACCGGCTCTGTGACC 720
DB 782 GCCATGCGCAACTCTATGAGATGACACCGGCTGTGAGGCAACCGGCTCTGTGACC 841
QY 721 AGGACTGTGCGAGCGCGCGCGAGCGGAGGAGGAAAGCGTCCCTCAGCCCTGAGAGAG 780
DB 842 AGGACTGTGCGAGCGCGCGCGAGCGGAGGAGGAAAGCGTCCCTCAGCCCTGAGAGAG 901
QY 781 CTGATACACTCTCTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840
DB 902 CTGATACACTCTCTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 961
QY 841 GTATTGCAATTTCTCTGTGAGATCCCGGCAAGACACTGGAGTATGATGAGCTTGAGG 900
DB 962 GTATT-----
QY 901 AATCATTTTCAAGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 960
DB 968 -----TATGCGCTTACTATGAGCATT 990
QY 961 TAAGATGTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
DB 991 TAAGATGTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1050
QY 1021 ATTCTATCTGTGATTTCAATGTGACACCTTGATTTTATCATTTTCAATGCTCCAGT 1080
DB 1051 ATTCTATCTGTGATTTCAATGTGACACCTTGATTTTATCATTTTCAATGCTCCAGT 1110
QY 1081 ATTGGATATTTTTCACAGATTTTCAATGATTTTCAATGATTTTCAATGATTTTCAAT 1140
DB 1111 ATTGGATATTTTTCACAGATTTTCAATGATTTTCAATGATTTTCAATGATTTTCAAT 1170
QY 1141 CAATTCACATCAATGAAATTCAGTCTGTGA 1171
DB 1171 CAATTCACATCAATGAAATTCAGTCTGTGA 1201

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RESULT 5
AAK52142
ID AAK52142 standard; cDNA; 1303 BP.
XX
AC AAK52142;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human polynucleotide SEQ ID NO 687.
XX
KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorder; arthritis; inflammation; SB.
XX
OS Homo sapiens.
XX
PN W0200157190-A2.
XX
PD 09-AUG-2001.
XX
PF 05-FEB-2001; 2001MO-US004098.
XX
PR 03-FEB-2000; 2000US-00496914.
XX
PR 27-APR-2000; 2000US-00560875.
XX
PR 20-JUN-2000; 2000US-00598075.

PR 19-JUL-2000; 2000US-00620325.
 PR 01-SEP-2000; 2000US-00654936.
 PR 15-SEP-2000; 2000US-00663561.
 PR 20-OCT-2000; 2000US-00693325.
 PR 30-NOV-2000; 2000US-00728422.

XX (HYSE-) HYSEO INC.

PI Tang YT, Liu C, Dirmnac RT, Aundi V, Zhou P, Xu C, Cao Y;
 PI Ma Y, Zhao QA, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
 PI Xue AJ, Yang Y, Wehrman T, Goodrich R;

XX MPI; 2001-476283/51.
 XX P-PSDB; AAM79009.

PT Nucleic acids encoding polypeptides with cytokine-like activities, useful
 in diagnosis and gene therapy.

XX Claim 1; Page: 2387-2388; 6221p; English.

XX The invention relates to polynucleotides (AAK51456-AAK51435) and the
 CC encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to
 CC cytokine, cell proliferation or cell differentiation or which may induce
 CC production of other cytokines in other cell populations. The
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,
 CC e.g. stem cell growth factor activity, haematopoiesis regulating
 CC activity, tissue growth factor activity, immunomodulatory activity and
 CC activity/inhibin activity and may be useful in the diagnosis and/or
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
 CC inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111
 CC (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the
 CC sequence listing were missing at the time of publication

XX SQ Sequence 1303 BP; 198 A; 426 C; 372 G; 307 T; 0 U; 0 Other;

Query Match 83.6%; Score 979; DB 4; Length 1303;
 Best Local Similarity 92.2%; Pred. No. 2e-222;
 Matches 1080; Conservative 0; Mismatches 0; Indels 91; Gaps 1;

QY 1 ATGAAGTCGCGCTTTCACCGCTGCGAAGACCACTCTGTGAAAAAGCACTCGGCG 60
 DB 166 ATGAAGTCGCGCTTTCACCGCTGCGAAGACCACTCTGTGAAAAAGCACTCGGCG 225
 QY 61 GTGATGGGGGGGGGCTCTTCAGACCGGCTCTCGGGCAACCTGTGGGCTGGGGCTG 120
 DB 226 GTGATGGGGGGGGGCTCTTCAGACCGGCTCTCGGGCAACCTGTGGGCTGGGGCTG 285
 QY 121 CTGGCGGCTCGGGGCTGGGGGTGTCTCGCGGCTGCACTGCGCCGCTCGGCTC 180
 DB 286 CTGGCGGCTCGGGGCTGGGGGTGTCTCGCGGCTGCACTGCGCCGCTCGGCTC 345
 QY 181 TTCTACATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 240
 DB 346 TTCTACATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 405
 QY 241 CCGGTGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 300
 DB 406 CCGGTGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 465
 QY 301 GACAACTCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 360
 DB 466 GACAACTCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 525
 QY 361 CTGCAACTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 420
 DB 526 CTGCAACTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 585
 QY 421 CGACGGGACATCACTCGGCTGTGGGCGCACTGGTGTGGGCGGCGGTGTGTGTGTGT 480
 DB 586 CGACGGGACATCACTCGGCTGTGGGCGCACTGGTGTGGGCGGCGGTGTGTGTGTGT 645
 QY 481 CTGGCTTTCTGGCGGCTACCTTTTCATGGGCTTGGGAAATTCTGACGTACTGCCCGGC 540

DB 646 CTGGCTTTCTGGCGGCTACCTTTTCATGGGCTTGGGAAATTCTGACGTACTGCCCGGC 705
 QY 541 ACCTGTGTGTGTATTCAGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 600
 DB 706 ACCTGTGTGTGTATTCAGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 765
 QY 601 GTGCTCTACTCCAGCTTCATGGGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 660
 DB 766 GTGCTCTACTCCAGCTTCATGGGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 825
 QY 661 GCCATGCGCACTCTATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 720
 DB 826 GCCATGCGCACTCTATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 885
 QY 721 AGGACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 780
 DB 886 AGGACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 945
 QY 781 CTGATCACTCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 840
 DB 946 CTGATCACTCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1005
 QY 841 GTTATTCATTTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 900
 DB 1006 GTTATTT----- 1011
 QY 901 AATCATTTTCAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 960
 DB 1012 -----TATCGGCTTACTATGACATT 1034
 QY 961 TAAGATGTCAAGAGAAAAAGAGAGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
 DB 1035 TAAGATGTCAAGAGAAAAAGAGAGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1094
 QY 1021 ATTTCTATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1080
 DB 1095 ATTTCTATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1154
 QY 1081 ATTTGGATATTTTTCACAGATTTTCAATTTTCAATTTTCAATTTTCAATTTTCAATTTT 1140
 DB 1155 ATTTGGATATTTTTCACAGATTTTCAATTTTCAATTTTCAATTTTCAATTTTCAATTTT 1214
 QY 1141 CAATTCACATTAACATGAATTCAGTGTGTGA 1171
 DB 1215 CAATTCACATTAACATGAATTCAGTGTGTGA 1245

RESULT 6
 AAT37402
 ID AAT37402 standard; DNA; 1488 BP.
 XX
 AC AAT37402;
 DT 11-MAR-1997 (first entry)
 XX
 DE Prostaglandin DP receptor coding sequence.
 XX
 KW Prostaglandin DP receptor; human; prostanoilid receptor; blood platelet;
 KW smooth muscle; nervous tissue; G protein-coupled receptor; modulator;
 KW mouse; prostaglandin-related disease; therapy; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 349..1429
 FT /tag= a
 FT /product= "prostaglandin DP receptor"
 XX
 PN W09623066-A2.
 XX
 PD 01-AUG-1996.
 XX

PF 23-JAN-1996; 96WO-CA000047.
 XX 26-JAN-1995; 95US-00378682.
 XX (MERI) MERCK FROST CANADA INC.
 PA Abramovitz M, Bole Y, Metters K, Sawyer N, Slietz DM;
 PI WPI; 1996-362690/36.
 DR P-PSDB; AAW03516.
 XX
 PT Human prostaglandin DP receptor and related DNA - used to identify
 PT receptor modulators to treat prostaglandin-related diseases.
 XX
 PS Claim 4; Page 41-42; 49pp; English.
 XX

CC This sequence represents the coding sequence for the human prostaglandin
 CC DP receptor. The DP receptor is the least ubiquitous and least abundant
 CC of the prostanoicid receptors. The DP receptors are thought to be
 CC distributed mainly in blood platelets, smooth muscle of various tissues,
 CC and nervous tissue (including the central nervous system). However, many
 CC of the actions and distribution of the DP receptor is species dependent.
 CC The encoded DP receptor is a G protein-coupled receptor which can
 CC specifically bind prostaglandin molecules. This sequence was isolated
 CC using primers (see AAT37403 and AAT37404) based on the N-terminal
 CC sequence, and an internal sequence from purified mouse DP. The human
 CC prostaglandin DP receptor can be used to identify modulators of the
 CC receptor. The identified modulators can then be used to treat
 CC prostaglandin-related diseases, and for modulating the effects of
 CC prostaglandins on the DP receptor
 XX

Sequence 1488 BP; 232 A; 482 C; 423 G; 351 T; 0 U; 0 Other;

Query Match 83.6%; Score 979; DB 2; Length 1488;
 Best Local Similarity 92.2%; Pred. No. 2,1e-222;
 Matches 1080; Conservative 0; Mismatches 0; Indels 91; Gaps 1;

QY 1 ATGAAGTCGCGCTTCTACCGCTGCAAGAACCACTCTGTGAAAAAGCACTCGGCG 60
 Db 350 ATGAAGTCGCGCTTCTACCGCTGCAAGAACCACTCTGTGAAAAAGCACTCGGCG 409
 QY 61 GTGATGAGGCGGAGTGTCTTACAGACCGGCTCTGTGGAACCTGTGCGCTGTG 120
 Db 410 GTGATGAGGCGGAGTGTCTTACAGACCGGCTCTGTGGAACCTGTGCGCTGTG 469
 QY 121 CTGGCGCGCTCGGCGCTGCGGCTGTGCTCGCGGCTGCACTGCGCGCTGCGCTG 180
 Db 470 CTGGCGCGCTCGGCGCTGCGGCTGTGCTCGCGGCTGCACTGCGCGCTGCGCTG 529
 QY 181 TTCTACATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 240
 Db 530 TTCTACATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 589
 QY 241 CCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 300
 Db 590 CCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 649
 QY 301 GACAATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 360
 Db 650 GACAATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 709
 QY 361 CTGCAACTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 420
 Db 710 CTGCAACTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 769
 QY 421 CGACGGACATCACTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 480
 Db 770 CGACGGACATCACTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 829
 QY 481 CTGGCTTTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 540
 Db 830 CTGGCTTTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 889

QY 541 ACCTGTGTCTTTATTCAGATGTCTCAAGAGAGGCTGCTGTGTGTGTGTGTGTGT 600
 Db 890 ACCTGTGTCTTTATTCAGATGTCTCAAGAGAGGCTGCTGTGTGTGTGTGTGTGT 949
 QY 601 GTGTCTTACTTCCAGCTCATGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 660
 Db 950 GTGTCTTACTTCCAGCTCATGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1009
 QY 661 GCCATGGGCAACCTTATGTGATGCAACGGCGGCTGAGCGGACCGGCTCTGACG 720
 Db 1010 GCCATGGGCAACCTTATGTGATGCAACGGCGGCTGAGCGGACCGGCTCTGACG 1069
 QY 721 AGGAGCTGTGCGAGCGCGCGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 780
 Db 1070 AGGAGCTGTGCGAGCGCGCGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1129
 QY 781 CTGGATCAGCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 840
 Db 1130 CTGGATCAGCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1189
 QY 841 GTTATTGCAATTTGTCTGTGAGTCCCGGCAAGACCTGTGAGTGTGAGGCTTGAG 900
 Db 1190 GTTATT-----
 QY 901 AATCATTTTCAAGTGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 960
 Db 1196 -----TATCGGCTTACTATGAGCATTT 1218
 QY 961 TAAAGATGTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
 Db 1219 TAAAGATGTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1278
 QY 1021 ATTCTATCTGTGATTTCAATTTGTGAGACCTGTGAGATTTTATTTATTTATTT 1080-
 Db 1279 ATTCTATCTGTGATTTCAATTTGTGAGACCTGTGAGATTTTATTTATTTATTT 1338
 QY 1081 ATTCTATCTGTGATTTTCAAGATTTTCAAGATTTTCAAGATTTTCAAGATTTT 1140
 Db 1339 ATTCTATCTGTGATTTTCAAGATTTTCAAGATTTTCAAGATTTTCAAGATTTT 1398
 QY 1141 CAATTCACATTAACAGAAATTCAGTCTGTGA 1171
 Db 1399 CAATTCACATTAACAGAAATTCAGTCTGTGA 1429

RESULT 7
 ADO30026
 ID ADO30026 standard; cDNA; 1077 BP.
 XX
 AC ADO30026;
 XX
 DT 29-JUL-2004 (first entry)
 XX
 XX Human GPCR PTGDR polynucleotide, SEQ ID NO:1128.
 XX
 KW G protein-coupled receptor; GPCR; drug screening; diagnosis;
 KW transgenic mouse; neurological disorder; adrenal gland disorder;
 KW colon disorder; intestinal disorder; cardiovascular disorder;
 KW muscular disorder; blood disorder; immune disorder; bone disorder;
 KW joint disorder; metabolic disorder; nutritive disorder; cancer;
 KW kidney disorder; liver disorder; lung disorder; breast disorder;
 KW ovary disorder; uterus disorder; prostate disorder; testis disorder;
 KW skin disorder; stomach disorder; pancreas disorder; spleen disorder;
 KW thymus disorder; thyroid disorder; antiparkinsonian; antianemic;
 KW cytostatic; antiinflammatory; vasotropic; antidiarrhoeic; antidiabetic;
 KW CNS; central nervous system; respiratory; antidiarrhoeic; antidiabetic;
 KW virocid; hepatotropic; antibacterial; antianemic; antidiarrhoeic;
 KW dermatological; antihyper; antihyper; antiallergic; anorectic;
 KW immunosuppressive; nephrotoxic; gene therapy; GPCR modulator; human;
 KW gene; ss.
 XX
 XX Homo sapiens.
 XX

MN MO200404000-A2.
 XX
 FD 13-MAY-2004.
 XX
 PF 09-SEP-2003; 2003WO-USO28226.
 PR 09-SEP-2002; 2002US-0409303P.
 PR 09-APR-2003; 2003US-0461329P.
 XX
 PA (PRIM-) PRIMAL INC.
 PI Gallanaris GA, Bergmann JE, Gragerov A, Hohmann J, Li F;
 PI Madisen L, McIlwain KU, Pavlova MN, Vassellatis D, Zeng H;
 DR WPI; 2004-390329/36.
 DR P-PSDB; ADO29614.
 XX
 PT Novel mammalian G protein coupled receptors, useful for identifying
 PT compounds that modulates diagnosing and treating disease condition
 PT associated with GPCR dysfunction e.g. autoimmune diseases, angina
 PT pectoris, Parkinson's disease.
 PS
 PS Claim 151: SEQ ID NO 1128; 542pp; English.
 XX
 CC The invention relates to human and mouse G protein-coupled receptors
 CC (GPCRs) and nucleic acids encoding them. The invention also relates to
 CC sequences at least 90% identical to the GPCR proteins and nucleic acids
 CC of the invention; methods of treating, preventing or diagnosing diseases
 CC associated with GPCRs of the invention; methods of screening for
 CC compounds useful in the treatment of GPCR-related diseases; a transgenic
 CC mouse comprising a GPCR gene of the invention; a mouse comprising a
 CC mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived
 CC from the transgenic mice; kits comprising several mice, each of which has
 CC a mutation in a different GPCR gene of the invention; and kits comprising
 CC probes which hybridise to GPCR polynucleotides of the invention. The
 CC invention further discloses variants of the GPCR polypeptides and vectors
 CC comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may
 CC be used in the diagnosis, treatment or prevention of a wide variety of
 CC diseases including neurological disorders (e.g., Alzheimer's disease,
 CC depression, diabetic neuropathy, Parkinson's disease or schizophrenia);
 CC disorders of the adrenal gland; disorders of the colon or intestine
 CC (e.g., Crohn's disease, diarrhoea, food poisoning or irritable bowel
 CC syndrome); cardiovascular disorders (e.g., angina, cardiac arrhythmia or
 CC myocardial infarction); muscular disorders; blood disorders (e.g.,
 CC anaemia or leukaemia); immune disorders (e.g., autoimmune disorders or
 CC AIDS); bone and joint disorders (e.g., osteoarthritis, rheumatoid
 CC arthritis, gout or osteoporosis); metabolic or nutritive disorders (e.g.,
 CC obesity, enzyme deficiency-related diseases or vitamin deficiency-related
 CC diseases); and disorders of the kidney, liver, lung, breast, ovary,
 CC uterus, prostate, testis, skin, stomach, pancreas, spleen, thymus and
 CC thyroid (e.g., cancers). The present sequence represents a GPCR-encoding
 CC nucleic acid form of the invention. Note: The full sequence data for this
 CC patent did not form part of the printed specification; those sequences
 CC not shown were obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 1077 BP, 169 A; 336 C; 310 G; 262 T; 0 U; 0 Other;
 Query Match 83.3%; Score 976; DB 122; Length 1077;
 Best Local Similarity 92.2%; Pred. No. 8-e-222;
 Matches 1077; Conservative 0; Mismatches 0; Indels 91; Gaps 11

[illegible]

XX AAA27056;
 AC 22-AUG-2000 (first entry)
 DT
 XX
 DE Human cell surface receptor protein cDNA sequence #13.
 KM Human; HCSR; cytosolic; antiarthritic; antineumatic; antiaesthetic;
 KM immunosuppressive; antiarteriosclerotic; antibacterial; antiparasitic;
 KM neuroprotective; nootropic; anticonvulsant; cancer; leukaemia; melanoma;
 KM rheumatoid arthritis; asthma; atherosclerosis; akathisia;
 KM Alzheimer's diseases; multiple sclerosis; epilepsy; ss.
 XX
 OS Homo sapiens.
 PH Key Location/Qualifiers
 FT CDS 130..1239
 FT /*tag= a
 FT /product= "HCSR-13"
 XX
 PN MO200028032-A2.
 XX 18-MAY-2000.
 XX
 PF 12-NOV-1999; 99MO-05026742.
 XX
 PR 12-NOV-1998; 98US-00191280.
 PR 07-DEC-1998; 98US-00206647.
 PR 08-MAR-1999; 99US-0123404P.
 XX
 XX (INCY-) INCYTE PHARM INC.
 XX
 PI Tang YT, Corley NC, Guegler KJ, Yue H, Baughn MR, Lal P;
 PI Hillman JL, Bandman O, Azimzai Y, Au-Young J;
 DR P-PSDB; AAY94346.
 XX
 PT New human cell surface receptor protein and polynucleotide useful for
 PT diagnosis, prevention and treatment of cancer, immune disorders,
 PT infection and neuronal disorders.
 XX
 PS Claim 9; Page 97; 97pp; English.
 XX
 CC The present sequence encodes a novel human cell surface receptor protein
 CC (HCSR) designated HCSR-13. The nucleotide sequence was identified in
 CC Incyte Clone 3576503 from the cDNA library BRONN0701, which was made from
 CC RNA isolated from bronchial tissue. A number of Incyte Clones were used
 CC to assemble the consensus sequence. BLAST analysis showed that the
 CC sequence is homologous to DR, prostanoic receptor 9940379. HCSR and its
 CC antagonist are useful for preventing or treating disorders associated
 CC with decreased or increased expression or activity of HCSR. Such
 CC disorders include cancers such as leukaemia and melanoma, immune
 CC disorders such as rheumatoid arthritis, asthma and atherosclerosis,
 CC bacterial and parasitic infections and neuronal disorders such as
 CC akathisia, Alzheimer's disease, multiple sclerosis and epilepsy.
 CC Polynucleotides encoding HCSR may be used as hybridisation probes to
 CC diagnose these conditions. Anti-HCSR antibodies may be used as
 CC antagonists, as a targeting or delivery mechanism for bringing
 CC pharmaceutical agents into contact with cells or tissues expressing HCSR
 CC and for diagnosis of HCSR-related disorders. HCSR and its catalytic or
 CC immunogenic fragments are useful for drug screening using libraries of
 CC compounds
 XX
 SQ Sequence 1264 BP; 189 A; 404 C; 368 G; 303 T; 0 U; 0 Other;
 Query Match 81.2%; Score 950.6; DB 3; Length 1264;
 Best Local Similarity 91.7%; Pred. No. 1,1e-215;
 Matches 1076; Conservative 0; Mismatches 4; Indels 93; Gaps 3;
 QY 1 ATGAAGTCGCGGTTCTTACCGCTGCAGAACACCACTCTGTGAAAAAGGCAACTCGGCG 60
 DB 130 ATGAAGTCGCGGTTCTTACCGCTGCAGAACACCACTCTGTGAAAAAGGCAACTCGGCG 189

QY 61 GTGATGCGCGGGGTGCTCTTACAGCACCGGCTCTGCGCAACCTGTGCGCTTGGGCTG 120
 DB 190 GTGATGCGCGGGGTGCTCTTACAGCACCGGCTCTGCGCAACCTGTGCGCGCTG 249
 QY 121 CTGGCGGCTCGGGGCTGGGGTGTGTCTCGCGCGTTCACCTGCGCCCTGCTCGGTC 180
 DB 250 CTGGCGGCTCGGGGCTGGGGTGTGTCTCGCGCGTTCACCTGCGCCCTGCTCGGTC 309
 QY 181 TTCTACATGCTGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 240
 DB 310 TTCTACATGCTGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 369
 QY 241 CCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
 DB 370 CCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 429
 QY 301 GACAACTCGTTGTGCAAGGCTTGCCTTCTTATGTCTTCTTGTGGGCTTCTCTGACA 360
 DB 430 GACAACTCGTTGTGCAAGGCTTGCCTTCTTATGTCTTCTTGTGGGCTTCTCTGACA 489
 QY 361 CTGCAACTCTGCGCAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGA 420
 DB 490 CTGCAACTCTGCGCAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGA 549
 QY 421 CGACGGCAATCACCCCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCT 480
 DB 550 CGACGGCAATCACCCCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCT 609
 QY 481 CTGGCTTTCTGCGCGCTACCTTTCATGAGGCTTGGGAAAGTTGCTGCAAGTACTGCCGCG 540
 DB 610 CTGGCTTTCTGCGCGCTACCTTTCATGAGGCTTGGGAAAGTTGCTGCAAGTACTGCCGCG 669
 QY 541 ACCTGCTGCTTATCCAGATGCTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600
 DB 670 ACCTGCTGCTTATCCAGATGCTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 729
 QY 601 GTGCTCACTCCAGGCTCATGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
 DB 730 GTGCTCACTCCAGGCTCATGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 789
 QY 790 GCCATGCGCAACTCTATGAGATGCAACCGCGGCTGCAAGGCAACCGCGGCTCTGCAAC 849
 DB 721 AGGACCTGTCGCAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 780
 QY 850 AGGACCTGTCGCAAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 909
 DB 781 CTGATCACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840
 QY 910 CTGATCACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 969
 DB 841 GTATTGCAATTTGTTCTGAGATCCCGCGCAAGACCTGGAGTAGTGGAGCTTGAGG 900
 QY 970 GTATT----- 975
 DB 901 AAACATTTTACGTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 960
 QY 976 -----TATCGGCTTACTATGAGCATTT 998
 DB 961 TAGGATGTCAGGAGAAAAACAGACCTCTGAAAGAGAGA-AGACCTCGAGCGCTTGC 1019
 QY 999 TAGGATGTCAGGAGAAAAACAGACCTCTGAAAGAGAGAGAGAGAGAGAGAGAGAGAG 1058
 DB 1020 GATTTCATCTGATGATTTCAATTTGAGACCTTGTGATTTTATCATTTTCAATTTCTCAG 1079
 QY 1059 GATTTCATCTGATGATTTCAATTTGAGACCTTGTGATTTTATCATTTTCAATTTCTCAG 1118
 DB 1080 TATTTCGATTTTTCACAGA-TTTTCATTTAGACTTCTTATGATGATGAGAGAGAGAG 1138
 QY 1119 TATTTCGATTTTTCACAGA-TTTTCATTTAGACTTCTTATGATGATGAGAGAGAGAGAG 1178

Qy 1139 AGCAATTCACCTACATGGAATCCAGTCGTGA 1171
| | | | | | | | | | | | | | | | | | | | | |
Db 1179 AGCAATTCACCTACATGGAATCCAGTCGTGA 1211

RESULT 9
AAA35113

ID	AAA35113	standard; DNA; 14607 BP.
1	1	1

AC AAA35113;

DT 28-JUL-2000 (first entry)

DE Human adenosine receptor related polynucleotide SEQ ID NO:2802.

KM Human; adenosine receptor; low adenosine antisense oligonucleotide; KM phosphorothioate; impaired respiration; inflammation; allergy; KM allergic disease; bronchoconstriction; inhibitor; antiinflammatory; KM antiallergic; antiasthmatic; cytoskeletal; analgesic; impaired airway; KM lung disease; ischaemic condition; pulmonary vasoconstriction; asthma; KM respiratory distress syndrome; pain; cystic fibrosis; emphysema; KM pulmonary hypertension; chronic obstructive pulmonary disease; COPD; KM cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.

Homo sapiens

PN W0200009525-A2.

PD 24-FEB-2000.

PF 03-AUG-1999; 99WO-US017712.

PR 03-AUG-1998; .98US-0095212P.
XX

PA (UYEC-) UNIV EAST CAROLINA.

PI NYCE JW;
VY

DR WPI; 2000-205971/18.

PT New ansense oligonucleotides useful for treating e.g. pulmonary
PT vasoconstriction, inflammation, allergies, asthma, hypertension,
PT bronchitis, emphysema, respiratory distress syndrome, ischemia or
PT cancers.

PS Disclosure; Page 1064-1068; 1343pp; English.

The present invention describes a new composition comprising an antisense oligonucleotide (ON) with low adenosine (up to 15%), which targets nucleic acids involved in bronchoconstriction, allergies, and/or inflammation. The ON can have anti-inflammatory, antiallergic, antiaesthetic, cytosstatic and analgesic activities. The compositions are useful for the treatment of diseases associated with inflammation, impaired airways, including lung disease and diseases whose secondary effects afflict the lungs of a subject. They can be used for treating e.g. ischemic conditions, pulmonary vasospasm, allergies, asthma, impaired respiration, respiratory distress syndrome, pain, cystic fibrosis, pulmonary hypertension, emphysema, chronic obstructive pulmonary disease (COPD), and cancers such as leukemias, lymphomas, carcinomas, and cancers which may metastasize to the lungs, including breast and prostate cancer. The reduction of the adenosine content of the ONs reduces side effects. The A-containing ONs break down with the release of deoxyadenosine which activates adenosine receptors causing bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the nucleotide sequences given in the sequence listing from the present invention, which correspond to SEQ ID NO:1 to 215, and then the last 185 sequences are also called SEQ ID NO:1 to 185, but the sequences differ from the previously named sequences. SEQ ID NO:11 to 1680 (AAA32323 to AAA33992) are specifically claimed ONs from the present invention. N.B. Sequences given in the disclosure of the present invention do not match up with their corresponding SEQ ID NO: sequences given in the sequence listing

Sequence	14607	BP;	3015	A;	4159	C;	3879	G;	3554	T;	0	U;	0	Other;
Query Match	72.5%	Score	848.4;	DB	3;	Length	14607;							
Best Local Similarity	94.4%	Pred. No.	5.1e-191;											
Matches	891;	Conservative	0;	Mismatches	51;	Indels	2;	Gaps	1;					

OY	1	ATGAAGTCGCGGCTTCTACGCTGCGAGAAACACACTCTGTGGAAAAAGGCAACTCGGCG	60
Db	845	ATGAAGTCGCGGCTTCTACGCTGCGAGAAACACACTCTGTGGAAAAAGGCAACTCGGCG	904
OY	61	GTATGATGGGCGGGGTGCTCTTACGACACGGGCTCTTGGGCAACTGTGTCGGCTTGGGCTG	120
Db	905	GTATGATGGGCGGGGTGCTCTTACGACACGGGCTCTTGGGCAACTGTGTCGGCTTGGGCTG	964
OY	121	CTGGGCGGCTCGGGGGCTGGGGGTGGTGTCTGGGGGGTCCACTGGCGCCGCTGCGCTCG	180
Db	965	CTGGGCGGCTCGGGGGCTGGGGGTGGTGTCTGGGGGGTCCACTGGCGCCGCTGCGCTCG	1022
OY	181	TTCTACATGTGCTGTGTGTGCTGACGGTCAACCGACTGTGCTGGGCAAGTGCTCTTAGC	240
Db	1025	TTCTACATGTGCTGTGTGTGCTGACGGTCAACCGACTGTGCTGGGCAAGTGCTCTTAGC	108
OY	241	CCGGTGTGTGCTGCTGCTTACGCTCAAGACCGAAGTCTGGGGTCTTGGCCCGCATTTG	300
Db	1085	CCGGTGTGTGCTGCTGCTTACGCTCAAGACCGAAGTCTGGGGTCTTGGCCCGCATTTG	1144
OY	301	GACAACTCTGTGTGTGCAAGCCTTGTGCTTTCATGTCTCTTGTGGCTCTCCCTGACA	360
Db	1145	GACAACTCTGTGTGTGCAAGCCTTGTGCTTTCATGTCTCTTGTGGCTCTCCCTGACA	1204
OY	361	CTGCAACTCTGGGCGATAGGCACTGGAAGTGGCTCTCCCTAGGGCAACCTTTCTTAC	420
Db	1205	CTGCAACTCTGGGCGATAGGCACTGGAAGTGGCTCTCCCTAGGGCAACCTTTCTTAC	1264
OY	421	CGACGGACATCACCTGTGCGCTGAGGCGCACTGTGTGCGCCCGGTGTGAGCGCTTCTC	480
Db	1265	CGACGGACATCACCTGTGCGCGCTGAGGCGCACTGTGTGCGCCCGGTGTGAGCGCTTCTC	1324
OY	481	CTGGCTTTCTGCGGGCTAACCTTTATGTGGCTTCCGGAAATTCTGTGTCACTATCGCCCGG	540
Db	1325	CTGGCTTTCTGCGGGCTAACCTTTATGTGGCTTCCGGAAATTCTGTGTCACTATCGCCCGG	1384
OY	541	ACCGGTGTCTTATTCAGATGTGTCAAGAGAGGCTGCTGTGGTGTCTGAGGATCTCT	600
Db	1385	ACCGGTGTCTTATTCAGATGTGTCAAGAGAGGCTGCTGTGGTGTCTGAGGATCTCT	1444
OY	601	GTGCTCTACTCCAGCCTTATGGCGCTGTGTCTTGTGCAACGCTGTGTGCAACTCTGGG	660
Db	1445	GTGCTCTACTCCAGCCTTATGGCGCTGTGTCTTGTGCAACGCTGTGTGCAACTCTGGG	1504
OY	661	GCCATGTGGCAACTCTTATGTGATGACACCGGTGTCAGCGGGCACCCGCTCTGTGACC	720
Db	1505	GCCATGTGGCAACTCTTATGTGATGACACCGGTGTCAGCGGGCACCCGCTCTGTGACC	1564
OY	721	AGGGACTGTGCGGAGCGCGCGGCGAGAGGGAAAGGTGCTCCCTCAGCCCTGTGGAGAG	780
Db	1565	AGGGACTGTGCGGAGCGCGCGGCGAGAGGGAAAGGTGCTCCCTCAGCCCTGTGGAGAG	1624
OY	781	CTGATATCACTCTGCTGTGAGCGCTGTATGACGAGTCTTCACTATGTGTCTTCTGCC	840
Db	1625	CTGATATCACTCTGCTGTGAGCGCTGTATGACGAGTCTTCACTATGTGTGTCTTCTGCC	1688
OY	841	GTAATGTGATTTGTTCTGTGAGTCCCGGCCAAGACACTGGAGTGTGAGGCTTTAGG	900
Db	1685	GTAATGTG--TGAGTCCCGGGGCCCGAGAGGGGCGCGCGTCCGCGCGTGTGCGGAGG	1742
OY	901	AAACATTTTAAGTGTGTCTCTCTCTTCTTCTCCAAAGTATGGG	944
Db	1743	GGGGCTGTGATTTGTGGTCCCTCCCTTTTCTGTAGTGTG	1786

RESULT 10

AAAF21235

ID AAF21235 standard; DNA; 14607 BP.
XX AAF21235;
AC
XX
XX
DT 14-MAR-2001 (first entry)
DE Human low adenosine antisense oligonucleotide related sequence #2802.
XX
XX Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
KM human; airway disorder; bronchoconstriction; lung inflammation;
KM surfactant depletion; respiratory; bronchodilator; antiinflammatory;
KM immunosuppressive; antiaesthetic; analgesic; hypotensive; cytostatic;
KM surfactant obstruction; pulmonary obstruction; impeded respiration;
KM respiratory hypoproduction; pulmonary vasoconstriction; asthma; RDS;
KM respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
KM pulmonary hypertension; emphysema; pain; pulmonary transplantation rejection;
KM chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
KM cancer; ss.
XX
XX Homo sapiens.
OS
XX MO200062736-A2.
XX
XX 26-OCT-2000.
XX
XX 24-MAR-2000; 2000MO-US008020.
XX
XX 06-APR-1999; 99US-0127958P.
XX
XX (UYEC-) UNIV EAST CAROLINA.
XX (NYCE/) NYCE J W.
XX
XX Nyce JW;
XX
XX WPI; 2000-679539/66.
XX
XX Low adenosine (A) content antisense oligonucleotides which do not trigger
PT adenosine receptors during metabolism, useful e.g. for treating cancers
PT and respiratory obstructions.
XX
XX
XX Disclosure; Page 1144-1147; 1592P; English.
XX
XX The present invention describes low adenosine (A) content antisense
CC oligonucleotides and compositions (I) comprising them. In the antisense
CC oligonucleotides the A is replaced by a 'Universal' or alternative base.
CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
CC immunosuppressive, antiaesthetic, hypotensive and cytostatic activities.
CC The antisense oligonucleotides and (I) can be used to down-regulate the
CC expression and/or activity of target polypeptides associated with
CC lung/respiratory disorders and malignancies, such as stimulating and
CC activating peptide factors and transmitters, transcription factors and
CC immunoglobulin and antibodies, antibody receptors, cytokines and
CC chemokines, endogenously produced specific and non-specific enzymes,
CC binding proteins, adhesion molecules and their receptors, cytokine and
CC chemokine receptors, adenosine receptors, bradykinin receptors, central
CC nervous system (CNS) and peripheral nervous and non-nervous system
CC receptors, CNS and peripheral nervous and non-nervous system peptide
CC transmitters, defensins, growth factors, vasoactive peptides and
CC receptors, binding proteins and malignancy associated proteins. The
CC antisense oligonucleotides may be used in this way to treat disorders
CC including respiratory obstruction (especially pulmonary obstruction
CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or
CC surfactant hypoproduction which are associated with a disease or
CC condition selected from pulmonary vasoconstriction, inflammation,
CC allergies, asthma, impeded respiration, respiratory distress syndrome
CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
CC and/or cancer. AAF21543 to AAF21543 represent human polynucleotide
CC fragments and antisense oligonucleotides used in the exemplification of
CC the present invention
XX
XX Sequence 14607 BP; 3015 A; 4159 C; 3879 G; 3554 T; 0 U; 0 Other;
SQ

Query Match 72.5%; Score 848.4; DB 3; Length 14607;
Best Local Similarity 94.4%; Pred. No. 5.1e-191;
Matches 891; Conservative 0; Mismatches 51; Indels 2; Gaps 1;
QY 1 ATGAGTGGCCGCTTCTACCGCTGCGAAGAACACCACTCTGTGGAAAAAGCACTGGCG 60
Db ATGAGTGGCCGCTTCTACCGCTGCGAAGAACACCACTCTGTGGAAAAAGCACTGGCG 904
QY 61 GTGATGGGGGGGTGCTCTTACAGACCGGCTCTTGGGCAACTGCTGGGCTTGGGGCTG 120
Db GTGATGGGGGGGTGCTCTTACAGACCGGCTCTTGGGCAACTGCTGGGCTTGGGGCTG 964
QY 121 CTGGCGCGCTGGGGGGGTGGGTGGGTGGGTGGGTGGGTGGGTGGGTGGGTGGGTGGGT 180
Db CTGGCGCGCTGGGGGGGTGGGTGGGTGGGTGGGTGGGTGGGTGGGTGGGTGGGTGGGT 1024
QY 181 TTCTACATGCTGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 240
Db TTCTACATGCTGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1084
QY 241 CCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 300
Db CCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1144
QY 301 GACAACTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 360
Db GACAACTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1204
QY 361 CTGCAACTCTGGGCACTGAGCACTGAGCACTGAGCACTGAGCACTGAGCACTGAGCACT 420
Db CTGCAACTCTGGGCACTGAGCACTGAGCACTGAGCACTGAGCACTGAGCACTGAGCACT 1264
QY 421 CGACGGCAATCACTCTGGGCTGGGCGCACTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 480
Db CGACGGCAATCACTCTGGGCTGGGCGCACTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1324
QY 481 CTGGCTTTCTGGGCGCTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTT 540
Db CTGGCTTTCTGGGCGCTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTT 1384
QY 541 ACCTGTGCTTTATCCAGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 600
Db ACCTGTGCTTTATCCAGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1444
QY 601 GTGCTTACTCAAGCTTCAAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 660
Db GTGCTTACTCAAGCTTCAAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1504
QY 661 GCGATGGCAACTCTATGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 720
Db GCGATGGCAACTCTATGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1564
QY 721 AGGCACTGTGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 780
Db AGGCACTGTGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1624
QY 781 CTGATCACTCTCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 840
Db CTGATCACTCTCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1684
QY 841 GTAATTTGATTTGTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 900
Db GTAATTTGATTTGTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1742
QY 901 AAACATTTTCACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 944
Db AAACATTTTCACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1786
RESULT 11
AB296929
ID AB296929 standard; DNA; 14607 BP.

AB296929;
17-OCT-2003 (first entry)
Human nucleic acid sequence.
Human: antisense; lung dysfunction; nasal airway dysfunction; antiinflammatory; steroid; ubiquinone; antiinflammatory; antiallergic; antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy; adenosine gene therapy; respiratory; lung; adenosine sensitivity; adenosine receptor; bronchodilation; bronchoconstriction; lung allergy; lung inflammation; respiratory disease; ds.
Homo sapiens.
WO200285308-A2.
31-OCT-2002.
23-APR-2002; 2002MO-US03135.
24-APR-2001; 2001US-0286137P.
(EPIG-) EPIGENESIS PHARM INC.
Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D, Miller S, Tang L, Shanabuddin S;
WPI; 2003-229219/22.
Pharmaceutical composition for treating ailments associated with impaired respiration, has oligo(s) antisense to specific gene(s) or its corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or ubiquinone.
Disclosure; SEQ ID NO 12171; 872pp; English.
The invention relates to a novel oligonucleotide composition, which has a first active agent comprising an oligonucleotide antisense to the initiation codon, coding region, 5' or 3' end genomic flanking regions, 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of junctions of genes encoding a polypeptide associated with lung and/or nasal airway dysfunction and a second active agent comprising an antiinflammatory steroid and ubiquinone. A composition of the invention has antiinflammatory, antiallergic, antiasthmatic, hypotensive, immunosuppressive, and cytostatic activity. The composition may have a use in antisense gene therapy. The composition is useful for treating or preventing a respiratory, lung or malignant disease or condition, also for enhancing the prophylactic or therapeutic respiratory effect of an antiinflammatory steroid in a subject, for reducing or depleting levels of, or reducing sensitivity to adenosine, reducing levels of adenosine receptor, producing bronchodilation, increasing levels of ubiquinone or lung surfactant in a subject's tissue, or treating bronchoconstriction, lung inflammation, lung allergies, or a respiratory disease or condition.
Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
Sequence 14607 BP; 3015 A; 4159 C; 3879 G; 3554 T; 0 U; 0 Other;

Query Match	72.5%	Score	848.4	DB 10	Length	14607	
Best Local Similarity	94.4%	Pred. No.	5.1e-191				
Matches 891; Conservative	0	Mismatches	51	Indels	2	Gaps	1

QY	1	ATGAAGTCGCGCTTACCGCTGCAGAAACACACTCTGTGTGAAAAAGGCAACTCGGCG	60
Db	845	ATGAAGTCGCGCTTACCGCTGCAGAAACACACTCTGTGTGAAAAAGGCAACTCGGCG	904
QY	61	GTGATGGCGGGGAGTCTCTTACGACACCGGCTCTCGGGCAACCTGCTGGCTCTGGGGCTTG	120
Db	905	GTGATGGCGGGGAGTCTCTTACGACACCGGCTCTCGGGCAACCTGCTGGCTCTGGGGCTTG	964

QY	121	CTGGCGGCGCTGGGGGCTGGGCTGGCTCGGGGGTCCATCGCCCGCTCGGCT	180
Db	965	CTGGCGGCGCTGGGGGCTGGGGTGGTGGCGGGGTCCACTGGCCCGCTCGGCT	1024
OY	181	TTTCAATGCTGGTGTGGGCTTGAACGGTCAACCACTTGGCTGGGCAAGTGGCTCTTAAG	240
Db	1025	TTTCAATGCTGGTGTGGGCTTGAACGGTCAACCACTTGGCTGGGCAAGTGGCTCTTAAG	1084
OY	241	CCGGTGGGCTGGGCGCTACGCTCAGAACCGAAGTCTGGGGGTGCTTGGCCCGCATGG	300
Db	1085	CCGGTGGGCTGGGCGCTACGCTCAGAACCGAAGTCTGGGGGTGCTTGGCCCGCATGG	1144
OY	301	GACAACTGGTGTGGCAAGCCTTGGCTTCTCAATGCTCTTGGGCTCTCTGACA	360
Db	1145	GACAACTGGTGTGGCAAGCCTTGGCTTCTCAATGCTCTTGGGCTCTCTCGACA	1204
OY	361	CTGCATCTCTGGGCAATGGCACTGGAGTGTGGCTCTCCCTAAGGCAACCTTTCTTCAAC	420
Db	1205	CTGCATCTCTGGGCAATGGCACTGGAGTGTGGCTCTCCCTAAGGCAACCTTTCTTCAAC	1264
OY	421	CGACGGGCATCACCCCTGGCGCTCTGGGGCACTTGGTGGGCCGGGTGGAGCGCCTTCTCC	480
Db	1265	CGACGGGCATCACCCCTGGCGCTCTGGGGCACTTGGTGGGCCCGGGTGGAGCGCCTTCTCC	1324
OY	481	CTGGCTTTCGGCGGCTACCTTTCAATGGGCTTCGGGAAGTTCTGCAATACCTGCCCCGGC	540
Db	1325	CTGGCTTTCGGCGGCTACCTTTCAATGGGCTTCGGGAAGTTCTGCAATACCTGCCCCGGC	1384
OY	541	ACCTGGTCTTTCATTCAGATGGTCCACGAGAGGGCTCTGGTGTGGTCTGGGGTACTCT	600
Db	1385	ACCTGGTCTTTCATTCAGATGGTCCACGAGAGGGCTCTGGTGTGGTCTGGGGTACTCT	1444
OY	601	GTGCTCTACTCCAGCGCTCATGGCGCTGTGGTCTCTGGCAACGTCGTGTGCAACTTCGGC	660
Db	1445	GTGCTCTACTCCAGCGCTCATGGCGCTGTGGTCTCTGGCAACGTCGTGTGCAACTTCGGC	1504
OY	661	GCCATGGCAACTCTATGCGATGCACTCGGCGGCTGACGCGGCAACCCGCGCTCTTGCACC	720
Db	1505	GCCATGGCAACTCTATGCGATGCACTCGGCGGCTGACGCGGCAACCCGCGCTCTTGCACC	1564
OY	721	AGGACGTGGCCGAGCGCGCGCGGAGCGGAGAGGAAGTCTCCCTCAAGCCCTTGAAGAG	780
Db	1565	AGGACGTGGCCGAGCGCGCGCGGAGCGGAGAGGAAGTCTCCCTCAAGCCCTTGAAGAG	1624
OY	781	CTGATCATCCTCCAGCTGGCTGGCGCTGATGACGCTGCTCTTCACTATGTGTTCTCTGCC	840
Db	1625	CTGATCATCCTCCAGCTGGCTGGCGCTGATGACGCTGCTCTTCACTATGTGTTCTCTGCC	1684
OY	841	GTAATTCATTGTTCTTGGAGTCCCGGCCCAAGACACTGGGAAGTAGTGAAGCTTGAAG	900
Db	1685	GTAATTCG--TGAGTCCCGCGGCCCGGAGGGGGCGCGCTCGGCGCGCTGGGTGGGAAG	1742
OY	901	AAACATTTTCAGTGTGCTGCTCTCTCTTTCCTCCAAAGTATGGG	944
Db	1743	GGGGCTCTGATTTGGTCCCTCTCCCTTTTCTCTCTAGTCTCG	1786

RESULT 12
ABD20778
ID ABD20778 standard; DNA; 14607 BP.

AC	ABD20778;
XX	
DT	29-JUL-2004 (first entry)

DE Human pulmonary and inflammatory target DNA #389.
XX
KW Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;
KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;
KW surfactant depletion; anti-allergic; anti-inflammatory; antiasthmatic;
KW analgesic; hypotensive; immunosuppressive; cystostatic; cystic fibrosis;
KW beta-adrenergic agonist; respiratory disease; pulmonary vasodilation;
KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension.

XX	emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
XX	pulmonary transplantation rejection; ds.
XX	
OS	Homo sapiens.
XX	
PN	WO200285309-A2.
XX	
PD	31-OCT-2002.
XX	
PF	23-APR-2002; 2002WO-US013143.
XX	
PR	24-APR-2001; 2001US-0286036P.
XX	
PA	(EPIG-) EPIGENESIS PHARM INC.
XX	
PI	Nyce JW, Li Y, Sandraesgra A, Katz E, Pabalan J, Aguilar D;
PI	Miller S, Tang L, Shahbuddin S;
DR	WPI; 2003-093058/08.
XX	
PT	Pharmaceutical composition for treating asthma, has antisense
PT	oligonucleotide containing less percentage of adenosine, targeted to
PT	nucleic acids associated with lung airway or lung dysfunction, and
PT	bronchodilating agent.
DS	Claim 15; SEQ ID NO 12171; 763pp; English.

This invention describes a novel composition (a) a first active agent, comprising oligonucleotides, effective for alleviating bronchoconstriction, respiratory tract inflammation, allergies and reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors, surfactant depletion or hyposecretion, when administered to a mammal. The oligonucleotides are derived from a gene encoding or regulating expression of a target polypeptide associated with lung airway or lung dysfunction or cancer and can be anti-sense to the corresponding mRNA. The invention also describes a kit, that comprises: (a) a delivery device, in separate containers, (b) the oligonucleotides, (c) instructions for adding a carrier and for use of the kit. The composition of the invention has antiallergic, antiinflammatory, antiasmatic, analgesic, hypotensive, immunosuppressive and cytostatic activity, is a beta-adrenergic agonist. The composition is useful for preventing or treating a respiratory, lung or malignant disease. The administered composition comprises oligo and is administered to reduce the production or availability, or to increase the degradation of the target mRNA or to reduce the amount of target polypeptide present in the lungs. The pulmonary obstruction, and/or bronchoconstriction and/or lung inflammation, allergies and/or surfactant hypoproduction are associated with a disease or condition such as pulmonary vasoconstriction, inflammation, allergies, asthma, impeded respiration, respiratory distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary transplantation rejection, pulmonary infections, bronchitis or cancer. The reduced adenosine content of the anti-sense oligos corresponding to thymidines present in the target RNA serves to prevent the breakdown of the oligonucleotides into products that free adenosine into the system e.g., lung, brain, heart, kidney, etc. tissue environment and thereby, to prevent any unwanted effects due to it.

SQ Sequence 14607 BP; 3015 A; 4159 C; 3879 G; 3554 T; 0 U; 0 Other;

Query Match	72.5%	Score 848.4	DB 11	Length 14607
Best Local Similarity	94.4%	Pred. No. 5.1e-191		
Matches 891; Conservative	0	Mismatches 51	Indels 2	Gaps 1

QY 1 ATGAAATGCGCGGTTCTACACCGCTGCAGAAACACACTGTGTGGAAAAAGCAACTCGGCG 60

Db 845 ATGAAATGCCCGCTTCTACCGCTGCCAGAACACCACTGTGTGAAAAAGCAACTCGGCG 904

QY 61 GTGATGGGCGGGGTGCTTTTCAGACACCGGCTCTGTGGCAACTGTGTGGCTGTGGGCTG 120

Db 905 GTGATGGGCGGGGTGCTTTTCAGACACCGGCTCTGTGGCAACTGTGTGGCTGTGGGCTG 964

QY 121 CTGGCGCGCTCGGGGCTGTGGGATGTGTCTGGCGGCTCCACTGTGCGCCGCTGCTCCGCTC 180

Db	965	CTGGCGGGCTTCGGGGCTGGGGTGTGCTTCGGGGGTCACTGGCCCGGTCCCTCGGT	10234
Qy	181	TTTCAACATGCTGTGTGTGTGGCTTGACGGTCAACGACTTGTGGGCAAGTGCCTCTAAGC	240
Db	1025	TTTCAACATGCTGTGTGTGTGGCTTGACGGTCAACGACTTGTGGGCAAGTGCCTCTAAGC	1084
Qy	241	CCGGTGTGTGCTGAGCTGAGTCCAGAACCCGAGTCTGCGGGTCTTGGCGCCGCATTG	300
Db	1085	CCGGTGTGTGCTGAGCTGAGTCCAGAACCCGAGTCTGCGGGTCTTGGCGCCGCATTG	1144
Qy	301	GACAACTGCTTGTGTGCAAGCCTTGCTTTCATGTCTCTTGGGCTCTCCTCGACA	360
Db	1145	GACAACTGCTTGTGTGCAAGCCTTGCTTTCATGTCTCTTGGGCTCTCCTCGACA	1204
Qy	361	CTGCAACTCTGTGGCATGAGCACTGGAATGCTGGCTCTCCTTAAGGCAACCTTTTCTTAC	420
Db	1205	CTGCAACTCTGTGGCATGAGCACTGGAATGCTGGCTCTCCTTAAGGCAACCTTTTCTTAC	1264
Qy	421	CGACGGCAACATCAACCTCGGCGCTGGGGGCACTGGTGGCCCCGGTGGAGAGGCTTTCAC	480
Db	1265	CGACGGCAACATCAACCTCGGCGCTGGGGGCACTGGTGGCCCCGGTGGAGAGGCTTTCAC	1324
Qy	481	CTGGCTTTTCGGCGGCTACCTTTTCAATGGAGCTCGGGAAGTTGCGACGATACGCGCCGAC	540
Db	1325	CTGGCTTTTCGGCGGCTACCTTTTCAATGGAGCTCGGGAAGTTGCGACGATACGCGCCGAC	1384

QY	541	ACCGGGGCTTTATCCAGATAGTGCACAGAGAGGGCTGGCTGGGCTGAGGGTAACTCT	600
Db	1385	ACCTGGCTTTATCCAGATAGTGCACAGAGAGGGCTGGCTGGGCTGAGGGTAACTCT	1444
QY	601	GTGCTTACTCCAGCCCTCATGGCGCTGCTGATCTCTGCCACCGTACTGTGCAACTTCGGC	660
Db	1445	GTGCTTACTCCAGCCCTCATGGCGCTGCTGATCTCTGCCACCGTACTGTGCAACTTCGGC	1504
QY	661	GCCATGGCGCAACTCTTATGCGATGCAACCGCGCTGCAGAGGGCAACCCGCGTCTCTGCACC	720
Db	1505	GCCATGGCGCAACTCTTATGCGATGCAACCGCGCTGCAGAGGGCAACCCGCGTCTCTGCACC	1564
QY	721	AGGAGCTGTGCCGAGCCGCGCGCGGAGCGGAGAGGGAACGTCCCTCAAGCCCTCTGAGAGAG	780
Db	1565	AGGAGCTGTGCCGAGCCGCGCGCGGAGCGGAGAGGGAACGTCCCTCAAGCCCTCTGAGAGAG	1624
QY	781	CTGGATCAACCTCCCTGCTGCTGTGGCGCTGATGACCGTGTCTTCACTATGTGTCTCTGCC	840
Db	1625	CTGGATCAACCTCCCTGCTGCTGTGGCGCTGATGACCGTGTCTTCACTATGTGTCTCTGCC	1684
QY	841	GTATTTGCAATTTGTTCTCTGAGTCCCGCCAGACACTTGGGAGTAGGTGAGCTTGAGG	900
Db	1685	GTATTTG--TGAGTCCCGCGGCCCCGAGGGGAGCGCGCTGGCGCGCTGGGTGGCGAGAG	1742
QY	901	AAACATTTTCAGTGCCTGCTCTCTCTTCTCCCAATATACGG	944
Db	1743	GAGGCTCTGGATTTGGTCCCTCCCTTTTCTCTGAGTCTCG	1786

RESULT 13
AAA35105
ID AAA35105 standard; DNA; 1216 BP

AC	AAA35105;
XX	
DT	28-JUL-2000 (first entry)

DE Human adenosine receptor related polynucleotide seq ID NO:2794.
XX

XX	cancer;leukemia; lymphoma; carcinoma; metastasis; ss.
OS	Homo sapiens.
PN	WO200009525-A2.
XX	
PD	24-FEB-2000.
PF	
PP	03-AUG-1999; 99WO-US017712.
PR	03-AUG-1998; 98US-0095212P.
PA	(UYEC-) UNIV EAST CAROLINA.
PI	Nyce JW;
DR	WPI; 2000-205971/18.
XX	
PT	New antisense oligonucleotides useful for treating e.g. pulmonary vaseoconstruction, inflammation, allergies, asthma, hypertension, bronchitis, emphysema, respiratory distress syndrome, ischemia or cancers.
XX	
PS	Disclosure; Page 1060; 1343p; English.
CC	The present invention describes a new composition comprising an antisense oligonucleotide (ON) with low adenosine (up to 15%), which targets nucleic acids involved in bronchoconstriction, allergies, and/or inflammation. The ON can have anti-inflammatory, antiallergic, antihistemic, cyostatic and analgesic activities. The compositions are useful for the treatment of diseases associated with inflammation, impaired airways, including lung disease and diseases whose secondary effects afflict the lungs of a subject. They can be used for treating e.g. ischemic conditions, pulmonary vasoconstriction, allergies, asthma, impeded respiration, respiratory distress syndrome, pain, cystic fibrosis, pulmonary hypertension, emphysema, chronic obstructive pulmonary disease (COPD), and cancers such as leukemias, lymphomas, carcinomas, and cancers which may metastasize to the lungs, including breast and prostate cancer. The reduction of the adenosine content of the ONs reduces side effects. The A-containing ONs break down with the release of deoxyadenosine which activates adenosine receptors causing bronchoconstriction and inflammation. AAA3213 to AAA5312 represent the nucleotide sequences given in the sequence listing from the present invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185 sequences are also called SEQ ID NO:1 to 185, but the sequences differ from the previously named sequences. SEQ ID NO:11 to 1680 (AAA3323 to AAA3392) are specifically claimed ONs from the present invention. N.B. Sequences given in the disclosure of the present invention do not match up with their corresponding SEQ ID NO: sequences given in the sequence listing
SO	Sequence 1216 BP; 153 A; 431 C; 371 G; 261 T; 0 U; 0 Other;
Query Match	72.3%; Score 847; DB 3; Length 1216;
Best Local Similarity	100.0%; Pred. No. 4.6e-191;
Matches 847; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
OY	1 ATGAAGTGGCGGTTCTACCGGTCCAGAAACACACCTCTGTGAAAAAAGCAACTGGGG 60
Dd	350 ATGANATGCCGTTTCACCGCTGCAGAACACCACTCTGTGTAAAAAAGCAACTGGGCG 409
OY	61 GTGATGGGCGGGGTGCTCTTCAGCACCGGCTCTCTGGGCAACTGCTGGCTCTGGGGCTG 120
Dd	410 GTGATGGGCGGGGTGCTCTTCAGCACCGGCTCTCTGGGCAACTGCTGGCTCTGGGGCTG 469
OY	121 CTGGGCGGCTCTGGGGCTGGGGGTGGTGCTTCGCGGCTCCACTGCGCCCGTGGCTTGGCTG 180
Dd	470 CTGGGCGGCTCTGGGGCTGGGGGTGGTGCTTCGCGGCTCCACTGCGCCCGTGGCTTGGCTG 529
OY	181 TTCTACATGCTGTGTGTGTGGCGCTGACCGGTCAACGACTTGTGGGCAAGGCTCTCTTAAGC 240
Dd	530 TTCTACATGCTGTGTGTGTGGCGCTGACCGGTCAACGACTTGTGGGCAAGGCTCTCTTAAGC 589

Qy	241	CCGATGGAGCGCGCTACGCTACAGAA	CCGAGAGTCTGCGGGGCTTGCGCCGATTG	300
Db	590	CCGATGGAGCTGCGCTGCTTACGCTCA	GAACCGGAGTCTGCGGGGCTTGCGCCGATTG	649
Qy	301	GACAACTGATGTGCGCAAGCCCTTG	CCCTTCTTCAATGTCCTTCTTGGGCTCTCTCGACA	360
Db	650	GACAACTGATGTGCGCAAGCCCTTG	CCCTTCTTCAATGTCCTTCTTGGGCTCTCTCGACA	709
Qy	361	CTGCAACTCCTGGCCATGAGCACTG	GAAGTCTGGCTTCTCCTTAGGGCACCTTCTTCTAC	420
Db	710	CTGCAACTCCTGGCCATGAGCACTG	GAAGTCTGGCTTCTCCTTAGGGCACCTTCTTCTAC	769
Qy	421	CGAGGGCAATCAACCTGCGCTGCGGG	GCATCTGATGGCCCGGATGGAGGCGCTTCTCC	480
Db	770	CGAGGGCAATCAACCTGCGCTGCGGG	GCATCTGATGGCCCGGATGGAGGCGCTTCTTCTCC	829
Qy	481	CTGGCTTTCTGCGCGCTACCTTTT	CGATGAGGCTTCTCGGAAAGTCTGACAGTACTGCCCCGGC	540
Db	830	CTGGCTTTCTGCGCGCTACCTTTT	CGATGAGGCTTCTCGGAAAGTCTGACAGTACTGCCCCGGC	889
Qy	541	ACCTGGTCTTTATTCAGATGCTCC	ACGAGAGGAGGCTTCGTGCTGGTGGTACTCT	600
Db	890	ACCTGGTCTTTATTCAGATGCTCC	ACGAGAGGAGGCTTCGTGCTGGTGGTACTCT	949
Qy	601	GTCGCTAATCTCCAACTCATTAG	CGCGCTGCTCTCTCCGACACCGGCTGTGAACCTCGGC	660
Db	950	GTCGCTAATCTCCAACTCATTAG	CGCGCTGCTCTCTCTCCGACACCGGCTGTGAACCTCGGC	1009
Qy	661	GCCATGCGCAACCTCTATGCGAT	CAACCGCGCGCTGACCGGCAACCGCGCTCTGCAAC	720
Db	1010	GCCATGCGCAACCTCTATGCGAT	CAACCGCGCGCTGACCGGCAACCGCGCTCTGCAAC	1069
Qy	721	AGGACTGTGCGGACCGCGCGCG	CGGACGGAGGAAAGCTCCCTCAGCCCTTGAGAG	780
Db	1070	AGGACTGTGCGGACCGCGCGCG	CGGACGGAGGAAAGCTCCCTCAGCCCTTGAGAG	1129
Qy	781	CTGATATCACTCCCTGCTGCTG	CGCGCTGATAGACGCTGCTTCACTATGTGTTCTCTGCCC	840
Db	1130	CTGATATCACTCCCTGCTGCTG	CGCGCTGATAGACGCTGCTTCACTATGTGTTCTCTGCCC	1189
Qy	841	GTAAATTG 847		
Db	1190	GTAAATTG 1196		
RESULT 14				
AAAF21227				
ID AAF21227 standard; DNA; 1216 BP.				
AAAF21227;				
14-MAR-2001 (first entry)				
Human low adenosine antisense oligonucleotide related sequence #2794.				
DE	XX	Low adenosine antisense oligonucleotide; phosphorothioate; allergy;		
KW	KW	human; airway disorder; bronchoconstriction; lung inflammation;		
KW	KW	surfactant depletion; respiratory; bronchodilator; antiinflammatory;		
KW	KW	immunosuppressive; antihistaminic; analgesic; hypotensive; cytostatic;		
KW	KW	respiratory obstruction; pulmonary obstruction; impeded respiration;		
KW	KW	surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;		
KW	KW	respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;		
KW	KW	pulmonary hypertension; emphysema; pulmonary transplantation rejection;		
KW	KW	chronic obstructive pulmonary disease; pulmonary infection; bronchitis;		
XX	XX	cancer; SR.		
XX	OS	Homo sapiens.		
XX	XX	W0200062736-A2.		
XX	XX	26-OCT-2000.		
XX	XX	24-MAR-2000; 2000WO-US008020.		
XX	PF			

XX	06-APR-1999;	99US-0127958P.
PR	(UYEC-) UNIV EAST CAROLINA.	
PA	(NYCE/) NYCE J W.	
XX		
PI	Nyce JW;	
XX		
XX	WPI: 2000-679539/66.	
DR		
XX		
PT	Low adenosine (A) content antisense oligonucleotides which do not trigger	
PT	adenosine receptors during metabolism, useful e.g. for treating cancers	
PT	and respiratory obstructions.	
PS	Disclosure: Page 1139; 1592pp; English.	
XX		
XX		
CC	The present invention describes low adenosine (A) content antisense	
CC	oligonucleotides and compositions (I) comprising them. In the antisense	
CC	oligonucleotides the A is replaced by a 'Universal' or alternative base.	
CC	(I) can have respiratory, bronchodilator, antiinflammatory, analgesic,	
CC	immunosuppressive, antisthmatic, hypotensive and cytostatic activities.	
CC	The antisense oligonucleotides and (I) can be used to down-regulate the	
CC	expression and or activity of target polypeptides associated with	
CC	lung/respiratory disorders and malignancies, such as stimulating and	
CC	activating peptide factors and transmitters, transcription factors,	
CC	immunoglobulins and antibodies, antibody receptors, cytokines and	
CC	chemokines, endogenously produced specific and non-specific enzymes,	
CC	binding proteins, adhesion molecules and their receptors, cytokine and	
CC	chemokine receptors, adenosine receptors, bradykinin receptors, central	
CC	nervous system (CNS) and peripheral nervous and non-nervous system	
CC	receptors, CNS and peripheral nervous and non-nervous system peptide	
CC	transmitters, defensins, growth factors, vasoactive peptides and	
CC	receptors, binding proteins and malignancy associated proteins. The	
CC	antisense oligonucleotides may be used in this way to treat disorders	
CC	including respiratory obstruction (especially pulmonary obstruction	
CC	and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or	
CC	surfactant hypoproduction which are associated with a disease or	
CC	condition selected from pulmonary vasoconstriction, inflammation,	
CC	allergies, asthma, impeded respiration, respiratory distress syndrome	
CC	(RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary	
CC	hypertension, emphysema, chronic obstructive pulmonary disease (COPD),	
CC	pulmonary transplantation rejection, pulmonary infections, bronchitis,	
CC	and/or cancer. AAF18434 to AAF21543 represent human polynucleotide	
CC	fragments and antisense oligonucleotides used in the exemplification of	
CC	the present invention	
XX		
XX		
SO	Sequence 1216 BP; 153 A; 431 C; 371 G; 261 T; 0 U; 0 Other;	
	Query Match 72.3%; Score 847; DB 3; Length 1216;	
	Best Local Similarity 100.0%; Pred. No. 4.6e-191;	
	Matches 847; Conservative 0; Mismatches 0; Indels 0; Gaps 0.	
QY	1 ATGAAGTGGCGGCTTACCGCGTCCAGAAACACACCTCTGTGGAAAAAGCAACTCGGGG	60
Db	350 ATGAAGTGGCGGCTTACCGCTCCAGAAACACACCTCTGTGGAAAAAGCAACTCGGGG	409
QY	61 GTGATGGCGGGGTGCTCTTCAGAACCGGCTCTTGCGCAACTGCTGGCCCTGGAGCTG	120
Db	410 GTGATGGCGGGGTGCTCTTCAGAACCGGCTCTTGCGCAACTGCTGGCCCTGGAGCTG	469
QY	121 CTGGCGGCGCTGGGGGCTGGGGGTGTGCTCGCGGCGTCCACTGCGCCCGTGCCTCGGTC	180
Db	470 CTGGCGGCGCTGGGGGCTGGGGGTGTGCTCGCGGCGTCCACTGCGCCCGTGCCTCGGTC	529
QY	181 TTCTACATGCTGGTGTGTGGCTGTACCGGTCAACCGACTGTGTTGGGAAGTCTCTCAAGC	240
Db	530 TTCTACATGCTGGTGTGTGGCTGTACCGGTCAACCGACTGTGTTGGGAAGTCTCTCAAGC	589
QY	241 CCGGTGTGCTGGCTGCTACGCTAGAACCGAGCTTGGGGTCTTGGCCGCCCATTTG	300
Db	590 CCGGTGTGCTGGCTGCTACGCTAGAACCGAGCTTGGGGTCTTGGCCGCCCATTTG	649
QY	301 GACAACTGTGTGCGCAACCTTGGCTTTCATGTCTTTTGGGCTCTCTCGACA	360

Db	650	GACAACTGTTGTGCCAAGCCTTGCCCTTTCTTATGTCCTTTTG66GCTCTCCGACA	709
Qy	361	CTGCAACTCTGSCCATGAGCACTGAGTGTGAGCTCTCCCTTAGGGCAACCCTTTCTTAC	420
Db	710	CTGCAACTCTGGCCATGAGCACTGAGTGTGAGCTCTCCCTTAGGGCAACCCTTTCTTAC	769
Qy	421	CGAAGGCAATACCCCTGCGCTG66GGCACTGATG6CCCCGGTGTGAGACGCTTCTCC	480
Db	770	CGAGGGCAATACCCCTGCGCTG66GGCACTGATG6CCCCGGTGTGAGACGCTTCTCC	829
Qy	481	CTGGCTTTCTGCGGCTACCTTTTCAATGAGGCTTCGGGAAAGTTGTCAGTACTG6CCGGC	540
Db	830	CTGGCTTTCTGCGGCTACCTTTTCAATGAGGCTTCGGGAAAGTTGTCAGTACTG6CCGGC	889
Qy	541	ACCTGTGCTTTATTCAGATGATGCACAGAGAGGACTCGCTGTGATGCTGAGGTACTCT	600
Db	890	ACCTGTGCTTTATTCAGATGATGCACAGAGAGGACTCGCTGTGATGCTGAGGTACTCT	949
Qy	601	GTGCTTACTCTCAAGCTCTATAGCGCTGCTGATCTCTCGCCACCGTGTGTCAACTTG6GC	660
Db	950	GTGCTTACTCTCAAGCTCTATAGCGCTGCTGATCTCTCGCCACCGTGTGTCAACTTG6GC	1009
Qy	661	GCCATGCGCAACCTCTTATGCGATGACACCGGCGGCTGACG66CAACCCGCGCTCTGACCC	720
Db	1010	GCCATGCGCAACCTCTTATGCGATGACACCGGCGGCTGACG66CAACCCGCGCTCTGACCC	1069
Qy	721	AGGACTGTGCGGAGCCGCGCGCGGAGCGGAGAGGAAAGTCCTCCCTCAAGCCCTTGAGAG	780
Db	1070	AGGACTGTGCGGAGCCGCGCGCGGAGCGGAGAGGAAAGTCCTCCCTCAAGCCCTTGAGAG	1129
Qy	781	CTGATCACTCTCTGCTGCTGAGCGGCTGATGACCGTGTCTTTCACTATGTGTTCTTG6CCC	840
Db	1130	CTGATCACTCTCTGCTGCTGAGCGGCTGATGACCGTGTCTTTCACTATGTGTTCTTG6CCC	1189
Qy	841	GTAATTG 847	
Db	1190	GTAATTG 1196	
RESULT 15			
ABZ96921			
ID	ABZ96921	standard; DNA, 1216 BP.	
AC	ABZ96921;		
XX			
DT	17-OCT-2003	(first entry)	
XX			
DE	Human nucleic acid sequence.		
XX			
KW	Human; antisense; lung dysfunction; nasal airway dysfunction;		
KW	antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;		
KW	antiallergic; hypotensive; immunosuppressive; cytostatic; gene therapy;		
KW	antisense gene therapy; respiratory; lung; adenosine sensitivity;		
KW	adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;		
KW	lung inflammation; respiratory disease; ds.		
XX			
OS	Homo sapiens.		
XX			
PN	WO200285308-A2.		
PD	31-OCT-2002.		
XX			
PF	23-APR-2002; 2002MO-US013135.		
XX			
PR	24-APR-2001; 2001US-0286137P.		
XX			
PA	(EPIDG-) EPIDGENESIS PHARM INC.		
PI	NYCE JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;		
PI	Miller S, Tang L, Shahabuddin S;		
XX			
DR	WPI; 2003-229219/22.		

XX Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.

XX Disclosure; SEQ ID NO 12163; 872bp; English.

XX The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5 and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC anti-inflammatory steroid and ubiquinone. A composition of the invention
CC has anti-inflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences

XX Sequence 1216 BP; 153 A; 431 C; 371 G; 261 T; 0 U; 0 Other;

XX Query Match 72.3%; Score 847; DB 10; Length 1216;

XX Best Local Similarity 100.0%; Pred. No. 4.6e-191;

XX Matches 847; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAAGTGGCGGCTTTACCGCTGCGAGAACACCACTTGTGAAAAAGGCAACTCGGCG 60
DB 350 ATGAAGTGGCGGCTTTACCGCTGCGAGAACACCACTTGTGAAAAAGGCAACTCGGCG 409
QY 61 GTATATGGGGGGGGGGGCTTACAGACCGGCTCTGGGGCAACCTGTGGGCGCTGGGGCTG 120
DB 410 GTATATGGGGGGGGGGGCTTACAGACCGGCTCTGGGGCAACCTGTGGGCGCTGGGGCTG 469
QY 121 CTGGCGCGCTCGGGGCTGGGGGCTGCTCGCGCGCTCACTGCGCCGCTGCGCTC 180
DB 470 CTGGCGCGCTCGGGGCTGGGGGCTGCTCGCGCGCTCACTGCGCCGCTGCGCTC 529
QY 181 TTCTACATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 240
DB 530 TTCTACATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 589
QY 241 CCGGTGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 300
DB 590 CCGGTGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 649
QY 301 GACAACCTGTTGTGCAAGGCTTGCCTTTTCAATGTCTTGTGGGCTCTCTCGACA 360
DB 650 GACAACCTGTTGTGCAAGGCTTGCCTTTTCAATGTCTTGTGGGCTCTCTCGACA 709
QY 361 CTGCAACTCTGTGGCATGTGCACTGAGAGTGTGGCTCTCTAGGGCACTCTTCTTAC 420
DB 710 CTGCAACTCTGTGGCATGTGCACTGAGAGTGTGGCTCTCTAGGGCACTCTTCTTAC 769
QY 421 CGACGGGCAATCAACCCGCGGCTGGGGGCACTGTGGGCGCGGCTGGAGGCGCTTCTC 480
DB 770 CGACGGGCAATCAACCCGCGGCTGGGGGCACTGTGGGCGCGGCTGGAGGCGCTTCTC 829
QY 481 CTGGCTTTCTGCGCGCTACCTTTTCAATGAGGCTTGTGGAAGTGTGTGAGTGTGAGTGTG 540
DB 830 CTGGCTTTCTGCGCGCTACCTTTTCAATGAGGCTTGTGGAAGTGTGTGAGTGTGAGTGTG 889
QY 541 ACCTGTGCTTTATCCAGATGTCTCACGAGAGGCTGCTGTGTGTGTGTGTGTGTGTGT 600

DB 890 ACCTGTGCTTTATCCAGATGTCTCACGAGAGGCTGCTGTGTGTGTGTGTGTGTGTGT 949
QY 601 GTGCTTACTCCAGCTCATGAGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 660
DB 950 GTGCTTACTCCAGCTCATGAGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1009
QY 661 GCCATGCGCAACCTCTATGCGATGCAACCGGCGGCTGACCGGCACTCCGCTCTGACAC 720
DB 1010 GCCATGCGCAACCTCTATGCGATGCAACCGGCGGCTGACCGGCACTCCGCTCTGACAC 1069
QY 721 AGGACTGTGCGGAGCGGCGGCGGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 780
DB 1070 AGGACTGTGCGGAGCGGCGGCGGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1129
QY 781 CTGATCACCTCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 840
DB 1130 CTGATCACCTCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1189
QY 841 GTATATG 847
DB 1190 GTATATG 1196

Search completed: April 22, 2005, 12:41:18
Job time : 716.49 secs

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OM nucleic - nucleic search, using sw model

Run on: April 22, 2005, 12:36:32 ; Search time 220.57 Seconds
(without alignments)
8686.931 Million cell updates/sec

Title: US-10-689-861-1

Perfect score: 1171
Sequence: 1 atgaagtcgcgcgtctaccg.....acatggaaccagctcgtga 1171

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA :
1: /cgn2_6/prodata/1/ina/5A COMB.seq : *
2: /cgn2_6/prodata/1/ina/5A COMB.seq : *
3: /cgn2_6/prodata/1/ina/6A COMB.seq : *
4: /cgn2_6/prodata/1/ina/6B COMB.seq : *
5: /cgn2_6/prodata/1/ina/PCTUS COMB.seq : *
6: /cgn2_6/prodata/1/ina/backfile1.seq : *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	979	83.6	1488	2	US-08-812-203-4	Sequence 4, Appl1
2	979	83.6	1488	3	US-09-300-864-4	Sequence 4, Appl1
3	979	83.6	1488	3	US-09-598-418-4	Sequence 4, Appl1
4	847	72.3	1216	4	US-09-016-434-1474	Sequence 1474, Ap
5	211	18.0	2236	1	US-08-239-431A-3	Sequence 3, Appl1
6	211	18.0	2236	1	US-09-267-423-3	Sequence 3, Appl1
7	209.4	17.9	2372	4	US-09-016-434-1441	Sequence 1441, Ap
8	209.4	17.9	6446	4	US-09-293-170-2	Sequence 2, Appl1
9	204.6	17.5	1077	4	US-09-826-509-558	Sequence 558, App
10	201.8	17.2	1356	1	US-08-134-012-5	Sequence 5, Appl1
11	201.8	17.2	1356	1	US-08-520-519-5	Sequence 5, Appl1
12	201.8	17.2	1356	3	US-09-039-798-5	Sequence 5, Appl1
13	201.8	17.2	1417	1	US-08-134-012-4	Sequence 4, Appl1
14	201.8	17.2	1417	1	US-08-520-519-4	Sequence 4, Appl1
15	201.8	17.2	1417	1	US-09-039-798-4	Sequence 4, Appl1
16	201.8	17.2	1417	4	US-09-016-434-1403	Sequence 1403, Ap
17	201.8	17.2	1488	1	US-08-134-012-6	Sequence 6, Appl1
18	201.8	17.2	1488	1	US-08-520-519-6	Sequence 6, Appl1
19	201.8	17.2	1488	3	US-09-039-798-6	Sequence 6, Appl1
20	201.4	17.2	1074	2	US-08-463-0818-29	Sequence 29, Appl1
21	201.4	17.2	1074	2	US-08-463-0818-29	Sequence 29, Appl1
22	201.4	17.2	1074	2	US-08-463-3908-29	Sequence 29, Appl1
23	201.4	17.2	1074	3	US-08-463-074B-29	Sequence 29, Appl1
24	201.4	17.2	1074	3	US-08-465-585C-29	Sequence 29, Appl1
25	201.4	17.2	1074	3	US-08-652-446-29	Sequence 29, Appl1
26	201.4	17.2	2450	2	US-08-463-0818-5	Sequence 5, Appl1
27	201.4	17.2	2450	2	US-08-461-379A-5	Sequence 5, Appl1

28	201.4	17.2	2450	2	US-08-462-3908-5	Sequence 5, Appl1
29	201.4	17.2	2450	3	US-08-463-074B-5	Sequence 5, Appl1
30	201.4	17.2	2450	3	US-08-465-585C-5	Sequence 5, Appl1
31	201.4	17.2	2450	3	US-08-652-446-5	Sequence 5, Appl1
32	107.2	9.2	1209	4	US-09-826-509-556	Sequence 556, App
33	107.2	9.2	1376	4	US-09-016-434-1361	Sequence 1361, Ap
34	107.2	9.2	1394	2	US-08-068-729-3	Sequence 3, Appl1
35	107.2	9.2	1394	3	US-09-255-671-3	Sequence 3, Appl1
36	107.2	9.2	1394	3	US-09-395-366-3	Sequence 3, Appl1
37	101.2	8.6	1467	4	US-09-826-509-560	Sequence 560, App
38	101.2	8.6	1958	1	US-08-115-365-1	Sequence 1, Appl1
39	101.2	8.6	1958	1	US-08-586-897-1	Sequence 1, Appl1
40	101.2	8.6	1958	4	US-09-016-434-1380	Sequence 1380, Ap
41	99	8.5	2442	1	US-08-390-162-5	Sequence 5, Appl1
42	99	8.5	2442	1	US-08-685-945B-5	Sequence 5, Appl1
43	82.6	7.1	2932	4	US-09-016-434-1419	Sequence 1419, Ap
44	82.6	7.1	2932	4	US-09-054-272-5	Sequence 5, Appl1
45	71.6	6.1	5688	3	US-09-293-170-7	Sequence 7, Appl1

ALIGNMENTS

RESULT 1
US-08-812-203-4
Sequence 4, Application US/08812203
Patent No. 5958723
GENERAL INFORMATION:
APPLICANT: ABRAMOVITZ, MARK
APPLICANT: BOIE, YVES
APPLICANT: SAWYER, NICOLE
APPLICANT: METTERS, KATHLEEN
APPLICANT: SLIPETZ, DEBORAH
TITLE OF INVENTION: DNA ENCODING PROSTAGLANDIN RECEPTOR DP
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: JOHN W. WALLEN, III
STREET: 126 E. LINCOLN AVE., P.O. BOX 2000
CITY: RAHWAY
STATE: NJ
COUNTRY: USA
ZIP: 07065-0900
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/812,203
FILING DATE: 06-MAR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/378,682
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: WALLEN III, JOHN W.
REGISTRATION NUMBER: 35,403
REFERENCE/DOCKET NUMBER: MRL 94/185
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908)594-3905
TELEX: (908)594-4720
INFORMATION FOR SEQ. ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1488 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-812-203-4
Query Match 83.6%; Score 979; DB 2; Length 1488;
Best Local Similarity 92.2%; Pred. No. 1e-243;
Matches 1080; Conservative 0; Mismatches 0; Indels 91; Gaps 1;

QY 1 ATGAAGTCCGCTGTTCTACCGCTGCGAGAACCACTCTGTGGAAGAAAGCAACTCGGCG 60
Db 350 ATGAAGTCCGCTGTTCTACCGCTGCGAGAACCACTCTGTGGAAGAAAGCAACTCGGCG 409
QY 61 GTGATGGGCGGGGCTCTTTCAGACCGGCTCTCTGGGCAACTGTGCGCTGCGGCTG 120
Db 410 GTGATGGGCGGGGCTCTTTCAGACCGGCTCTCTGGGCAACTGTGCGCTGCGGCTG 469
QY 121 CTGGCGGCTCGGGGCTGGGGGCTGCTCGGGGCTCACTGGGCGGCTGCGCTGCTG 180
Db 470 CTGGCGGCTCGGGGCTGGGGGCTGCTCGGGGCTCACTGGGCGGCTGCGCTGCTG 529
QY 181 TTCTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
Db 530 TTCTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 589
QY 241 CCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
Db 590 CCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 649
QY 301 GACAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
Db 650 GACAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 709
QY 361 CTGCAACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420
Db 710 CTGCAACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 769
QY 421 CGACGGCACTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
Db 770 CGACGGCACTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 829
QY 481 CTGAGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
Db 830 CTGAGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 889
QY 541 ACCTGCTGCTTATTCAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
Db 890 ACCTGCTGCTTATTCAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 949
QY 601 GTGCTCTACTCCAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
Db 950 GTGCTCTACTCCAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1009
QY 661 GCCATGGGCAACCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720
Db 1010 GCCATGGGCAACCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1069
QY 721 AGGGAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
Db 1070 AGGGAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1129
QY 781 CTGGAATCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840
Db 1130 CTGGAATCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1189
QY 841 GTATATGCAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900
Db 1190 GTATAT----- 1195
QY 901 AAACATTTTCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
Db 1196 -----TATCGGCTTACTATGAGATTT 1218
QY 961 TAAGATGTCAAGAGAAAAAGACCTTGAAGAGCAAGACCTCGAGCTTGGCG 1020
Db 1219 TAAGATGTCAAGAGAAAAAGACCTTGAAGAGCAAGACCTCGAGCTTGGCG 1278
QY 1021 ATTTCTATCTGATTTCAATGAGACCTTGGATTTTATCATTTTTCAGATCTCAGT 1080
Db 1279 ATTTCTATCTGATTTCAATGAGACCTTGGATTTTATCATTTTTCAGATCTCAGT 1338

QY 1081 ATTGCGATATTTTTTCAAGATTTTCAATAGACTCTTATGATACGAGACCGGTGAC 1140
Db 1339 ATTGCGATATTTTTTCAAGATTTTCAATAGACTCTTATGATACGAGACCGGTGAC 1398
QY 1141 CAATTCACCTAACATGGAATCCAGTCTGGA 1171
Db 1399 CAATTCACCTAACATGGAATCCAGTCTGGA 1429

RESULT 2
US-09-300-864-4
Sequence 4, Application US/09300864
Patent No. 6214972
GENERAL INFORMATION:
APPLICANT: ABRAMOVITZ, MARK
APPLICANT: BOLE, YVES
APPLICANT: SAWYER, NICOLE
APPLICANT: METTERS, KATHLEEN
TITLE OF INVENTION: DNA ENCODING PROSTAGLANDIN RECEPTOR DP
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESSES:
ADDRESSEE: JOHN W. MALLEN, III
STREET: 126 E. LINCOLN AVE., P.O. BOX 2000
CITY: RAHWAY
STATE: NJ
COUNTRY: USA
ZIP: 07065-0900
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/300,864
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/378,682
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: WALLEN III, JOHN W.
REGISTRATION NUMBER: 35,403
REFERENCE/DOCKET NUMBER: MRL 94/185
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908)594-3905
TELEX: (908)594-4720
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1488 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-300-864-4

Query Match 83.6%; Score 979; DB 3; Length 1488;
Best Local Similarity 92.2%; Pred. No. 1e-243;
Matches 1080; Conservative 0; Mismatches 0; Indels 91; Gaps 1;

QY 1 ATGAAGTCCGCTGTTCTACCGCTGCGAGAACCACTCTGTGGAAGAAAGCAACTCGGCG 60
Db 350 ATGAAGTCCGCTGTTCTACCGCTGCGAGAACCACTCTGTGGAAGAAAGCAACTCGGCG 409
QY 61 GTGATGGGCGGGGCTCTTTCAGACCGGCTCTCTGGGCAACTGTGCGCTGCGGCTG 120
Db 410 GTGATGGGCGGGGCTCTTTCAGACCGGCTCTCTGGGCAACTGTGCGCTGCGGCTG 469
QY 121 CTGGCGGCTCGGGGCTGGGGGCTGCTCGGGGCTCACTGGGCGGCTGCGCTGCTG 180
Db 470 CTGGCGGCTCGGGGCTGGGGGCTGCTCGGGGCTCACTGGGCGGCTGCGCTGCTG 529
QY 181 TTCTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240

[illegible]

RESULT 3
US-09-598-418-4
; Sequence 4, Application US/09598418
; Patent No. 6395499
; GENERAL INFORMATION:

```

1  APPLICANT: ABRAMOVITZ, MARK
2  BOIE, YVES
3  SAWYER, NICOLE
4  METTERS, KATHLEEN
5  TITLE OF INVENTION: SLIPNETZ, DEBORAH
6  NUMBER OF SEQUENCES: 4
7  CORRESPONDENCE ADDRESS:
8  ADDRESSEE: JOHN W. WALLEN, III
9  STREET: 126 E. LINCOLN AVE., P.O. BOX 2000
10 CITY: RAHWAY
11 STATE: NJ
12 COUNTRY: USA
13 ZIP: 07065-0900
14 COMPUTER READABLE FORM:
15 MEDIUM TYPE: floppy disk
16 COMPUTER: IBM PC compatible
17 OPERATING SYSTEM: PC-DOS/MS-DOS
18 SOFTWARE: Patent In Release #1.0, Version #1.25
19 CURRENT APPLICATION DATA:
20 APPLICATION NUMBER: US/09/598, 418
21 FILING DATE: 20-Jun-2000
22 CLASSIFICATION: <Unknown>
23 ATTORNEY/AGENT INFORMATION:
24 NAME: WALLEN III, JOHN W.
25 REGISTRATION NUMBER: 35,403
26 REFERENCE/DOCKET NUMBER: MRL 94/185
27 TELECOMMUNICATION INFORMATION:
28 TELEPHONE: (908) 594-3905
29 TELEX: (908) 594-4720
30 INFORMATION FOR SEQ ID NO: 4:
31 SEQUENCE CHARACTERISTICS:
32 LENGTH: 1488 base pairs
33 TYPE: nucleic acid
34 STRANDEDNESS: single
35 TOPOLOGY: linear
36 MOLECULE TYPE: DNA (genomic)
37 SEQUENCE DESCRIPTION: SEQ ID NO: 4:
38 US-09-598-418-4
39
40 Query Match      83.6%; Score 979; DB 3; Length 1488;
41 Best Local Similarity 92.2%; Pred. No. 1e-243;
42 Matches 1080; Conservative 0; Mismatches 0; Indels 91; Gaps 1
43
44 QY 1 ATGAAGTCGCGGTCTACCGCTGCAGAAACACACTTGTGGAAAAAGCACTCGGCG 60
45 DB 350 ATGAAGTCGCGGTCTACCGCTGCAGAAACACACTTGTGGAAAAAGCACTCGGCG 409
46
47 QY 61 GTGATGGGCGGGGTGCTCTTACGACCGGGCTCTTGGGCAACTGCTGCGGCGTGTG 120
48 DB 410 GTGATGGGCGGGGTGCTCTTACGACCGGGCTCTTGGGCAACTGCTGCGGCGTGTG 469
49
50 QY 121 CTGGCGGGGCTCGGGGGCTGGGGTGTGCTCGGGGGGTCCACTGGGCGCGCTCGGGTTC 180
51 DB 470 CTGGCGGGGCTCGGGGGCTGGGGTGTGCTCGGGGGGTCCACTGGGCGCGCTCGGGTTC 529
52
53 QY 181 TTCTACATGCTGTGTGTGAGCTTACGAGTCAACGACTTGTGAGGCAAGTGCTCTTAAGC 240
54 DB 530 TTCTACATGCTGTGTGTGAGCTTACGAGTCAACGACTTGTGAGGCAAGTGCTCTTAAGC 589
55
56 QY 241 CCGGTGTGTGCTGGCTGCTACGCTCAAGAACCGAGTCTGCGGGGTGCTTGGCGCGCATTTG 300
57 DB 590 CCGGTGTGTGCTGGCTGCTACGCTCAAGAACCGAGTCTGCGGGGTGCTTGGCGCGCATTTG 649
58
59 QY 301 GACAACTCGTTGTGSCCAAGCCTTGACCTTCTATGTCCTTCTTGGGCTCTCTCGACA 360
60 DB 650 GACAACTCGTTGTGSCCAAGCCTTGACCTTCTATGTCCTTCTTGGGCTCTCTCTCGACA 709
61
62 QY 361 CTGCAACTCTCTGGCCATGAGCACTGAGTGTGCTCTCCCTTAGGCAACCTTTCTTCTAC 420
63 DB 710 CTGCAACTCTCTGGCCATGAGCACTGAGTGTGCTCTCCCTTAGGCAACCTTTCTTCTAC 769
64
65 QY 421 CGAGCGCAATCAACCTTGCGCTGCGGCGCACTGAGTGGCCCGGTGTGAGCGCTTCTCC 480

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Db      950 GTGCTCTACTCCAGCCTCATGCGCGTGTCTCTCCACCGTGTGTGCAACTTCGGC 1009
Qy      661 GCCATGCGCAACCTCTATGCGATGCAACCGCGCGCTGACGGGACCCGCGCTCTGCAAC 720
Db      1010 GCCATGCGCAACCTCTATGCGATGCAACCGCGCGCTGACGGGACCCGCGCTCTGCAAC 1069
Qy      721 AGGAGCTGTGCGGAGCGCGCGGAGCGGAGGAGGAGAGCGTCCCTCAGCCCTGAGAGAG 780
Db      1070 AGGAGCTGTGCGGAGCGCGCGGAGCGGAGGAGGAGAGCGTCCCTCAGCCCTGAGAGAG 1129
Qy      781 CTGATGATCCTCTCTGCTGTGCGGCGCTGATGACCGTGTCTTCACTATGTTCTTGTCCC 840
Db      1130 CTGATGATCCTCTCTGCTGTGCGGCGCTGATGACCGTGTCTTCACTATGTTCTTGTCCC 1189
Qy      841 GTATTTG 847
Db      1190 GTATTTG 1196

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RESULT 5

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US-08-239-431A-3
; Sequence 3, Application US/08239431A
; Patent No. 5716835

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GENERAL INFORMATION:

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; APPLICANT: Regan, John W.
; APPLICANT: Gil, Daniel W.
; APPLICANT: Woodward, David F.
; TITLE OF INVENTION: NOVEL HUMAN EP PROSTAGLANDIN RECEPTOR
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson and Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: USA

```

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; ZIP: 92660

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COMPUTER READABLE FORM:

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; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS

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; SOFTWARE: FastSeq Version 1.5

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/239,431A

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; FILING DATE: 05-MAY-1994

```

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; CLASSIFICATION: 435

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; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER:

```

FILING DATE:

```

; ATTORNEY/AGENT INFORMATION:
; NAME: Israelson, Ned A.

```

```

; REGISTRATION NUMBER: 29,655

```

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; REFERENCE/DOCKET NUMBER: ALRGN.053A

```

```

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-235-8550

```

```

; TELEFAX: 619-235-0176

```

TELEX:

```

; INFORMATION FOR SEQ ID NO: 3:

```

```

; SEQUENCE CHARACTERISTICS:
; LENGTH: 2296 base pairs

```

```

; TYPE: nucleic acid

```

```

; STRANDEDNESS: single

```

```

; TOPOLOGY: linear

```

```

; MOLECULE TYPE: cDNA

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```

; HYPOTHETICAL: NO

```

```

; ANTI-SENSE: NO

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; FRAGMENT TYPE:

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; ORIGINAL SOURCE:

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; NAME/KEY: Coding Sequence

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; LOCATION: 157...1230

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; OTHER INFORMATION:

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US-08-239-431A-3

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Query Match      18.0%; Score 211; DB 1; Length 2296;
Best Local Similarity 59.4%; Pred. No. 1,6e-44;
Matches 484; Conservative 0; Mismatches 295; Indels 36; Gaps 6;

```

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Qy      48 AGGCACTGCGCGGTATGAGCGGGGTGCTTTCAGACATCCGCTCTGGGCAACTGTCT 107
Db      219 AGGCGAAGCCCAAGCATAGCTCCGTATGTTCTGCGCGGGGTCTGGGAACCTCAT 278
Qy      108 GGGCTTGGGAGCTGCTGAGCGGCTCGGGGCTGGGGT--GGTGTCTGGCGCTCCACTGCGC 165
Db      279 AGCATGGGAGCTCTGAGCGGCGCGCTGGGGGAGAGTGGGGTGCAGCCGCGCGAG 338
Qy      166 CCGCTGCC--CTCGGTCTTACATGCTGTGTGTGAGCTGCAGCCGACTGTGTGG 224
Db      339 GAGCTCCCTCTCTCTTGTTCACAGTGTGTGAGCCAGCTGTGTGTACAGCACTGTCTCG 398
Qy      225 CAAGTGTCTCTTAAGCCCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 284
Db      399 GACCTGTCTATCAGCCAGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 458
Qy      285 GCTTGGCGCGGATTTGACACTCGTTTGTGCAAGCCTTGCCCTTCTTATGTCCTTCTT 344
Db      459 ACTGGCGCC-----GAGAGCGCGCGGTGACACTTCTTGTGCGCACTGACTTCTT 512
Qy      345 TGGGCTCTCTCGACACTGCAACTCTGTGGCAATGAGCACTGAGTGTGCTCTCCCTAG 404
Db      513 CAGCTGTGCGCAGATGCTCATGCTCTTGCACATGAGCCCTGAGCGCTACTCTCGATCG 572
Qy      405 GCACCTTTCTTCTACCGACGAGCATCACTCGCTGTGGGCGCACTGTGGCCCGGT 464
Db      573 GCACCCCTTCTTCTACCGACGAGCATCACTCGCTGTGGGCGCTGTGGGCGCTGTGTGT 632
Qy      465 GGTAGCGGCTTCTCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 524
Db      633 CATTAAGAGTCTCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 692
Qy      525 GCAGTATGCTCCCGGACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 584
Db      693 CAGTATGCTCCCGGACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 754
Qy      585 GGTGTGGGTACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 644
Db      735 ---GACCGCTTACCTGCACTGTGACCGCACCCGTGTGTGTGTGTGTGTGTGTGTGT 791
Qy      645 GCTGTGCACTCGGCGGCAATGCGCACTGTATGAGTGCACCGCGG--GCTGCAAGCG 702
Db      792 CGCTGCACTTCAAGTATTTCTCACTCATTCGCAATCGCAATCGCGGAGAG 851
Qy      703 CACCGCGCTCTGCAACGAGACTGTGCGGCGCGCGGAGCGGAGGAGAGCGTCC 762
Db      852 CCGCTGCGACCTTCCCTGTGGAGTGGCGGGGCGGCGCGCGCGCGGAGAGGAG 911
Qy      763 CTTGAGCCCC--TGAAGAGCTGATCACTCTGTGTGTGTGTGTGTGTGTGTGTGTGT 818
Db      912 AAGGATGTCATGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 971
Qy      819 CTTCATATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 853
Db      972 CTTCGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1006

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RESULT 6

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US-09-267-423-3
; Sequence 3, Application US/09267423
; Patent No. 6395878

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GENERAL INFORMATION:

```

; APPLICANT: Regan, John W.
; APPLICANT: Gil, Daniel W.

```

```

; APPLICANT: Woodward, David F.

```

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; TITLE OF INVENTION: No. 6395878e1 Human Prostaglandin EP Receptor

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; FILE REFERENCE: 17023 DIV CIP

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; CURRENT APPLICATION NUMBER: US/09/267,423

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; CURRENT FILING DATE: 1999-03-12

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EARLIER APPLICATION NUMBER: 09/019,393
EARLIER FILING DATE: 1998-02-05
EARLIER APPLICATION NUMBER: 08/239,431
EARLIER FILING DATE: 1994-05-05
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 3
LENGTH: 2296
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (157)...(1233)
US-09-267-423-3

Query Match 18.0%; Score 211; DB 3; Length 2296;
Best Local Similarity 59.4%; Pred. No. 1.6e-44;
Matches 484; Conservative 0; Mismatches 295; Indels 36; Gaps 6;

48 AGGCAACTCGCGGATGAGGCGGGGCTCTTCAGCAGCGGCTCTCTGAGCACTGCT 107
219 AGCGGAAGCCAGCCATCAGCTCCGTCATGTTCTCGCGGGGCTGCGGAACTCAT 278
108 GGGCTTGGGGCTGTGGCGGCTCGGGCTGGGGT--GGTCTGGCGGCTCACTGCGC 165
279 AGCACTGGCGCTGTGGCGGCTGGCGGAGCGTGGGAGCGCGCGCGCAG 338
166 CCGCTGCC-CTCGGCTCTTACATGCTGATGATGAGGCTGACGAGTCAAGCTTGG 224
339 GAGCTCCTCTCTCTTGTTCACAGTGTGACGAGCTGATGACCACTGCTCGG 398
225 CAAGTCTCTTAAGCCCGGTGTGTGCTGCTGCTTACAGCTCAAGCGAGTCTGCGGT 284
399 GAGCTCCTCTCTCTTGTTCACAGTGTGACGAGCTGATGACCACTGCTCGG 458
285 GCTTGGCGCGCATGAGCACTGCTGTGTGCAAGCTTGGCTTCTTCACTGCTTCTT 344
459 ACTGGCGCC-----GAGAGCGCGCGGTGACCTTCTTGGCTTCCCATGACTTCTT 512
345 TGGGCTCTCTCGACATGCACTCTGCGCATGAGGCACTGAGTGGCTGCTCCCTAGG 404
513 CAGCTGGGCAAGTGTCTATGCTCTTTCGCAATGAGCCCTGAGGCTTCTGATCGG 572
405 GCAACCTTCTTCTTACAGCGGCAATCACTGCGCTGCGCGCACTGTGTGCGCGGT 464
573 GCAACCTTCTTCTTACAGCGGCAATCACTGCGCTGCGCGCACTGTGTGCGCGGT 632
465 GGTGAGCGCTTCTCTCTGCTTCTGCGCGCTACCTTCTTCACTGAGGCTTGGT 524
633 CATCTAATGAGTCTCTCTGCTCTGCTGCTGCGCTGCTGCTGCTGCTGCTGCTGCT 692
525 GAGTACTGCGCGGCACTGCTGCTTATCCAGATGTGTCAAGAGAGGCTGCTGCTGCT 584
693 CAGTACTGCGCGGCACTGCTGCTTATCCAGATGTGTCAAGAGAGGCTGCTGCTGCT 744
585 GGTGAGCGCTTCTCTCTGCTTCTGCTGCTTATCCAGATGTGTCAAGAGAGGCTGCT 644
735 ---GACGCTTACCTGAGCTGTACAGCGCACTGCTGCTGCTTCTTCTGCTGCTGCT 791
645 GGTGAGCGCTTCTCTCTGCTTCTGCTGCTTATCCAGATGTGTCAAGAGAGGCTGCT 702
792 CAGTACTGCGCGGCACTGCTGCTTATCCAGATGTGTCAAGAGAGGCTGCTGCTGCT 851
703 CAGTACTGCGCGGCACTGCTGCTTATCCAGATGTGTCAAGAGAGGCTGCTGCTGCT 762
852 CAGTACTGCGCGGCACTGCTGCTTATCCAGATGTGTCAAGAGAGGCTGCTGCTGCT 911
763 CAGTACTGCGCGGCACTGCTGCTTATCCAGATGTGTCAAGAGAGGCTGCTGCTGCT 818
912 AAGGAGTGTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 971
819 CTTGACTATGTGCTTCTGCGCGGCTTATGCTGCTTATGCTGCTTATGCTGCTTATGCT 853

Db 972 CTTGCGGCTGCTCTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCT 1006

RESULT 7

US-09-016-434-1441
Sequence 1441, Application US/09016434

Patent No. 6500938

GENERAL INFORMATION:

APPLICANT: Janice Au-Young

TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING

TITLE OF INVENTION: PATHWAY GENE EXPRESSION

NUMBER OF SEQUENCES: 1490

CORRESPONDENCE ADDRESS:

ADDRESSEE: INCYTE PHARMACEUTICALS, INC.

STREET: 3174 PORTER DRIVE

CITY: PALO ALTO

STATE: CALIFORNIA

COUNTRY: USA

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/016,434

FILING DATE: HEREWITH

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Zeller, Karen J.

REGISTRATION NUMBER: 37,071

REFERENCE/DOCKET NUMBER: PA-0002 US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (650) 855-0555

TELEFAX: (650) 845-4166

INFORMATION FOR SEQ ID NO: 1441:

SEQUENCE CHARACTERISTICS:

LENGTH: 2372 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

IMMEDIATE SOURCE:

LIBRARY: GENBANK

CLONE: 9639719

US-09-016-434-1441

Query Match 17.9%; Score 209.4; DB 4; Length 2372;
Best Local Similarity 59.3%; Pred. No. 4.1e-44;
Matches 483; Conservative 0; Mismatches 296; Indels 36; Gaps 6;

48 AGGCAACTCGCGGATGAGGCGGGGCTCTTACAGACCGGCTCTCTGAGCACTGCT 107
219 AGCGGAAGCCAGCCATCAGCTCCGTCATGTTCTGCGCGGGGCTCTGGGAACTCAT 278
108 GGGCTTGGGGCTGTGGCGGCTCGGGCTGGGGT--GGTCTGGCGGCTCACTGCGC 165
279 AGCACTGGCGCTGTGGCGGCTGGCGGAGCGTGGGAGCGTGGGAGCGCGCGAG 338
166 CCGCTGCC-CTCGGCTCTTACATGCTGATGATGAGGCTGACGAGTCAAGCTTGG 224
339 GAGCTCCTCTCTCTTGTTCACAGTGTGACGAGCTGATGACCACTGCTCGG 398
225 CAAGTCTCTTAAGCCCGGTGTGTGCTGCTGCTTACAGCTCAAGCGAGTCTGCGGT 284
399 GAGCTCCTCTCTCTTGTTCACAGTGTGATGAGGCTGATGAGGAGGAGGAGGAGGAG 458
285 GCTTGGCGCGCATGAGCACTGCTGTGTGCAAGCTTGGCTTCTTCACTGCTTCTTCT 344

Db	459	ACTGGGCGCC-----GAGAGCCGCGGTCACCTTACCTTGGCTTGGCCATGACCTTCTT	51.2
Qy	345	TGGGCTCTCTCGACACTGCAACTCCTGGCCATAGCAGCTGGAATGCTGGCTTCCCTAAG	40.4
Db	513	CAGCCTTGGCAGAGATGCTATGCTCTTTCGCGCAATGAGCCCTGGAGCCGCTAACCTTCGATCCG	57.2
Qy	405	GCACCTTTCCTTACACGAGGACATACACCTGGGCGCTGGGGGCACTGGTGGCCCGGT	46.4
Db	573	GCACCCCTACTTCACAGACGCGCGCTTCGCGCTCCGGGGGCGCTGGCCGTGCTGCCTGT	63.2
Qy	465	GGTGAAGCGCTTCTCCCTGGCTTTCGCGGCTACCTTTCATAGGGCTTCGGGAAGTTGCT	52.4
Db	633	CATCATAGAGTCTCCCTGCTCTTCTGCTCGCTGCGGCTGCTGAGATATAGGACAGTACGT	65.2
Qy	525	GCAGTACTGCGCCCGCACCTGGTGCTTTATCCAGATGATCCACAGAGAGGGCTCGCTGTC	58.4
Db	693	CCAGTACTGCGCCCGGAGCTTGGGCTTCATCCGGGACCGGGCG-----73.4	73.4
Qy	585	GATGCTGGGGTACTCTGATCTACTATCCAGACCTCATAGGGGCTGCTGCTCGGCACCGT	64.4
Db	735	---GACCGTTTACCTGCACTGTACCCCAACCTGCTGCTGCTTCTATGTCTCGATGCT	79.1
Qy	645	GCTGTGCAACTCTCGGCGCATGGCGCAACCTTATGCGATGACACGGGCG--GCTGCAAGCG	70.2
Db	792	CGCTGCAACTTCAGTGTATTTCTCAACTTCATCCGATGACACCGCCGAAGCCGGAGAAAG	85.1
Qy	703	CACCCGCGCTCTGTGACCAAGGAGATGTGCGAGACCGCGCGCGAGACGAGAGGAAGCGTCC	76.2
Db	852	CCGCTGCGGACCTTCCCTGGGAGTGGCCGGGGCGGCCCGGGGCGCCGACAGAGAGAGGGA	91.1
Qy	763	CCTCAGCCCC---TGGAGAGCTGGATCACTCTGCTGCTGGCGCTGATGACCGTGT	81.8
Db	912	AAGGTGTTCATAGGCGAGAGAGACGAGACCACTCATTTCTGGCTATCATGACCATAC	97.1
Qy	819	CTTACATATGTTCTCTCCCGCTATTCGATTTTG	85.3
Db	972	CTTGCCGCTGCTCTTGGCTTTTACGATTTTGG	100.6

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RESULT 8
US-09-293-170-2
; Sequence 2, Application US/09293170
; Patent No. 6383777
; GENERAL INFORMATION:
; APPLICANT: Breyer, Richard M.
; APPLICANT: Ma, Lijun
; APPLICANT: Kennedy, Chris
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR HIGH YIELD
; FILE REFERENCE: 22000.0094
; CURRENT APPLICATION NUMBER: US/09/293.170
; EARLIER FILING DATE: 1999-04-16
; EARLIER APPLICATION NUMBER: 60/081.989
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 6446
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (300)..(2126)
; OTHER INFORMATION: Description of Artificial Sequence:/note =
; OTHER INFORMATION: synthetic construct
; US-09-293-170-2

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Query Match	17.9%	Score 209.4	DB 3	Length 6446
Best Local Similarity	59.3%	Pred. No. 6.7e-44		
Matches 483	Conservative	0	Mismatches 296	Indels 36
	Gaps	6		
QY	48	AGGCAACTGGGCGGATGGGGGGGTCCTTTCAGCACCGGCGCTCTGGGGAACCTCT	107	

Db	596	AGGGAAAGCCAGACGANTCAGACTCCGTCATGTTCTCGGAGCGGGGGTGTGGGAAACCTCAT	655
Oy	108	GAGCCTTGGAGGTCTGTGGCGCGCTCGGGGCTGGGCT--GTGCTGGCGGCTTCACCTGGCC	165
Db	656	AGCACTGGCGCTGTGGCGCGCCCTCGGCGGGGAGACGTGGGGTGCAGCGCGCGCGCAG	715
Oy	166	CCGCTGCC-CTCGGCTTTTACATGCTGTGTGTGTGGCTGACGGTCAACCACTTGTGGG	224
Db	716	GAGCTCCCTCTCCCTTGTTCACAGCTGTGTACCGAGCTGTGTTCACCCGACCTGTCCGG	775
Oy	225	CAAGTGCCTCTTAAGCCCGGTTGGTGGCTGGGCTGACCTAGCTACGAGAACGGAGCTTGGGGT	284
Db	776	GACCTGCTTATCAGCCCACTGTGTACTGTGGCTTGTGTATGCGCGGAAACAGACCTGTGTGGC	835
Oy	285	GCTTGGCGCCGATTTGACAACACTGTTGTGCAAGCCTTGCCTTCTTCACTGTCTTCTT	344
Db	836	ACTGGCGCCC-----GAGAGCCCGCGGTGACCACTTCTGCTTTTCCGCACTGACCTTTT	889
Oy	345	TGGGCTCTCTTCGACACTGTCACACTCTTGGCCATGGCACTGGAGTGTGGACTCTCCCTAGG	404
Db	890	CAGCCTGGCCACGATGTGTCATGTCTTTCGCCATGCGCCCTGGAGGCTACCTCTGATGG	949
Oy	405	GCACCCCTTTCTTTCACCGAGCGGCACATCACCTTGGCGCTGGGGCGCACTGTGGCCCGGT	464
Db	950	GCACCCCTACTTTCACAGAGCGCCCGTCTCGGACTCCGGGGGGCTTGGCGCTGTGCTCTGT	1009
Oy	465	GGTGAAGGCGCTTTCCTCCCTGGCTTCTTGGGCTTACCGGCTACCTTTCAATGGGCTTTCGGGAAGTTCGT	524
Db	1010	CATTTATGACAGTCTCCCTGCTCTTCTCTCGCTGCGCTGCTGTGACATATGGGACAGTACGT	1065
Oy	525	GCAGTACTGCCCCCGGACACTGGTACTTTTATTCACATGATGGTCCACAGAGAGGGCTCGCTGTC	584
Db	1070	CCAAGTACTGCCCGGGAGACTGTGTCTTCACTCCGACAGGGCG-----111111	
Oy	585	GGTGTGAGGGTACTCTGTGCTTACTCCAGCCTTCATGAGCGCTGTGTGCTCTCGCACCGT	644
Db	1112	---GACGGTTTACTCGAGAGCTGTACCGCACTCCGTCTGTGTTCATTTGTCTGTGGTCT	1168
Oy	645	GCTGTGCAACCTCGGCGCCATGCGCAACTTCTATGCAATGCACCGGCG--GCTGCACGG	702
Db	1169	CGCTGCAACTTTCAGTGTCACTTCACTCACTCATCCGATGACCGCGAGACCGGAGAG	1228
Oy	703	CACCCGCGCTCTGACACAGAGGACTGTGCGAGCCGCGCGCGAGACGGAGGGAAAGCTTC	762
Db	1229	CCGCTGTGGGACCTTCTCCCTGGGCACTGTGCGCGGGCGGCGCCCGGGGACCGCAGAGAGGGGA	1288
Oy	763	CTTACGCCCC---TGGAGGAGCTGTGATCACTCTCTGTGTGGCGCTGATGACCGTGTCT	818
Db	1289	AAAGGTGTCCATGGCGGAGAGACGAGACCACTCATTTCTCTGTGCTATCATGACCATTCAC	1348
Oy	819	CTTCACTATGTTGTCTCTGCGCCGTAATTTGATTTG	853
Db	1349	CTTGTGCGGTCTGCTCTTGTGCTTTACAGATTTTGG	1383

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1 RESULT 9
2 US-09-826-509-558
3 : Sequence 558, Application US/09826509
4 : Patent No. 6806054
5 :
6 : GENERAL INFORMATION:
7 :
8 : APPLICANT: Lehmann-Bruinsma, Karin
9 :
10 : APPLICANT: Lin, I-Lin
11 :
12 : TITLE OF INVENTION: No. 6806054-Endogenous, Constitutively Activated Known G
13 :
14 : TITLE OF INVENTION: Protein-Coupled Receptors
15 :
16 : FILE REFERENCE: AEN-207
17 :
18 : CURRENT APPLICATION NUMBER: US/09/826,509
19 :
20 : CURRENT FILING DATE: 2001-04-05
21 :
22 : PRIOR APPLICATION NUMBER: 60/195,747
23 :
24 : PRIOR FILING DATE: 2000-04-07
25 :
26 : PRIOR APPLICATION NUMBER: 09/170,496
27 :
28 : PRIOR FILING DATE: 1998-10-13
29 :
30 : NUMBER OF SEQ ID NOS: 589

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SOFTWARE: PatentIn Version 2.1
 SEQ ID NO 558
 LENGTH: 1077
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-09-826-509-558

Query Match 17.5%; Score 204.6; DB 4; Length 1077;
 Best Local Similarity 58.9%; Pred. No. 4.9e-43;
 Matches 480; Conservative 0; Mismatches 299; Indels 36; Gaps 6;

QY 48 AGGCACTGGGGGATGGGGGGGATGCTTTCAAGACCGGCTCTCTGGCACTGCT 107
 DB 63 AGGCGAAGCCAGCCATCAGCTCCCTCAATGTTCTGGCCGGGATGCGGGAACCTCAT 122
 QY 108 GGCCTGGGGGCTGCTGGCGGCTCGGGGCTGGGGT--GGTGCCTGGGGGCTCACTGCGC 165
 DB 123 AGCATGAGGCTGCTGGCGCGCGCTGGGCGGAGAGTGGGGTGAAGCGCGCGCGAG 182
 QY 166 CGGCTGCC-CTCGGCTTTTCAATGCTGGTGGTGGCTGAACGGTCACTGCTGGG 224
 DB 183 GAGCTCCCTCTCTCTGTTTCAAGTGTGGTGAACGAGCTGGTGTTCACCGACTGCTCG 242
 QY 225 CAAGTGCCTCTTAAGCCCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 284
 DB 243 GACCTGCCTCATAGCCAGTGGTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 302
 QY 285 GGTGGGCGCCGATGGAGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 344
 DB 303 ACTGGGCGCC-----GAGAGCGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCT 356
 QY 345 TGGGCTCTCTCGACACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 404
 DB 357 GAGCTGGGCAAGATGCTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 416
 QY 405 GCACTCTTTCTTCAACGAGGCAATCACTGCTGCTGCTGCTGCTGCTGCTGCTGCT 464
 DB 417 GCACCCCTTCTTCAACGAGGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 476
 QY 465 GGTGAGCGGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 524
 DB 477 CATCTATGAGTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 536
 QY 525 GCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 584
 DB 537 CAGTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 578
 QY 585 GGTGCTGGGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 644
 DB 579 ---GACCGCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 635
 QY 645 GGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 702
 DB 636 GCGCTGCACTTCAAGTCTTCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 695
 QY 703 CACCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 762
 DB 696 CGGCTGCGGACCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 755
 QY 763 CCTGAGCCCC---TGGAGGAGCTGATCACTGCTGCTGCTGCTGCTGCTGCTGCTGCT 818
 DB 756 AAGGATGCTCAATGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 815
 QY 819 CTTCACTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 853
 DB 816 CTTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 850

RESULT 10
 US-08-134-012-5
 Sequence 5, Application US/08134012
 Patent No. 551652
 GENERAL INFORMATION:

APPLICANT: Abramovitz, Mark
 APPLICANT: Boie, Yves
 APPLICANT: Grygorczyk, Richard
 APPLICANT: Metters, Kathleen
 APPLICANT: Rushmore, Thomas H.
 APPLICANT: Sliet, Deborah M.
 TITLE OF INVENTION: DNA ENCODING PROSTAGLANDIN RECEPTOR IP
 NUMBER OF SEQUENCES: 6
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: John Wallen
 STREET: 126 E. Lincoln Avenue
 CITY: Rahway
 STATE: New Jersey
 COUNTRY: USA
 ZIP: 07065
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/134,012
 FILING DATE: 06-OCT-1993
 CLASSIFICATION: 530
 ATTORNEY/AGENT INFORMATION:
 NAME: Wallen, John W
 REGISTRATION NUMBER: 35,403
 REFERENCE/DOCKET NUMBER: 19098
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (908) 594-3905
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1356 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 US-08-134-012-5

Query Match 17.2%; Score 201.8; DB 1; Length 1356;
 Best Local Similarity 61.4%; Pred. No. 2.9e-42;
 Matches 380; Conservative 0; Mismatches 227; Indels 12; Gaps 3;

QY 98 GCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 157
 DB 53 GCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 112
 QY 158 CACTGCGCC---CGTGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 214
 DB 113 CACGGCGACCGGCGCGCCCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 172
 QY 215 ACTTGTGGGCAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 274
 DB 173 ACTGCTGCGGACAGAGCTTCTGAGCCCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 232
 QY 275 GTCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 334
 DB 233 CCTGCTGCGGCT---GGCCGAGCGGCGCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 289
 QY 335 TGTCTCTTCTTGGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 394
 DB 290 TACCTTCTTGGGCTTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 349
 QY 395 TCTCCCTGAGGCACTGCTTCTTCAACGAGCATATCACTGCTGCTGCTGCTGCTGCTGCT 454
 DB 350 TGGCGCTGAGCCACCTCTTCACTTCAAGGAGCTGAGAGGAGGAGGAGGAGGAGGAGGAG 409
 QY 455 TGGCCCGGCTGCTGAGCGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 514
 DB 410 CGCTGCAAGCATCTAAGCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 469
 QY 515 GGAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 574

(732) 594-3905

OY 695 TGCAGCGGCACCCGCGCTC 713
| | | | | | | | | |
Db 706 AGAAGCGCCACCAAGGCTC 724

RESULT 14

US-08-520-519-4
Sequence 4, Application US/08520519
Patent No. 5728808
GENERAL INFORMATION:
APPLICANT: Abramovitz, Mark
APPLICANT: Boie, Yves
APPLICANT: Grygorczyk, Richard
APPLICANT: Metters, Kathleen
APPLICANT: Rushmore, Thomas H.
APPLICANT: Slipetz, Deborah M.
TITLE OF INVENTION: DNA ENCODING PROSTAGLANDIN RECEPTOR IP
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Jack L. Tribble
STREET: 126 E. Lincoln Avenue
CITY: Rahway
STATE: New Jersey
COUNTRY: USA
ZIP: 07065-0907
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/520,519
FILING DATE: 29-AUG-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Tribble, Jack L.
REGISTRATION NUMBER: 32,633
REFERENCE/DOCKET NUMBER: 19098DA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-5321
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1417 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-520-519-4

Query Match 17.2%; Score 201.8; DB 1; Length 1417;
Best Local Similarity 61.4%; Pred. No. 3e-42;
Matches 380; Conservative 0; Mismatches 227; Indels 12; Gaps 3;

OY 98 GGAACCTGTGAGCCCTGTGAGGCTGCGGCGCTCGGGGCTGTGCTCGCGGCTC 157
| | | | | | | | | |
Db 115 GACACCTGATGTTCTGTGGCGGCTGTGTGGGCAACGGGCTGCGCTGATCTTGAAGC 174
| | | | | | | | | |
OY 158 CACTGGCC--CGTGCCTCGCTTCTTACATGCTGTGTGGCTTGACGGTCAACG 214
| | | | | | | | | |
Db 175 CACGGGACCGGGCGCCCTTGGGCTTGGCGGTGCTGGTCAACGGACTGGCGGCAACG 234
| | | | | | | | | |
OY 215 ACTGTGTGGCAAGTCTCTTAAGCCGGTGTGTGCTGTGCTTCAAGCTCAAGACCGA 274
| | | | | | | | | |
Db 235 ACCTGTGGGCAACAGCTTCTAGGCCGGCGCTGTTCGTGGGCTTATGGCGCAAGCT 294
| | | | | | | | | |
OY 275 GTCTGGGGTGTGGCGCGCATTTGACAACTCGTTTSCAAGCCTTGCCCTTCTTA 334
| | | | | | | | | |
Db 295 CCTGTGGGCT--GCGCCGAGGGGCGCCCGCTGTGCAATGCTTGTGCTTGGCA 351
| | | | | | | | | |
OY 335 TGTCTTCTTTGGGCTCTCTCGACACTGCAACTCTGCGCATGGAAGTGTGCTG 394
| | | | | | | | | |
Db 352 TGACCTTCTTGGGCTGTGGGCTCATGCTATCTTGTGCGATGGCGGTGAGCGCTGCC 411
| | | | | | | | | |

OY 395 TCTCCCTAAGGACCCCTTCTTCTACCAAGGACATCACTGCGCTGGGGCACTGG 454
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Db 412 TGGCGCTGAGCCACCCCTTACTTACGGCAGTGAACGGGCCCCCGCTGGCGCTGG 471
| | | | | | | | | |
OY 455 TGGCCCGGTGTGAGCGCTTCTCCCTGCTTCTGCGGCTTACTTTATGAGGCTTG 514
| | | | | | | | | |
Db 472 CGCTGCACGACATCTACGCTTCTGTGCTCTTCTGCGGCTGCGCCCTGCGGCTGG 531
| | | | | | | | | |
OY 515 GGAATTGTGACATCTGCGCCCGGACCTGTGCTTTATCCAGATGTGTCCAGAGAG 574
| | | | | | | | | |
Db 532 GCCAACACGACAGTACTGCGCGGACGCTGTGTCTTCTCCGATGCGC-----TGGG 585
| | | | | | | | | |
OY 575 GCTGCTGTGAGTGTGGGTACTGTGCTCTACTTCAAGCCATGAGCGCTGCTGTC 634
| | | | | | | | | |
Db 586 CCGAGCCGGGCGGCGGCTTCTGCTGCTTACGCGCGGCTGTGGCTGTGCTG 645
| | | | | | | | | |
OY 635 TGCACACGCTGTGTCACCTCGGCGCATGCGCAACTTATGCGATGACCGGCGGC 694
| | | | | | | | | |
Db 646 CTGCATCTTCTCTGCAACGGCTCGTCACTGAGCTCTGCGCATGTACCGCAGC 705
| | | | | | | | | |
OY 695 TGCAGCGGCACCCGCGCTC 713
| | | | | | | | | |
Db 706 AGAAGCGCCACCAAGGCTC 724

RESULT 15

US-09-039-798-4
Sequence 4, Application US/09039798
Patent No. 6365360
GENERAL INFORMATION:
APPLICANT: Abramovitz, Mark
APPLICANT: Boie, Yves
APPLICANT: Grygorczyk, Richard
APPLICANT: Metters, Kathleen
APPLICANT: Rushmore, Thomas H.
APPLICANT: Slipetz, Deborah M.
TITLE OF INVENTION: DNA ENCODING PROSTAGLANDIN RECEPTOR IP
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESSES:
ADDRESSEE: J. Mark Hand
STREET: 126 E. Lincoln Avenue
CITY: Rahway
STATE: New Jersey
COUNTRY: USA
ZIP: 07065-0907
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/039,798
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/520,519
FILING DATE: 29-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Hand, J. Mark
REGISTRATION NUMBER: 36,545
REFERENCE/DOCKET NUMBER: 19098DB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (732) 594-3905
TELEFAX: (732) 594-4720
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1417 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-09-039-798-4

Query Match	17.2%;	Score 201.8;	DB 3;	Length 1417;
Best Local Similarity	61.4%;	Pred. No. 3e-42;		
Matches 380; Conservative	0;	Mismatches 227;	Indels 12;	Gaps 3;

QY	98	GCACCTGCGGCGCCCTGGGGGCTGTGAGCGCGCTCGGGGCTGGGGGTGAGTCTCGCGGCGTC	1.57
Db	115	GCACCTGATGTTTCGTGGCGGGGTGTGTGTGGGCAAGGGGCTGGCCCTGGGCATCTGTAGCG	1.74
QY	158	CACTCGCGC---CGTCGCTTCGTGTTCTTACATGCTGTGTGTGGCCCTGACGGTCA	2.14
Db	175	CAGGGGCAACGGGGCGCCCTCGGGCTTCGCGTGTCTGTATCCAGGCACTGGCGGGCCACCG	2.34
QY	215	ACTTGTGGGGCAAGGGCCCTTAAACCGCGGTGTGTCTGGCTGCTTAACGCTCAGAACCGGA	2.74
Db	235	ACCTGCTGGGACACAGCTTCTGTAGCGCCGGCCGTTGTGTGACCTTATGCGGGCAACGCT	2.94
QY	275	GTCCTGGGGTGTCTTGGCGCCCGCATTTGACAACTCGTTGTGCAAGCCTTCGCTTCTTCA	3.34
Db	295	CCCTGCTGGGGCCT---GGCCGAGGGGGGCCCGCCCTGTGTGGATGCTTGGCCTTCCGCA	3.51
QY	335	TGTCTCTTCTTTTGGGCTCTCTCTGACACTGCAACTCTCGGCGATGAGCACTGAGTGTGCG	3.94
Db	352	TGACCTTCTTCGGCCCTGGCGTGCATGCTCATCTCTTGGCATGAGCGGTGAGGGGCTGGC	4.11
QY	395	TCACCTTAAAGGACCCCTTCTTCTTACACCAAGGACATACCTGTGGCTGGGGGCACTGG	4.54
Db	412	TGGCGCTGAGCACCCCTTACCTTACGGGCACTGGAAGGGCCCGCTGCGCCCGGCTGG	4.71
QY	455	TGCGCCCGGTGTGAGCGGCTTCTCCCTGAGCTTTTGTGCGGCTACTTTCATGTGGGCTTGC	5.14
Db	472	CGGTGCAGACATCTACGCTTCTGTGGTCTCTTCTGTGGCGGTGGCCCTGTGGGCTTGG	5.31
QY	515	GGAACTTCTGTAAGTACTGTGCCCCGGGACCTGTGTCTTATCAAGTGTCCAGAGAGG	5.74
Db	532	GGCAACACAGCAAGTACTGTGCCCGGAGGTGTGTCTTCTCCGATGTGC-----TGGG	5.85
QY	575	GCTCGGTGTGGGTGCTGGGGTACTGTGTGTCTTATTCAGGCTCATGGCGGTGTGTGTTC	6.34
Db	586	CCGACGCGGGCGGCGCGCTTCTGTGCTGTGACCTTACGCGCGCTGTGTGCTTGTGTGG	6.45
QY	635	TGCGCACGCTGTGTGCAACTGTGGCGCATGTGGCAACTTATTCAGATGCAATGCAACGGGAGC	6.94
Db	646	CTGCGCATTTCTCTGTGCAACGGCTGTGTATCCCTCAGGCTCTGCGCATGTACGCGAGC	7.05
QY	695	TGAGAGGCAACCGCGCTC	7.13
Db	706	AGAAAGCCACAGAGGCTC	7.24

Search completed: April 22, 2005, 18:00:07
Job time : 226.57 secs

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QY 285 GCTTGGCCCGGCAATTGGACAATCTGTTGGCAAGCCTTGCCCTTCTTCAATGTCCTTCTT 344
 |||||
 DB 459 ACTGGGGCC-----GAGAGCCGCGGCGGACCTTACTTGTGCCATGACCTTCTT 512
 |||||
 QY 345 TGGGCTCTCCCTGACACTGCACTCCCTGCGCATGGACATGGAGTGGCTGCTCCCTAGG 404
 |||||
 DB 513 CAGCTGGCCACAGATGCTATGCTCTTGGCATGGCCCTGAGCGCTACTCTTGATCGG 572
 |||||
 QY 405 GCACCCCTTCTTCTACCGACGAGCAATCACTGCGCTGGGCGCACTGCTGGCCCGGT 464
 |||||
 DB 573 GCACCCCTTACTTCTACAGCGCGCGCTCTGGGCTCGGGGCGCTGGCGCTGCTGT 632
 |||||
 QY 465 GGTGAGCGCTTCTCCCTGCTTCTGCGGCTACTCTTCAATGAGCTTCGGAAATTGCT 524
 |||||
 DB 633 CATCTATGCACTCTCCCTGCTCTTCTGCTGCTGCGCTGCTGACTATGGGCACTACGT 692
 |||||
 QY 525 GCAGTACTGCGCCGCGGACCTGCTGCTTATCCAGATGCTCAAGAGAGGCTCGCTGC 584
 |||||
 DB 693 CCAGTACTGCGCCGAGACCTGCTGCTTCACTCCGCAAGGCG----- 734
 |||||
 QY 585 GGTGCTGGGGTACTCTGCTCTACTCTCAAGCTCATGCGCTGCTGCTCGCCACCGT 644
 |||||
 DB 735 ---GACCGCTTACTGCAAGCTGACGCAACCTGCTGCTCTCTCATTTGCTCGGAGCT 791
 |||||
 QY 645 GCTTGCAACTCTGCGCGCATGCGCAACTCTATGCGATGACCGGCG--GCTGCAAGCG 702
 |||||
 DB 792 CGCTGCAACTCTGAGTCTATCTCAACTCATCCGATGCAACGCGCAAGCGGAGAG 851
 |||||
 QY 703 CACCGCGCTCCGCAACGAGGACCTGAGCGGCGCGGCGGAGCGGAGGAGCTCC 762
 |||||
 DB 852 CGGCTGCGAATCTTCCCTGGGCAATGCGCGGCGGCGCGCGGCGCGGAGAGGAGGA 911
 |||||
 QY 763 CCTCAAGCCCC--TGAAGAGCTGATCACTCTGCTGCTGCGCTGATGACCGTGTCT 818
 |||||
 DB 912 AAGGATGTCATGGGAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 971
 |||||
 QY 819 CTTCACTATGTTCTCTGCGCGTAAATGCAATTTG 853
 |||||
 DB 972 CTTGCGCGTGTGCTCTGCTTCAAGATTTTG 1006
 |||||

Search completed: April 22, 2005, 21:25:19
 Job time : 777.996 secs

Db 735 -----GACGGCTTACCTGAGCTGTATACCGCAACCTGCTGCTCTCTCATTTGTCTGGGTCT 791
Qy 645 GCTGTGCAACCTTGGCGCCATGCGCAACCTTATGAGATGACCGGGCG--GCTGCAAGCGG 702
Db 792 CGCTGTGCAACCTTCAAGTGTATCTTCAACCTTCATCCGATGACACCGCGCAAGCGGGAAG 851
Qy 703 CACCGCGGCTCTGCAACGAGGACGTGGCGGACCGCGCGGACGAGGAGGAAGGTCTC 762
Db 852 CGCTGTGCAACCTTCTGCTGAGTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 911
Qy 763 CCTCAAGCCCC--TGAGAGAGCTGATACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 818
Db 912 AAGGCTGTCCATGCGGAGGAGAGACGACCACTCATTTCTCTGCTATATATGACCATAC 971
Qy 819 CTTCATATGTGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 853
Db 972 CTTCGCGCTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1006

RESULT 14

US-10-305-720-1441
; Sequence 1441, Application US/10305720
; Publication No. US20040010136A1
; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice K.; Seilhamer, Jeffrey J.
; TITLE OF INVENTION: Composition for the Detection of Signaling Pathway Gene Expression
; FILE REFERENCE: PA-0002-1 CON
; CURRENT APPLICATION NUMBER: US/10/305,720
; PRIOR FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: 09/016,434
; PRIOR FILING DATE: 1998-01-30
; NUMBER OF SEQ ID NOS: 1490
; SOFTWARE: PERL Program
; SEQ ID NO 1441
; LENGTH: 2372
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Genbank ID No. US20040010136A1 g639719
US-10-305-720-1441

Query Match 17.9%; Score 209.4; DB 17; Length 2372;
Best Local Similarity 59.3%; Pred. No. 9e-51;
Matches 483; Conservative 0; Mismatches 296; Indels 36; Gaps 6;

Qy 48 AGGCACTGCGCGGTGATGCGCGGTGCTCTTCAAGACCGGCTCTGCGCAACCTGCT 107
Db 219 AGCGGAAGCCGACGATACGCTCCGTCATGTTCTGCGCGGGGTCTGCGGAACCTCAT 278
Qy 108 GCGCTTGGGCTGCTGCGCGCTGCGCGCTGCGGT--GGTCTGCGCGGCTCCATGCGC 165
Db 279 AGCACTGGGCTGCTGCGCGCTGCGCGCGGAGAGTGGGTGAGACCGCGCGCAG 338
Qy 166 CCGCTGCC--CTCGCTCTTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 224
Db 339 GAGCTCCCTCTCTTGTTCACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 398
Qy 225 CAGTGTCTCTAAGCCCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 284
Db 399 GACCTGCTCATAGCCGAGTGTACTGCTTGTGAGCGCGGAGACCAAGACCTGTGGG 458
Qy 285 GCTTGGCGCGCATTTGAGCACTGCTGTGTGCAAGCTTGTGCTTCTTATGCTCTTCTT 344
Db 459 ACTGGGCGCC-----GAGAGCGCGGTGACCTTCTTGTGCGCAATGCTTCTT 512
Qy 345 TGGGCTCTCTGCACTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 404
Db 513 CACCTGTGCGACATGCTATGCTTGTGCGCATGCGCTTGTGAGCGCTTCTTCAATCGG 572
Qy 405 GCAACCTTCTTCTTACGAGGAGCATCACTGCGCTGCGGCGCACTGCTGCGCGCT 464

Db 573 GCAACCTTCTTCTTACAGCGCGCGGTCTGCGCTTCGCGGAGCGCTGCGCTGCTGCT 632
Qy 465 GGTGAGCGCTTCTCTCGGTGCTTCTGCGCGGCTTACCTTTCATGAGGCTTGGGAAGTCTG 524
Db 633 CATCTATGAGTGTCTCTGCTGCTTCTGCTGCGCTGCGCTGCTGCTGCTGCTGCTGCTGCT 692
Qy 525 GCAATGAGCGCGCGGACCTGCTGCTTATCCAGATGTGTCAAGAGAGGCTCTGCTGCT 584
Db 693 CCAATGAGCGCGGAGCTGCTGCTTATCCGAGCGCGG----- 734
Qy 585 GGTGCGGAGTCTGCTGCTTCTTCAAGCTTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCT 644
Db 735 -----GACCGCTTACCTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 791
Qy 645 GCTGTGCAACCTTGGCGCATGCGCAACCTTATGAGATGACCGGCG--GCTGCAAGCGG 702
Db 792 CGCTGTGCAACCTTCAAGTGTATCTTCAACCTTATCGCATGACCGCGCAAGCGGGAAG 851
Qy 703 CACCGCGCTCTGCAACGAGGACGTGCGGACCGCGCGGCGGAGGAGGAGGCTCTC 762
Db 852 CGCTGTGCAACCTTCTGCTGAGTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 911
Qy 763 CCTCAAGCCCC--TGAGAGAGCTGATACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 818
Db 912 AAGGCTGTCCATGCGGAGGAGAGACGACCACTCATTTCTCTGCTATATATGACCATAC 971
Qy 819 CTTCATATGTGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 853
Db 972 CTTCGCGCTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1006

RESULT 15

US-10-755-889-91
; Sequence 91, Application US/10755889
; Publication No. US20040171823A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ASSOCIATED WITH THE NF-KB
; FILE REFERENCE: D0284 NP
; CURRENT APPLICATION NUMBER: US/10/755,889
; PRIOR FILING DATE: 2004-01-13
; PRIOR APPLICATION NUMBER: U.S. 60/440,068
; PRIOR FILING DATE: 2003-01-14
; PRIOR APPLICATION NUMBER: U.S. 60/469,757
; PRIOR FILING DATE: 2003-05-12
; NUMBER OF SEQ ID NOS: 823
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 91
; LENGTH: 2372
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-755-889-91

Query Match 17.9%; Score 209.4; DB 18; Length 2372;
Best Local Similarity 59.3%; Pred. No. 9e-51;
Matches 483; Conservative 0; Mismatches 296; Indels 36; Gaps 6;

Qy 48 AGGCACTGCGCGGTGATGCGCGGTGCTCTTCAAGACCGGCTCTGCGCAACCTGCT 107
Db 219 AGCGGAAGCCGACGATACGCTCCGTCATGTTCTGCGCGGGGTCTGCGGAACCTCAT 278
Qy 108 GCGCTTGGGCTGCTGCGCGCTGCGCGCTGCGGT--GGTCTGCGCGGCTCCATGCGC 165
Db 279 AGCACTGGGCTGCTGCGCGCTGCGCGCGGAGAGTGGGTGAGACCGCGCGCAG 338
Qy 225 CAGTGTCTCTAAGCCCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 284
Db 399 GACCTGCTCATAGCCGAGTGTACTGCTTGTGAGCGCGGAGACCAAGACCTGTGGG 458

TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (157) ... (1233)
US-10-352-684A-35

Query Match 17.9%; Score 209.4; DB 17; Length 2372;
Best Local Similarity 59.3%; Pred. No. 9e-51;
Matches 483; Conservative 0; Mismatches 296; Indels 36; Gaps 6;

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QY 48 AGGCACTGGGGGATGATGGGCGGGGCTCTTTCAGACACCGGCTCTCTGGGCAACCTGCT 107
DB 219 AGGCGAAAGCCAGCCATCAGCTCCGTCATGTTCTCGCGGGGTGCTGGGAACTTCAT 278
QY 108 GGCCTTGAGGCTCTGGCGGCTCGGGGCTGGGGT--GGTCTCGCGGCTCCACTGCGC 165
DB 279 AGGACTGGGCTCTGGCGGCGCGGCTGGCGGGGAGTGGGGGTCAGCCCGCGCGAG 338
QY 166 CCGCTGCC-CTGGGCTTCTTACATGCTGTGTGTGTGGCTTACCGGTCACCGACTTGTGG 224
DB 339 GAGCTCCCTCTCTTGTTCACGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 398
QY 225 CAGTCTCTCTTAAAGCCCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 284
DB 399 GACTGCTCTATGAGCCCACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 458
QY 285 GCTTGGCGCCGATGAGCACTGTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 344
DB 459 ACTGGGGGCC-----GAGAGCGCGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 512
QY 345 TGGGCTCTCTGTGACACTGTGACCTCTGTGCGCATGTGCACTGAGTGTGCTTCTTCC 404
DB 513 GACCTGTGCGACATGTCTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 572
QY 405 GCACTCTTCTTACCGAGGCAATCATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 464
DB 573 GCACTCTTCTTACCGAGGCGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 632
QY 465 GGTGAGCGCTTCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 524
DB 633 CATCTATGAGTCTCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 692
QY 525 GCAGTACTGCGCGGACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 584
DB 693 CAGTACTGCGCGGACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 744
QY 585 GGTGTGGGGTACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 644
DB 735 ---GACCGCTTACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 791
QY 645 GGTGTGCACTCTGGGCGGACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 702
DB 792 CGCTGTCAACTTATGATGTCTTCTCACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 851
QY 703 CACCGCGCTCTGTGACAGGGACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 762
DB 852 CCGCTGTGAGCTTCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 911
QY 763 CCTCAAGCCC---TGAAGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 818
DB 912 AAGGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 971
QY 819 CTTCACTATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 853
DB 972 CTTGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1006
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RESULT 13
US-10-366-288-35
Sequence 35, Application US/10366288
Publication No. US2003021628A1
GENERAL INFORMATION:

```
APPLICANT: Powell, Douglas  
APPLICANT: Welch, Nadine S.  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING  
TITLE OF INVENTION: AIDS AND HIV-RELATED DISORDERS USING 1414, 1481, 1553,  
TITLE OF INVENTION: 34021, 1720, 1683, 1552, 1682, 1675, 12825, 9952, 5816,  
TITLE OF INVENTION: 10002, 1611, 1371, 14324, 126, 270, 312, 167, 326, 18926,  
TITLE OF INVENTION: 6747, 1793, 1784 OR 2045 MOLECULES  
FILE REFERENCE: MP102-025P1R0N0NIM  
CURRENT APPLICATION NUMBER: US/10/366,288  
CURRENT FILING DATE: 2003-02-13  
PRIOR APPLICATION NUMBER: 60/357,391  
PRIOR FILING DATE: 2002-02-15  
PRIOR APPLICATION NUMBER: 60/380,249  
PRIOR FILING DATE: 2002-05-13  
PRIOR APPLICATION NUMBER: 60/391,306  
PRIOR FILING DATE: 2002-06-25  
PRIOR APPLICATION NUMBER: 60/406,297  
PRIOR FILING DATE: 2002-08-27  
PRIOR APPLICATION NUMBER: 60/412,007  
PRIOR FILING DATE: 2002-09-19  
PRIOR APPLICATION NUMBER: 60/417,508  
PRIOR FILING DATE: 2002-10-10  
PRIOR APPLICATION NUMBER: 60/432,318  
PRIOR FILING DATE: 2002-12-10  
NUMBER OF SEQ ID NOS: 52  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 35  
LENGTH: 2372  
TYPE: DNA  
ORGANISM: Homo Sapien  
US-10-366-288-35
```

Query Match 17.9%; Score 209.4; DB 17; Length 2372;
Best Local Similarity 59.3%; Pred. No. 9e-51;
Matches 483; Conservative 0; Mismatches 296; Indels 36; Gaps 6;

```
QY 48 AGGCACTGGGGGATGATGGGCGGGGCTCTTTCAGACACCGGCTCTCTGGGCAACCTGCT 107
DB 219 AGGCGAAAGCCAGCCATCAGCTCCGTCATGTTCTCGCGGGGTGCTGGGAACTTCAT 278
QY 108 GGCCTTGAGGCTCTGGCGGCTCGGGGCTGGGGT--GGTCTCGCGGCTCCACTGCGC 165
DB 279 AGGACTGGGCTCTGGCGGCGCGGCTGGCGGGGAGTGGGGGTCAGCCCGCGCGAG 338
QY 166 CCGCTGCC-CTGGGCTTCTTACATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 224
DB 339 GAGCTCCCTCTCTTGTTCACGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 398
QY 225 CAGTCTCTCTTAAAGCCCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 284
DB 399 GACTGCTCTATGAGCCCACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 458
QY 285 GGTGTGGGGTACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 644
DB 735 ---GACCGCTTACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 791
QY 645 GGTGTGCACTCTGGGCGGACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 702
DB 792 CGCTGTCAACTTATGATGTCTTCTCACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 851
QY 703 CACCGCGCTCTGTGACAGGGACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 762
DB 852 CCGCTGTGAGCTTCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 911
QY 763 CCTCAAGCCC---TGAAGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 818
DB 912 AAGGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 971
QY 819 CTTCACTATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 853
DB 972 CTTGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1006
```

Db 723 ---GACCCTTACCTGACAGCTGACGCAACCCCTGCTGCTTCTCATTTGTCGGTGT 789
Qy 645 GCTGTGCAACCTTGGGCGCATGCGCAACCTTATGAGATGCAACCGGCG--GCTGCAAGCG 702
Db 790 CGCTGTGCAACCTTCAAGTATTTCTCAACCTTCACTGACCGCATGCAACCGCGGAAG 849
Qy 703 CACCGCGCTCTCTGCAACGAGGACTGTGCGAGCCGCGCGCGGAGGAGGAGGCTCC 762
Db 850 CCGCTGCGGACCTTCCCTTGGGAGTGGCCGCGGCGGCGCGCGCGGAGAGAGGGA 909
Qy 763 CCTCAGCCCC---TGAGAGAGCTGATGATCACTCTGCTGCTGCTGCTGATGACCTGTCT 818
Db 910 AAGGCTGTCCATGCGGAGAGAGACCGACCACTTCTCTGCTATGATGACATGAC 969
Qy 819 CTTGACTATGTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 853
Db 970 CTTGCGCGTCTGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1004

RESULT 11
US-10-225-567A-290
Sequence 290, Application US/10225567A
Publication No. US20030113798A1
GENERAL INFORMATION:
APPLICANT: Lifespan Biosciences
APPLICANT: Brown, Joseph P.
APPLICANT: Burner, Glenna C.
APPLICANT: Rouher, Christine L.
TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
FILE REFERENCE: 1920-4-4
CURRENT FILING DATE: US/10/225,567A
PRIOR APPLICATION NUMBER: 60/257,144
PRIOR FILING DATE: 2000-12-19
NUMBER OF SEQ ID NOS: 2292
SOFTWARE: Patent in version 3.1
SEQ ID NO 290
LENGTH: 2372
TYPE: DNA
ORGANISM: Homo sapiens
US-10-225-567A-290

Query Match 17.9%; Score 209.4; DB 15; Length 2372;
Best Local Similarity 59.3%; Pred. No. 9e-51;
Matches 483; Conservative 0; Mismatches 296; Indels 36; Gaps 6;
Qy 48 AGCAACTGCGGCGGTGATGCGGCGGCTCTTACAGCAACCGGCTCTGCGCAACCTGCT 107
Db 219 AGCGGAAAGCCCAAGCATGAGTCCGTCATGTTCTGCGCGGCGGCTCTGCGGAACTCAT 278
Qy 108 GCGCCCTGCGGCTGCTGCGGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGG 165
Db 279 AACACTGCGGCTGCTGCGGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGG 338
Qy 166 CCGCTGCGC-CTGCGCTCTTACATGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 224
Db 339 GAGCTTCCCTCTCTTCTTCAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 398
Qy 225 CAGTGTCTCTTACAGCCGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 284
Db 399 GACGTGCTCTATCAGCCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 458
Qy 285 GCTTGGCGCGCATGAGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 344
Db 459 ACTGGGCGCC---GAGAGCGCGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 512
Qy 345 TGAGGCTCTCTGCACTGCACTCTCTGCGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 404
Db 513 CAGCTGCGCAGATGCTATGCTTCTGCGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 572
Qy 405 GAACCTTCTTCTTACAGAGGAGCATCACTGCGCTGCGGCGCACTGCTGCTGCTGCTGCTGCT 464
Db 573 GCACCCCTTCTTCTTACAGAGGCGGCTGCTGCGCTGCGGCGGCGCTGCGCTGCTGCTGCTGCT 632

Qy 445 GGTAGCGCTTCTCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 524
Db 633 CATCTATGAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 692
Qy 525 GCAGTACTGCGCGGCACTGCTGCTTATTCAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 584
Db 693 CAGTACTGCGCGGCACTGCTGCTTATTCAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 734
Qy 585 GGTGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 644
Db 735 ---GACCCTTACCTGCAAGCTGATGCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 791
Qy 645 GCTGTGCAACCTTGGGCGCATGCGCAACCTTATGAGATGCAACCGGCG--GCTGCAAGCG 702
Db 792 CGCTGTGCAACCTTCAAGTATTTCTCAACCTTCACTGACCGCATGCAACCGCGGAAG 851
Qy 703 CACCGCGCTCTCTGCAACGAGGACTGTGCGAGCCGCGCGGAGGAGGAGGAGGCTCC 762
Db 852 CCGCTGCGGACCTTCCCTTGGGAGTGGCCGCGGCGGCGCGCGGAGAGAGGGA 911
Qy 763 CCTCAGCCCC---TGAGAGAGCTGATGATCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 818
Db 912 AAGGCTGTCCATGCGGAGAGAGACCGACCACTTCTCTGCTATGATGACATGAC 971
Qy 819 CTTGACTATGTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 853
Db 972 CTTGCGCGTCTGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1006

RESULT 12
US-10-352-684A-35
Sequence 35, Application US/10352684A
Publication No. US20030215452A1
GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals Inc.
APPLICANT: Carroll, Joseph M.
APPLICANT: Healy, Aileen
APPLICANT: Kelly, Louise M.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
TITLE OF INVENTION: HEMATOLOGICAL DISORDERS USING 131, 148, 199, 12303, 13906,
TITLE OF INVENTION: 15513, 17822, 302, 5677, 194, 14393, 28059, 7366, 12212,
TITLE OF INVENTION: 1981, 261, 12416, 270, 1410, 137, 1871, 13051, 1847, 1849,
TITLE OF INVENTION: 15402, 340, 10217, 837, 1761, 8990 OR 13249 MOLECULES
FILE REFERENCE: MP102-019P1RNDNMIM
CURRENT APPLICATION NUMBER: US/10/352,684A
PRIOR FILING DATE: 2003-01-28
PRIOR APPLICATION NUMBER: US 60/354,333
PRIOR FILING DATE: 2002-02-04
PRIOR APPLICATION NUMBER: US 60/360,258
PRIOR FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: US 60/364,476
PRIOR FILING DATE: 2002-03-15
PRIOR APPLICATION NUMBER: US 60/375,626
PRIOR FILING DATE: 2002-04-26
PRIOR APPLICATION NUMBER: US 60/386,494
PRIOR FILING DATE: 2002-06-06
PRIOR APPLICATION NUMBER: US 60/390,965
PRIOR FILING DATE: 2002-06-24
PRIOR APPLICATION NUMBER: US 60/392,480
PRIOR FILING DATE: 2002-06-28
PRIOR APPLICATION NUMBER: US 60/394,128
PRIOR FILING DATE: 2002-07-03
PRIOR APPLICATION NUMBER: US 60/399,783
PRIOR FILING DATE: 2002-07-31
PRIOR APPLICATION NUMBER: US 60/403,221
PRIOR FILING DATE: 2002-08-13
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 62
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 35
LENGTH: 2372

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? PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/239,431
? PRIOR FILING DATE: EARLIER FILING DATE: 1994-05-05
? NUMBER OF SEQ ID NOS: 10
? SOFTWARE: FastSeq for Windows Version 3.0
? SEQ ID NO 3
? LENGTH: 2296
? TYPE: DNA
? ORGANISM: Homo sapiens
? FEATURE:
? NAME/KEY: CDS
? LOCATION: (157)...(1233)
? GS-10-108-714-3

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Query Match	18.0%	Score 21;	DB 13;	length 2296;
Best Local Similarity	59.4%;	Pred. No. 3e-51;		
Matches 484;	Conservative	0;	Mismatches 295;	Indels 36;
				Gaps 6

QY	48	AGGCAACTCGGCGGGGATGAGGCGGGGGTCTCTTTCAGACCGGCTCTTGGGCAACTCGT	107
Db	219	AGGGGAAAGCCAGCATCAAGCTCCGTATGTTCTCGGCGGGGGTGTCTGGGAACTTCAT	278
QY	108	GGCCCTGGAGCTGCTGGCGCGCTCGGGCTGGGGT--GATGTCGGAGGCTCACTGGCG	165
Db	279	AGCACTGGCGCTGTGGCGCGCCGCTGGCGGGGGAGCTGGGGGTTCACGCGCGGCGCAG	338
QY	166	CCGATGCC--CTCGGCTTCTTACATGCTGGTGTGTGGCTTGAACGGTACACGATTTGCTGG	224
Db	339	GAGCTCCCTCTCTGTGTTCACGTGTGTGTACGAGCTGGGTTCACCGACCTGCTCG	398
QY	225	CAAGTGCCTCTTAAGCCCGGTGTGTGTGCTGCTACGCTCAGAACCGGAGTCTGGGT	284
Db	399	GACCTGCTTATCAGGCCAGTGGTATCTGGCTTTCGATCGCGGAGACAGACCTGTGTGG	458
QY	285	GCTTGGCGCGCGCATTTGGAACACTCGTTGTGCCAAGCTTTGCGCTTCTTCAATGCTCTT	344
Db	459	ACTGGCGGCC-----GAGACCGCGCGCTTGCACCTATCTTTCGTTTCGCTATGACCTTCTT	512
QY	345	TGGGCTCTCTCGACACTGCGAACTCTGGGCCATGGCACTGGAGTGTGGTCTCTCCCTAG	404
Db	513	CAGCTTGGCCAGATGCTCATGCTCTTGGCATGGCCCTGGAGCGCTACCTTCTGCATCG	572
QY	405	GCACCCCTTCTTCTACCGACGGCAATGACCTGTGCGCTGGAGCGCACTGTGTGCCCCGT	464
Db	573	GCACCCCTACTTTCACGACCGCGGCTGTGCGGCTCCGAGGGGCTGGCGTGTGCTGT	632
QY	465	GGTGAAGGCTTCTCTCGGCTTCTTGTGGCGCGTACCTTTCAATGGGCTTGGGAAGTTGT	524
Db	633	CATTTATGCAATCTCCCTGCTCTTCTGTCTGCTGCGCTGTGGACTATGGGCAATGATGT	692
QY	525	GCAGTATCGCCCCGGGCACTGGTGTATTATCCAGATGTGTCAACGAGAGGGGTGCTGTG	584
Db	693	CGAGTACTGCCCCGGGACTGTGTCTTATTCGGGACGGGG-----734	734
QY	585	GGTGTGGGGTACTCTGTGCTTACTCTCAGGCTCATGGAGGCTGTGATCTTGCCACCGT	644
Db	735	---GACGCTTACTCGAGCTGTAGCGCACCTGTGCTGTCTTCATTTCTGTGCTCT	791
QY	645	GCTGTGAACCTCGGGCGCATGGCCCAACTGTATGCAATGACCGGGG--GCTGAGCGG	702
Db	792	CGCTGGAATTCAGTGTCAATTTCAACTATTCGCAATGACCGGCTCAAGCCGGAGAG	851
QY	703	CACCCGCGCTCTTACACGAGGACTGTGCCAGCGCGCGGAGCGGAGGAGGAAGCTGCC	762
Db	852	CCGCTGGGAACTTCCCTGGGCAATGTGGCGGGGGCGCCCGGGGCGCCGAGAGAGGGGA	911
QY	763	CTTCAGCCCC---TGAAGAGCTGATCACTTCTGTGCTGTGGCTGATGACGTGCT	818
Db	912	AAGGTTTCATGCGGAGAGAGACGACCACTATTTCTCTGGCTATCATGACCATAC	971
QY	819	CTTCACATATGTTCTTCGCGCCGTAATTCGATTGG	853
Db	972	CTTGGCGGTGCTCTTGGCTTTCACGATTTTGG	1006

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RESULT 10
US-10-684-206-37
? Sequence 37, Application US/10684206
? Publication No. US20050032725A1
? GENERAL INFORMATION:
? APPLICANT: Rao, Patricia
? APPLICANT: Szymanska, Grazyna
? TITLE OF INVENTION: Molecules Associated
? TITLE OF INVENTION: Cells and Methods of
? FILE REFERENCE: TLM-021CP
? CURRENT APPLICATION NUMBER: US/10/684, 206
? CURRENT FILING DATE: 2003-10-10
? PRIOR APPLICATION NUMBER: US 60/417102
? PRIOR FILING DATE: 2002-10-09
? PRIOR APPLICATION NUMBER: US 60/417103
? PRIOR FILING DATE: 2002-10-09
? PRIOR APPLICATION NUMBER: US 60/417243
? PRIOR FILING DATE: 2002-10-09
? PRIOR APPLICATION NUMBER: US 60/419575
? PRIOR FILING DATE: 2002-10-18
? PRIOR APPLICATION NUMBER: US 60/424777
? PRIOR FILING DATE: 2002-11-08
? NUMBER OF SEQ ID NOS: 40
? SOFTWARE: FastSeq for Windows Version 4.0.
? SEQ ID NO 37
? LENGTH: 2395
? TYPE: DNA
? ORGANISM: Homo sapiens
US-10-684-206-37

```

Query Match	18.0%;	Score 211;	DB 19;	Length 2395;
Best Local Similarity	59.4%;	Pred. No. 3.1e-51;		
Matches 484;	Conservative 0;	Mismatches 295;	Indels 36;	Gaps 6;

QY	48	AGGCAACTCGGCGGGTGAATGGGCGGGGGAGTCTCTTACGACACGGGCTCTCGGGCAACTCTCT	107
Db	217	AGGGGAAAGCCCAAGCCATCAAGTCCCTGTCATTTCTCGGCGGGGGGTGCTGGGGAACTCAT	276
QY	108	GAGCCTTGGGCTGCTGGGCGCGCTCGGGGCTGGGGT--GGTGTGCGGGCGTTCACCTGGCG	165
Db	277	AGCATGGGCGCTGTGGCGCGCCCTGTGGCGGGGGAGACGTGGGGTGTACAGCGCGCGCGCAG	336
QY	166	CCGCTGGC-CTCGGTCTTTACATGCTGGTGTGTGGCTTGAACGGTCAACCACTTGGCTGG	224
Db	337	GAGTCTCCTCTCTTGTTCACGCTGGTGTACCGAGTGTGTTCACGACCTGTCTGG	396
QY	225	CAATGCTCTCTTAAGCCCGGGTGTGCTGGCTGACCTACGCTCAGAAACCGAGATCTTGGGGT	284
Db	397	GACTGCTCTATACGCCCAATGTGTATCTGTCTGTATCCGGGGAAACAGACCTGTGTGG	456
QY	285	GCTTGGCGCCGCAATTGACAACTCTGTTGTGCAAAGCTTGCCTTCTTCAATGTCTCTT	344
Db	457	ACTGGCCGCC-----GAGAGCCCGCGGGTGCACTTACTTCCCTTTCGCATGACCTTCTT	510
QY	345	TGGGCTTCCGCGACATGCAACTCCGAGCATGAGCACTGGAGTGTGGCTCTCCCTTAG	404
Db	511	CAGCTTGGCCACATGTCTCATGTCTTGGCCATGAGCCTTGAAGGCTTACTCTGTGATGG	570
QY	405	GCACCTTTTCTTACCGAGCGACATCACCTTGGCGCTTGGGCGCACTGTATGCCCGGT	464
Db	571	GCACCTCTACTTTCACAGCGCGCGTCTGGCGCTCGGGGGGCTGGCGGTGTGCTGT	630
QY	465	GGTGAAGGCTTCTCTCGGCTTCTTGGCGCTACCTTTATATGGAGCTTGGGAAAGTTGT	524
Db	631	CATTTATGAGTCTCCCTGTCTTCTCTGTCTGTGCTGCTGTGTGAATAATGGCAATAGT	690
QY	525	GCAGTATGCCCCGGGACCTGATGCTTTATCCATATGATGTTCACAGAGAGGGGCTGCTGTG	584
Db	691	CCAGTATGCCCCGGGACCTGTGTCTTCACTCCGCAAGGGG-----	732
QY	585	GGTGTGGGGTACTGTGTCTTACTCCAGCTTCATGGCGGTGTGTGTCTTGGCCACCGT	644


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; SEQ ID NO 24136
; LENGTH: 964
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL355833.1
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.9
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.96
; OTHER INFORMATION: EST HUMAN HIT: A1460323.1, EVALUATE 1.00e-108
; OTHER INFORMATION: SWISSPROT HIT: Q13258, EVALUATE 1.00e-128
; OTHER INFORMATION: NT HIT: U31332.1, EVALUATE 0.00e+00
US-10-029-386-24136

Query Match      70.9%; Score 830; DB 16; Length 964;
Best Local Similarity 100.0%; Pred. No. 5.8e-234;
Matches 830; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 CCGCTGCGCAAGAACACACCTCTGTGAAAAAGGCACTCGGCGGTATATGGGCGGGGTGCT 77
DB 964 CCGCTGCGCAAGAACACACCTCTGTGAAAAAGGCACTCGGCGGTATATGGGCGGGGTGCT 905
QY 78 CTTACAGACACCGGCTCTCTGCGGCAACCTGCTGCGCTGCGGCTCTGCGGCGCT 137
DB 904 CTTACAGACACCGGCTCTCTGCGGCAACCTGCTGCGCTGCGGCTCTGCGGCGCT 845
QY 138 GGGGTGTGTCTGCGGCGCTGCTGCTGCGGCGCTGCGGCGCTGCTGCTGCTGCTG 197
DB 844 GGGGTGTGTCTGCGGCGCTGCTGCTGCGGCGCTGCGGCGCTGCTGCTGCTGCTG 785
QY 198 TGGCTGAGGTACCGACCTGCTGCGGCAAGTGTCTCTAAGCCGCGGTGTGCTGCTG 257
DB 784 TGGCTGAGGTACCGACCTGCTGCGGCAAGTGTCTCTAAGCCGCGGTGTGCTGCTG 725
QY 258 CTAACGCTCAGAAACCGAGTCTGCGGCGCTGCGGCGGCAATTGAGCAACTGTTGAGCA 317
DB 724 CTAACGCTCAGAAACCGAGTCTGCGGCGCTGCGGCGGCAATTGAGCAACTGTTGAGCA 665
QY 318 AGCTTTCGCTTCTTATGTCCTTCTTTGAGCTCTCTGAGCACTGCAACTCTGAGCAAT 377
DB 664 AGCTTTCGCTTCTTATGTCCTTCTTTGAGCTCTCTGAGCACTGCAACTCTGAGCAAT 605
QY 378 GGCACGTGAGTGTGCTCTCTCTAGGAGCACTCTTCTTCTAACCAGCAATACCT 437
DB 604 GGCACGTGAGTGTGCTCTCTCTAGGAGCACTCTTCTTCTAACCAGCAATACCT 545
QY 438 GCGCTGAGGAGCACTGCTGAGGCGCGGTGTGAGCGCTTCTCTGAGCTTCTGCGGCT 497
DB 544 GCGCTGAGGAGCACTGCTGAGGCGCGGTGTGAGCGCTTCTCTGAGCTTCTGCGGCT 485
QY 498 ACCTTTCATGGCTTCTGAGAAAGTTCTGTGAGTACTGCCCCGAGCACTGTGCTTTATCA 557
DB 484 ACCTTTCATGGCTTCTGAGAAAGTTCTGTGAGTACTGCCCCGAGCACTGTGCTTTATCA 425
QY 558 GATGTGTCACAGAGAGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 617
DB 424 GATGTGTCACAGAGAGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 365
QY 618 CATGGGCTGTGTGCTCTGCGCAACCGTGTGTGCAACTCGGAGGCAATGCGCAACTCTTA 677
DB 364 CATGGGCTGTGTGCTCTGCGCAACCGTGTGTGCAACTCGGAGGCAATGCGCAACTCTTA 305
QY 678 TGCAGTGAACCGGAGCGCTGCAAGCGGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCT 737
DB 304 TGCAGTGAACCGGAGCGCTGCAAGCGGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCT 245
QY 738 GCGCGCGAGACGGAGGAGAGCGTCCCTCAAGCCCTGAGAGAGTGAATCACTCTGCT 797
DB 244 GCGCGCGAGACGGAGGAGAGCGTCCCTCAAGCCCTGAGAGAGTGAATCACTCTGCT 185
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; Sequence 10081, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR GI
; FILE REFERENCE: AEOMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 10081
; LENGTH: 597
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO CHR14.3
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.5
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.6
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.3
; OTHER INFORMATION: NT HIT: U31332.1, EVALUATE 0.00e+00
; OTHER INFORMATION: EST HUMAN HIT: A1460323.1, EVALUATE 1.00e-108
; OTHER INFORMATION: SWISSPROT HIT: Q13258, EVALUATE 1.00e-92
US-10-029-386-10081

Query Match      50.4%; Score 590; DB 16; Length 597;
Best Local Similarity 100.0%; Pred. No. 2.9e-163;
Matches 590; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 258 CTAACGCTCAGAAACCGAGTCTGCGGCGCTGCTGCGGCGGCAATTGAGCAACTGTTGAGCA 317
DB 1 CTAACGCTCAGAAACCGAGTCTGCGGCGCTGCTGCGGCGGCAATTGAGCAACTGTTGAGCA 60
QY 318 AGCTTTCGCTTCTTATGTCCTTCTTTGAGCTCTCTGAGCACTGCAACTCTGAGCAAT 377
DB 61 AGCTTTCGCTTCTTATGTCCTTCTTTGAGCTCTCTGAGCACTGCAACTCTGAGCAAT 120
QY 378 GGCACGTGAGTGTGCTCTCTCTAGGAGCACTCTTCTTCTAACCAGCAATACCT 437
DB 121 GGCACGTGAGTGTGCTCTCTCTAGGAGCACTCTTCTTCTAACCAGCAATACCT 180
QY 438 GCGCTGAGGAGCACTGCTGAGGCGCGGTGTGAGCGCTTCTCTGAGCTTCTGCGGCT 497
DB 181 GCGCTGAGGAGCACTGCTGAGGCGCGGTGTGAGCGCTTCTCTGAGCTTCTGCGGCT 240
QY 498 ACCTTTCATGGCTTCTGAGAAAGTTCTGTGAGTACTGCCCCGAGCACTGTGCTTTATCA 557
DB 241 ACCTTTCATGGCTTCTGAGAAAGTTCTGTGAGTACTGCCCCGAGCACTGTGCTTTATCA 300
QY 558 GATGTGTCACAGAGAGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 617
DB 301 GATGTGTCACAGAGAGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
QY 618 CATGGGCTGTGTGCTCTGCGCAACCGTGTGTGCAACTCGGAGGCAATGCGCAACTCTTA 677
DB 361 CATGGGCTGTGTGCTCTGCGCAACCGTGTGTGCAACTCGGAGGCAATGCGCAACTCTTA 420
QY 678 TGCAGTGAACCGGAGCGCTGCAAGCGGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCT 737
DB 421 TGCAGTGAACCGGAGCGCTGCAAGCGGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
QY 738 GCGCGCGAGACGGAGGAGAGCGTCCCTCAAGCCCTGAGAGAGTGAATCACTCTGCT 797
DB 481 GCGCGCGAGACGGAGGAGAGCGTCCCTCAAGCCCTGAGAGAGTGAATCACTCTGCT 540
QY 798 GGTGGGCTGATGATACCGTGTCTTCACTAATGTTCTGCGCCGTAATTG 847
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Db 422 GACAACTGCTGTCGCAAGCTTTCCTTCTTCAATGTCCTTCTTGGAGCTCTCTCCAGCA 481
Qy 361 CTGCAACTCTGCGCATGAGCATGAGAGTGTGCTCTCCCTAGAGGCACTCTTCTTCTAC 420
Db 482 CTGCAACTCTGCGCATGAGCATGAGAGTGTGCTCTCCCTAGAGGCACTCTTCTTCTAC 541
Qy 421 CGACGGCAATCACTCTGCGCTGAGGCGCACTGTGTGCCCCGGTGTGTAGAGCCCTTCTCC 480
Db 542 CGACGGCAATCACTCTGCGCTGAGGCGCACTGTGTGCCCCGGTGTGTAGAGCCCTTCTCC 601
Qy 481 CTGAGCTTTCGCGGCGTCACTTTCATGAGGAGTTCGAGAGTTCGAGTCTGCCCCGGC 540
Db 602 CTGAGCTTTCGCGGCGTCACTTTCATGAGGAGTTCGAGAGTTCGAGTCTGCCCCGGC 661
Qy 541 ACCTGTGCTTTATCCAGATGATCCAGAGAGGCTCGCTGTCTGAGGCTGAGTCTCT 600
Db 662 ACCTGTGCTTTATCCAGATGATCCAGAGAGGCTCGCTGTCTGAGGCTGAGTCTCT 721
Qy 601 GTGCTTACTCTCAAGCTCATGAGGCTGTGTGTCTCGCCACCGTGTGTGCAACTTCGCG 660
Db 722 GTGCTTACTCTCAAGCTCATGAGGCTGTGTGTCTCGCCACCGTGTGTGCAACTTCGCG 781
Qy 661 GCCATGGCAACCTCTATGAGATGCAACGGCGCTGAGAGGCAACCGCGCTCTCTGACC 720
Db 782 GCCATGGCAACCTCTATGAGATGCAACGGCGCTGAGAGGCAACCGCGCTCTCTGACC 841
Qy 721 AGGAGCTGTGCGCAGCGCGCGCGAGAGGAGGAGACCTCTCCCTCAGCCCTGAGAGAG 780
Db 842 AGGAGCTGTGCGCAGCGCGCGCGAGAGGAGGAGACCTCTCCCTCAGCCCTGAGAGAG 901
Qy 781 CTGAGTACCTCTCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 840
Db 902 CTGAGTACCTCTCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 961
Qy 841 GTATATGCAATTTTCTCTGAGTCCCGCCAGACACTGTGAGTGTGTGTGTGTGTGTGTGT 900
Db 962 GTATAT-----TATCGCGCTTACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 967
Qy 901 AAACATTTTCAGTGTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 960
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Qy 1081 ATTTGGAATTTTTCACAGAGATTTTCAATTTAGAGCTTTAGGATTCAGAGAGCGGTGAG 1140
Db 1111 ATTTGGAATTTTTCACAGAGATTTTCAATTTAGAGCTTTAGGATTCAGAGAGCGGTGAG 1170
Qy 1141 CAATTCACATCAATGAGATTCAGATCTGTGA 1171
Db 1171 CAATTCACATCAATGAGATTCAGATCTGTGA 1201

RESULT 3
US-10-128-558-263
; Sequence 263, Application US/10128558
; Publication No. US20040219521A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wang, Zhiwei
; APPLICANT: Weng, Gezhi
; APPLICANT: Boyle, Bryan J
; APPLICANT: Drmanac, Radoje T
; TITLE OF INVENTION: Novel Nucleic Acids and
; FILE REFERENCE: 812A
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; CURRENT APPLICATION NUMBER: US/10/128,558
; CURRENT FILING DATE: 2002-04-22
; PRIOR APPLICATION NUMBER: US 60/339,453
; PRIOR FILING DATE: 2001-12-11
; PRIOR APPLICATION NUMBER: US 09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: PCT/US00/35017
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: PCT/US01/02623
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: US 09/496,914
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: US 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: PCT/US01/03800
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: US 09/515,126
; PRIOR FILING DATE: 2000-02-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 412
; SOFTWARE: PC_FU_genes Version 6.0
; SEQ ID NO 263
; LENGTH: 1253
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-128-558-263
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Query Match 83.6%; Score 979; DB 18; Length 1253;
Best Local Similarity 92.2%; Pred. No. 7.3e-278;
Matches 1080; Conservative 0; Mismatches 0; Indels 91; Gaps 1;
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Qy 1 ATGAGTTCGCGCTTCTTACCGCTCCAGAGACCACTCTGTGAGAGAGAGAGAGAGAGAGAG 60
Db 122 ATGAGTTCGCGCTTCTTACCGCTCCAGAGACCACTCTGTGAGAGAGAGAGAGAGAGAG 181
Qy 61 GTATATGCGCGGAGTGTCTTTCAGACACCGGCTCTGTGAGAGAGAGAGAGAGAGAGAG 120
Db 182 GTATATGCGCGGAGTGTCTTTCAGACACCGGCTCTGTGAGAGAGAGAGAGAGAGAGAG 241
Qy 121 CTGAGCGCGCTCGGAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 180
Db 242 CTGAGCGCGCTCGGAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 301
Qy 181 TTCTATAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 240
Db 302 TTCTATAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 361
Qy 241 CCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 300
Db 362 CCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 421
Qy 301 GACAACTGTTGTGCAAGGCTTGTGCTTCTTATGATGCTTCTTGTGAGCTCTCTGACA 360
Db 422 GACAACTGTTGTGCAAGGCTTGTGCTTCTTATGATGCTTCTTGTGAGCTCTCTGACA 481
Qy 361 CTGCAACTCTGCGCATGAGCATGAGAGTGTGCTCTCCCTAGAGGCACTCTTCTTCTAC 420
Db 482 CTGCAACTCTGCGCATGAGCATGAGAGTGTGCTCTCCCTAGAGGCACTCTTCTTCTAC 541
Qy 421 CGACGGCAATCACTCTGCGCTGAGGCGCACTGTGTGCCCCGGTGTGTAGAGCCCTTCTCC 480
Db 542 CGACGGCAATCACTCTGCGCTGAGGCGCACTGTGTGCCCCGGTGTGTAGAGCCCTTCTCC 601
Qy 481 CTGAGCTTTCGCGGCGTCACTTTCATGAGGAGTTCGAGAGTTCGAGTCTGCCCCGGC 540
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Qy 541 ACCTGTGCTTTATCCAGATGATCCAGAGAGGCTCGCTGTGTGTGTGTGTGTGTGTGTGT 600
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PRIOR FILING DATE: 2000-02-28
 Remaining Prior Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 412
 SOFTWARE: PL_FL_genes Version 6.0
 SEQ ID NO 24
 LENGTH: 1505
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (231) ..(1505)
 US-10-128-558-24

Query Match 84.8%; Score 992.8; DB 18; Length 1505;
 Best Local Similarity 92.3%; Pred. No. 6,7e-282;

Matches 1069; Conservative 0; Mismatches 57; Indels 32; Gaps 1;

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 DB 291 GTGATGGCGGGGCTCTTCAAGCACCGGCTCTGCGCAACTGCTGGCCCTGGGGCTG 350
 QY 121 CTGGCGCGCTCGGGGCTGGGGTGTGTCTCGCGGCTCCACTGGCCCGCTGGCTGTG 180
 DB 351 CTGGCGCGCTCGGGGCTGGGGTGTGTCTCGCGGCTCCACTGGCCCGCTGGCTGTG 410
 QY 181 TTCTACATCTGGTGTGTGGCTGACGGTCAACCGATTGTGGGCAAGTGCCTCTAACG 240
 DB 411 TTCTACATCTGGTGTGTGGCTGACGGTCAACCGATTGTGGGCAAGTGCCTCTAACG 470
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 DB 471 CCGGTGTCTGGCTGCTCAAGCTCAAGAACCGAGTCTGGGGTCTTGGCCCGCATTTG 530
 QY 301 GACAACTCGTGTGGCAAGCTTGGCTTCTATGTCCTTTTGGGGCTCTCTGAGA 360
 DB 531 GACAACTCGTGTGGCAAGCTTGGCTTCTATGTCCTTTTGGGGCTCTCTGAGA 590
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 DB 361 CTGCAACTCTGCGCAGTGAAGTGTGCTCTCTTGAAGGCAACCTTCTCTTAC 420
 QY 591 CTGCAACTCTGCGCAGTGAAGTGTGCTCTCTTGAAGGCAACCTTCTCTTAC 650
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 QY 651 CGACGGCACATCACTCGCGCTGGGCGCACTGTGGCCCGGTGTGAAGCGCTTCTCC 710
 DB 481 CTGGCTTTTGGCGGCTACTCTTCAAGGGCTTGGGAAAGTCTGTGAAGTACCGCGGCG 540
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 DB 541 ACTGTGTCTTATCCAGATGTCCAGAGAGGGCTCGTCTGCTGGTGTGGGATCTCT 600
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 DB 601 GTGCTTACTCCAGCTCATGCGCTGTGTCTTCCGCAACGCTGTGTGCAACTCTGGG 660
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QY 841 GTAATTG-----CATTTGCTCGAGTCCCCG 868
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 QY 1049 CCTTGAATTTTATCATTTTCAGATCTCCAGTATTTGGAAATTTTTCACAAATTTT 1108
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RESULT 2 US-10-276-774-1020

; Sequence 1020; Application US/10276774
 ; Publication No. US20040053245A1
 ; GENERAL INFORMATION:

; APPLICANT: Hyseq, Inc.

; APPLICANT: Tang, Y. Tom et al

; TITLE OF INVENTION: No. US20040053245A1el Nucleic Acids and Polypeptides

; FILE REFERENCE: 212/2-030

; CURRENT APPLICATION NUMBER: US/10/276,774

; PRIOR FILING DATE: 2002-11-18

; PRIOR APPLICATION NUMBER: 09/560,875

; PRIOR FILING DATE: 2000-04-27

; PRIOR APPLICATION NUMBER: 09/496,914

; NUMBER OF SEQ ID NOS: 2700

; SOFTWARE: Custom

; SEQ ID NO 1020

; LENGTH: 1253

; TYPE: DNA

; ORGANISM: Homo sapiens

Query Match 83.6%; Score 979; DB 17; Length 1253;
 Best Local Similarity 92.2%; Pred. No. 7.3e-278;

Matches 1080; Conservative 0; Mismatches 0; Indels 91; Gaps 1;

QY 1 ATGAAGTCGCGCTTCTACCGCTGCGCAGAAACACCACTCTGTGAAAAAGCAACTCGGCG 60
 DB 122 ATGAAGTCGCGCTTCTACCGCTGCGCAGAAACACCACTCTGTGAAAAAGCAACTCGGCG 181
 QY 61 GTGATGGCGGGGCTCTTTCAGACCGGCTCTGGGCAACCTGCGCCCTGGGGCTG 120
 DB 182 GTGATGGCGGGGCTCTTTCAGACCGGCTCTGGGCAACCTGCGCCCTGGGGCTG 241
 QY 121 CTGGCGCGCTCGGGGCTGGGGTGTGTCTGCGGCGCTCACTGCGCGCTGCTCGGTC 180
 DB 242 CTGGCGCGCTCGGGGCTGGGGTGTGTCTGCGGCGCTCACTGCGCGCTGCTCGGTC 301
 QY 181 TTCTACATCTGTGTGTGGCTTGAACGCTCACTGCTGTGGGCAAGTGTCTCTAACG 240
 DB 302 TTCTACATCTGTGTGTGGCTTGAACGCTCACTGCTGTGGGCAAGTGTCTCTAACG 361
 QY 241 CCGGTGTGTGGCTGTGGCTCAAGACCGAGTGTGGGGTGTGGCGCGCGGATTTG 300
 DB 362 CCGGTGTGTGGCTGTGGCTCAAGACCGAGTGTGGGGTGTGGCGCGCGGATTTG 421
 QY 301 GACAACTCGTGTGGCAAGCTTTCATGATCTCTTCTTGGGCTCTCTGAGCA 360

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 22, 2005, 15:32:17 ; Search time 771.996 Seconds
(without alignments)
9208.852 Million cell updates/sec

Title: US-10-689-861-1

Perfect score: 1171

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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 5633728 segs, 3035525691 residues

11267456

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	992.8	84.8	1505	US-10-128-558-24	Sequence 24, Appl
2	979	83.6	1253	US-10-276-774-1020	Sequence 1020, Ap
3	979	83.6	1253	US-10-128-558-263	Sequence 263, App
4	847	72.3	1216	US-10-305-720-1474	Sequence 1474, App
5	830	70.9	964	US-10-029-386-24136	Sequence 24136, A
6	590	50.4	597	US-10-029-386-10081	Sequence 10081, A
7	371	31.7	371	US-10-029-386-23781	Sequence 23781, A
8	335	28.6	495	US-10-225-567A-286	Sequence 286, App
9	211	18.0	2396	US-10-108-714-3	Sequence 3, Appl
10	211	18.0	2395	US-10-684-206-37	Sequence 37, Appl
11	209.4	17.9	2372	US-10-225-567A-290	Sequence 290, App

12	209.4	17.9	2372	17	US-10-352-684A-35	Sequence 35, Appl
13	209.4	17.9	2372	17	US-10-366-286-35	Sequence 35, Appl
14	209.4	17.9	2372	17	US-10-305-720-1441	Sequence 1441, Ap
15	209.4	17.9	2372	18	US-10-755-889-91	Sequence 91, Appl
16	209.4	17.9	6446	17	US-10-139-686A-2	Sequence 2, Appl
17	208	17.5	501	16	US-10-029-386-10432	Sequence 10432, A
18	204.6	17.5	1077	16	US-09-825-509-558	Sequence 558, App
19	204.6	17.5	1077	19	US-10-925-095-558	Sequence 558, App
20	203.4	17.4	2824	17	US-10-108-260A-1464	Sequence 1464, Ap
21	201.8	17.2	1417	17	US-10-305-720-1403	Sequence 1403, Ap
22	201.8	17.2	1862	15	US-10-225-567A-284	Sequence 284, App
23	186.4	15.9	1242	18	US-10-349-528-3	Sequence 3, Appl
24	185	15.8	1360	9	US-09-917-800A-1482	Sequence 1482, Ap
25	108.8	9.3	1209	18	US-10-472-362-2	Sequence 2, Appl
26	108.8	9.3	1209	19	US-10-681-029-7	Sequence 7, Appl
27	108.8	9.3	3318	9	US-09-781-311-1	Sequence 1, Appl
28	107.2	9.2	1140	19	US-10-681-029-1	Sequence 1, Appl
29	107.2	9.2	1309	10	US-09-825-509-556	Sequence 556, App
30	107.2	9.2	1209	19	US-10-925-095-556	Sequence 556, App
31	107.2	9.2	1376	15	US-10-225-567A-288	Sequence 288, App
32	107.2	9.2	1376	17	US-10-305-720-1361	Sequence 1361, App
33	107.2	9.2	1376	18	US-10-473-974-179	Sequence 179, App
34	107.2	9.2	1473	14	US-10-243-501-1	Sequence 1, Appl
35	107.2	9.2	1473	14	US-10-243-501-2	Sequence 2, Appl
36	103.4	8.8	1473	14	US-10-243-351-1	Sequence 1, Appl
37	101.2	8.6	1467	10	US-09-825-509-560	Sequence 560, App
38	101.2	8.6	1467	19	US-10-925-095-560	Sequence 560, App
39	101.2	8.6	1554	15	US-10-320-351-1	Sequence 1, Appl
40	101.2	8.6	1554	15	US-10-320-351-2	Sequence 2, Appl
41	101.2	8.6	1958	15	US-10-225-567A-295	Sequence 295, App
42	101.2	8.6	1958	17	US-10-295-027-1109	Sequence 1109, App
43	101.2	8.6	1958	17	US-10-305-720-1380	Sequence 1380, App
44	101.2	8.6	1958	18	US-10-755-889-169	Sequence 169, App
45	101.2	8.6	1958	18	US-10-783-528-38	Sequence 38, Appl

ALIGNMENTS

RESULT 1
US-10-128-558-24
Sequence 24, Application US/10128558
Publication No. US20040219551A1
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Wang, Zhiwei
APPLICANT: Weng, Gezhi
APPLICANT: Boyle, Bryan J
APPLICANT: Drmanac, Radjoje T
TITLE OF INVENTION: Novel Nucleic Acids and
FILE REFERENCE: 812A
CURRENT APPLICATION NUMBER: US/10/128,558
CURRENT FILING DATE: 2002-04-22
PRIOR APPLICATION NUMBER: US 60/339,453
PRIOR FILING DATE: 2001-12-11
PRIOR APPLICATION NUMBER: US 09/488,725
PRIOR FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: US 09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: PCT/US00/35017
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: US 09/491,404
PRIOR FILING DATE: 2000-01-25
PRIOR APPLICATION NUMBER: PCT/US01/02623
PRIOR FILING DATE: 2001-01-25
PRIOR APPLICATION NUMBER: US 09/496,914
PRIOR FILING DATE: 2000-02-03
PRIOR APPLICATION NUMBER: US 09/560,875
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: PCT/US01/03800
PRIOR FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: US 09/515,126

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 22, 2005, 10:55:17 ; Search time 4391.64 Seconds

(without alignments)
10149.570 Million cell updates/sec

Title: US-10-689-861-1

Perfect score: 1171

Sequence: 1 atgaagtcgcccgttctaccg.....acatggaatccagtcgtgta 1171

Scoring table: IDENTITY_NUC

Gapop 10_0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*

1: gb_est1: *
2: gb_est2: *
3: gb_hic: *
4: gb_est3: *
5: gb_est4: *
6: gb_est5: *
7: gb_est6: *
8: gb_gsa1: *
9: gb_gsa2: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	1142.6	97.6	1229	6	CD013871	CD013871 90116594
2	654	55.8	1053	5	BQ068035	BQ068035 AGENCOURT
3	554.4	47.3	3190	3	AK032488	AK032488 Mus muscu
4	393	33.6	495	7	CR747669	CR747669 CR747669
C 5	375.4	32.1	1996	3	AK016503	AK016503 Mus muscu
C 6	361.8	30.9	948	6	BY716183	BY716183 BY716183
C 7	333	28.4	486	1	A1460323	A1460323 ac95a01.x
8	333	28.4	520	1	AA105532	AA105532 mc57a09.r
9	313	26.7	632	2	BB622854	BB622854 BB622854
C 10	212	26.6	589	8	AZ291373	AZ291373 RPCI-23-1
11	211	18.0	1077	9	AY410679	AY410679 Homo sapi
12	203.4	17.4	1038	3	BC017857	BC017857 Homo sapi
C 13	203.4	17.4	2020	3	CR601077	CR601077 full1-1eng
14	202.4	17.3	565	8	B2120059	B2120059 CH230-523
C 15	192.6	16.4	1032	5	BM925026	BM925026 AGENCOURT
16	188	16.1	652	5	BX498371	BX498371 DKP2p779E
C 17	186.2	15.9	658	6	BY724253	BY724253 BY724253
18	185.6	15.8	765	1	AU132613	AU132613 AU132613
19	183.6	15.7	2509	3	AK086904	AK086904 Mus muscu
C 20	182.6	15.6	2653	3	AK036474	AK036474 Mus muscu
21	181.4	15.5	1077	9	AY410681	AY410681 Mus muscu
C 22	181.4	15.5	2619	3	AK054132	AK054132 Mus muscu
23	181.2	15.5	615	5	BP381970	BP381970 BP381970
C 24	176.4	15.1	571	8	AZ357037	AZ357037 1M0098023

25	170.6	14.6	1062	5	BM925058	BM925058 AGENCOURT
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27	166.2	14.2	635	7	CF131282	CF131282 UI-HF-FQO
28	162.6	13.9	603	7	CK820125	CK820125 if31906.y
29	161.8	13.8	1019	1	AL552370	AL552370 AL552370
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C 31	154.2	13.2	577	4	BM354213	BM354213 if31906.y
32	150.2	12.8	562	6	CB609359	CB609359 AMGNNUC:N
33	150.2	12.8	573	4	BM273260	BM273260 if28C08.y
34	144.2	12.3	655	2	BB625385	BB625385 BB625385
35	139	11.9	771	4	BG919027	BG919027 602816763
36	132	11.3	479	2	AW240093	AW240093 pcr1c.pko
37	130.4	11.1	364	4	BM386608	BM386608 ha97906.g
38	125.4	10.7	584	8	BH341188	BH341188 CH230-S1K
39	125.4	10.7	639	8	BH315818	BH315818 CH230-S0L
40	125	10.7	482	5	BM986638	BM986638 EST594232
41	121.6	10.4	520	1	AA818108	AA818108 UI-R-A0-a
42	121.6	10.4	653	7	CN484094	CN484094 hw42a07.y
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45	112.6	9.6	624	8	BH335976	BH335976 CH230-S0N

ALIGNMENTS

RESULT 1
CD013871
LOCUS CD013871 1229 bp mRNA linear EST 21-OCT-2003
DEFINITION 90116594 Single gene library Homo sapiens cDNA, mRNA sequence.
ACCESSION CD013871
VERSION CD013871.1 GI:37777401
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1229)
Jin, P., Fu, G.K., Wilson, A.D., Yang, J., Chien, D., Hawkins, P.R.,
Au-Young, J. and Stuve, L.L.
PCR isolation and cloning of novel splice variant mRNAs from known
drug target genes
Genomics 83 (4), 566-571 (2004)
CONTACT: Jin, P.
Incyte Corporation
3160 Porter Drive, Palo Alto, CA 94304, USA
Tel: 650 621 8639
Fax: 650 621 8965
Email: pjin@incyte.com.

FEATURES

source
Location/Qualifiers
1..1229
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="Single gene library"
/note="Vector: pDrive Cloning Vector; RT-PCR was performed
using gene-specific primers flanking the open-reading
frame. PCR products were subcloned into pDrive Cloning
Vector and sequenced completely using M13 forward and
reverse primers. Sequencing gaps were closed by
re-sequencing using primers flanking the gapped areas."

ORIGIN

Query Match: 97.6%; Score 1142.6; DB 6; Length 1229;
Best Local Similarity 99.5%; Pred. No. 6.1e-271;
Matches 1167; Conservative 0; Mismatches 4; Indels 2; Gaps 2;
Qy 1 ATGAAGTCGCGGTTCTACCGTGCAGAACACCACTCTGTGGAAAGGCAACTCGGCG 60
Db 4 ATGAAGTCGCGGTTCTACCGTGCAGAACACCACTCTGTGGAAAGGCAACTCGGCG 63
Qy 61 GTGATGGCGGGGTCTCTTTCAGACCGGCTCTCTGGCAACCTCTGCGCCCTGGGGCTG 120

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Db 64 GTGATGGCGGGTGTCTTTACAGCACCGGCTCTCTGGGCAACCTGCTGGCCCTGGGGCTG 123
Qy 121 CTGGCGCGCTCGGGCTGGGGTGGTGTCTCGCGCGTCCACTGCGCGCCGCTGCCCTCGGTG 180
Db 124 CTGGCGCGCTCGGGGCTGGGGTGGTGTCTCGCGCGTCCACTGCGCGCCGCTGCCCTCGGTG 183
Qy 181 TTCTACATGCTGGTGTGGCGCTGACCGGTACCGACTTGTCTGGCAAGTGCCTCTTAAGC 240
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Qy 361 CTGCAACTCTCTGGCCATGGCACTGGAGTGTCTGGCTCTCTCTAGGCAACCTTCTTCTAC 420
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Qy 421 CGACGGCAATCACCTGCGCTGGCGGCACTGGTGGCCCGGTGGTGGAGCCCTTCTCC 480
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Qy 841 GTAATTGCATTTGTTCTGGAGTCCCGCAGACACCTGGAGTAGGTGAGGCTTGAGG 900
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Qy 961 TAAAGGATGTCAAGGAGAAAAACAGGACCTCTGAAGAAGCAGA - AGACCTCCAGCCTTGC 1019
Db 964 TAAAGGATGTCAAGGAGAAAAACAGGACCTCTGAAGAACAGAGAGACCTCCGAGCCTTGC 1023
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Qy 1080 TATTTTCGGATATTTTTCACAAAG - TTTTTCATTAGACCTCTTAGGTACAGGAGCCGCTGC 1138
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Qy 1139 AGCAATTCACATPAACATGAATCCAGTCTGTGA 1171
Db 1144 AGCAATTCACATPAACATGAATCCAGTCTGTGA 1176
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RESULT 2

BQ068035

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BQ068035 1053 bp mRNA linear EST 02-APR-2002
AGENCOURT 6792268 NIH_MGC_121 Homo sapiens cDNA clone IMAGE:5769056
5' mRNA sequence.

BQ068035
BQ068035.1 GI:19897081
EST.

Homo sapiens (human)

Homo sapiens

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1053)

NIH-MGC http://mgi.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Life Technologies, Inc.

cDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM12829 row: o column: 09

High quality sequence stop: 645.

Location/Qualifiers

FEATURES

source

1..1053

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/clones="IMAGE:5769056"

/lab_host="DH10B"

/clone_lib="NIH_MGC_121"

/note="Organ: brain; Vector: pCMV-SPORT6; Site 1: NotI;

Site 2: EcoRV (destroyed); RNA source anonymous pool of 3

fetal brains, female age 20 weeks, female age 24 weeks,

and male age 26 weeks. Library is oligo-dT primed and

directionally cloned (EcoRV site is destroyed upon

cloning). Average insert size 1.7 kb, insert size range

0.7-3.5 kb. Library is normalized and enriched for

full-length clones and was constructed by C. Gruber

(Invitrogen). Research Genetics tracking code 017. Note:

this is a NIH_MGC Library."

ORIGIN

Query Match 55.8%; Score 654; DB 5; Length 1053;

Best Local Similarity 96.0%; Pred. No. 2.5e-150;

Matches 714; Conservative 0; Mismatches 25; Indels 5; Gaps 4;

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Db 122 ATGAAGTCGCGGTTTACCGCTGCCAGAACACCACTCTGTGGAAAAAGGCAACTCGGCG 181

Qy 61 GTGATGGCGGGGTCTCTTTCAGCAACCGGCTCTCTGGGCAACCTGCTGGCCCTGGGGCTG 120

Db 182 GTGATGGCGGGGTCTCTTTCAGCAACCGGCTCTCTGGGCAACCTGCTGGCCCTGGGGCTG 241

Qy 121 CTGGCGCGCTCGGGGCTGGGGTGGTGTCTCGGGGCTCCACTGCGCGCCGCTCGGCTCGGTC 180

Db 242 CTGGCGCGCTCGGGGCTGGGGTGGTGTCTCGGGGCTCCACTGCGCGCCGCTCGGCTCGGTC 301

Qy 181 TTCTACATGCTGTGTGGCTTGAACGCTTACCGACTTCTGCTGGCAAGTGCCTCTTAAGC 240

Db 302 TTCTACATGCTGTGTGGCTTGAACGCTTACCGACTTCTGCTGGCAAGTGCCTCTTAAGC 361

Qy 241 CCGGTGTGTGGCTGGCTTACCTAGCTCAGAACCGGAGTGTGGGGTGTGGCCCGCCGATTTG 300

Db 362 CCGGTGTGTGGCTGGCTTACCTAGCTCAGAACCGGAGTGTGGGGTGTGGCCCGCCGATTTG 421

Query Match		47.3%; Score 554.4; DB 3; Length 3190;
Best Local Similarity		71.1%; Pred. No. 1.3e-125;
Matches 829; Conservative		0; Mismatches 231; Indels 106; Gaps 3;
QY	12	GTCTACCGCTCCGAGAACACCACTCTGTGTGAAAGGCAAACTCGGGGGTATGGGGG 71
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QY	72	GGTGTCTTTCAGCACCGGCTCTCGGCAACCTGTGGCCCTGGGGCTGCTGGCGGCTC 131
DB	192	TGTGTCTTTCGGTGGGGCTTCTGGGCAATCTTCTGGGCTGGGTGCTGCTGGCGGCTC 251
QY	132	GGGGTGGGGTGGTGTCTCGCGCGCTCCACTGGCGCGCTCGCTCGCTCTTCTACATGCT 191
DB	252	GGGACTGGGGTCTTGGCGGCGAGGCGCACTACACCGCGCGCTCGCTCTTATGTGCT 311
QY	192	GGTGTGGCTTGACGGTCAACGACTTGTGTGGCAAGTGCCTCTTAAGCCCGGTGGTGT 251
DB	312	CGTGTGGCTTGACGGTCAACGACTTGTGTGGCAATGTCTGTATCAGCCCGATGGTCT 371
QY	252	GGCTGCTACGCTCAGAACCGAGTCTGGGGTGTGTGGCCCGCATTTGGACAACCTGTT 311
DB	372	GGCTGCTACGCGCAAAACAGAGCTAAAGAACTGTGCTGCTCAGGCAATCAGTT 431
QY	312	GTGCCAAGCTTTCGCTCTTCTCATGTCTTCTTTGGGCTCTCTCGCACTGCAACTCTCT 371
DB	432	ATGCGAAAGTTTTCGCTCTCTGATGTCTTCTTTGGGCTAGCTCGACTTACAGTGT 491
QY	372	GGCCATGGCACTTGGAGTGTGCTCTCTTACAGGCACTTCTTCTTACCGAGCGAAT 431
DB	492	GGCTATGGCGGTGGAGTGTGCTGTCTGTGGACACCCCTTCTTCTACCAAGGCACT 551
QY	432	CACCTTGGCGCTGGGGCACTGGTGGCCCGGTGTGAGCGCTTCTCCCTGGCTTCTG 491
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QY	492	CGCGCTACCTTTTCATGGGCTTCGGGAAGTTCGTGCAGTACTCCCGCGGCACCTGGTGT 551
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DB	967	----- 966
QY	912	GTGTGTCTCTCTCTTCTCCCAAGTATCGCGCTTACTATGAGGCAATTTAAGATGCA 971
DB	967	-----TATGTGCGCTACTATGAGGCTTTAACTTG--- 997
QY	972	AGGAGAAACAGGACCTCTGAAGAGCAGAGAGCTCCGAGCCCTTGGATTTCTATCTG 1031
DB	998	-----AGAACAAAGCTGAAGGAGACTCAGAGAGCTCCAGAGCTTGGCTTTCTGTCTG 1051
QY	1032	TGATTTCAATTGTGGACCTTGGATTTTATCATTTTTCAGATCTCCAGTATTTCCGATAT 1091
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Best Local Similarity		100.0%; Pred. No. 5.9e-86;
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QY	1	ATGAAGTCGGCTTCTACCGTCCAGAACACCCTCTGTGAAAAAGGCAACTCGGGC 60
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/note="Organ: brain; Vector: pCMV-SPORT6; Site: 1: NotI; Site 2: EcoRV (destroyed); RNA source anonymous pool of 3 fetal brains, female age 20 weeks, female age 24 weeks, and male age 26 weeks. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.7 kb, insert size range 0.7-3.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 017. Note: this is a NIH_MGC Library."		
ORIGIN		
Query Match		33.6%; Score 393; DB 7; Length 495;
Best Local Similarity		100.0%; Pred. No. 5.9e-86;
Matches 393; Conservative		0; Mismatches 0; Indels 0; Gaps 0;
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QY	61	GTGATGGCGGGGTGCTCTTTCAGCACCGGCTCTCTGGGCAACCTGCTGGCGCTG 120


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Db 400 CGTGTGTGGCTTGAACGGTCAACGAGTCTGCTGGGCAAGTGTCTGATCAGCCCGATGTCT 341
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QY 252 GGCTGCTACGCTCAGAACCGGAGTCTGGGGGTGCTTGGCCCGCATTTGGACAACTCGT 311
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Db 340 GGCTGCTACGCGCAAAACAGAGCTTAAGAACTGCTGCTGCTCAGGCAATCAGTT 281
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Db 280 ATGCGAAACGTTTCGCTTCTCATGTCCTTCTTTGGGCTAGCTGACCTTACAGCTGT 221
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QY 372 GSCCATGGACATGGAGTGTGCTCTCCCTAGGACACCTTCTTCTACCGAGCGACAT 431
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Db 220 GGTATAGGCGGTGGAGTGTGCTGTCTTGGGACACCTTCTTCTACCAAGGACAGT 161
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QY 432 CACCTTGGCCCTGGGCGCACTGGTGGCCCGGCTGGTGGAGCGCTTCTCCTCGCTTCTG 491
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Db 160 CACCTTGGCCCGGAGTGTGCTGGTGGCACGGTGGTGGCGGCTTCTGCTTGGCTTCTG 101
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QY 492 CGCGTACCTTTCATGGGCTTGGGAAGTTCGTGCAAGTACTGCCCGGCACTGTGTGTT 551
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Db 100 TCGGCTCCCTTGTGCTTGGTGGTGGGAAGTTCGTGCAAGTACTGCCAGGCACTGTGT 41
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QY 552 TATCCAGATGTCACAGGAGGCTGCTGTGGTG 588
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RESULT 7

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LOCUS AI460323/c 486 bp mRNA linear EST 09-MAR-1999
DEFINITION a095a01.x1 Schiller meningioma Homo sapiens cDNA clone
IMAGE:1953576 3' similar to SW:PD2R_HUMAN Q13258 PROTAGLANDIN D2
RECEPTOR ;, mRNA sequence.

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ACCESSION AI460323
VERSION AI460323.1 GI:4313204
KEYWORDS EST.
SOURCE Homo sapiens (human)

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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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REFERENCE 1 (bases 1 to 486)
AUTHORS Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M.,
Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F.,
Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.

```

```

WashU-NCI human EST Project
Unpublished (1997)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.edu
This clone is available royalty-free through LNL ; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
Possible reversed clone: polyt not found
Seq primer: -40UP from Gibco
High quality sequence stop: 423.
Location/Qualifiers
i. .486
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1953576"
/sex="female"
/tissue_type="meningioma"

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```

FEATURES source

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```

/dev_stage="72 years"
/lab_host="SOUR"
/clone_lib="Schiller meningioma"

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```

/Note="Organ: brain; Vector: pBluescript SK- (Stratagene);
Site 1: EcoRI; Site 2: XhoI; Double-stranded cDNA was
prepared from human_meningioma using primer
5'-GAGAGAGAGAGAGAGAACTAGTCTGAGT(18)-3'. An EcoRI
adaptor was used on the 5' end of the cDNA as follows:
5'-AATTCGACGAG-3'. The library was size-selected and
went through one round of amplification. Average insert
size is 1.7 kb, with a range from 0.4-12 kb. Tumor
identification by consensus pathology. This library was
constructed by Dr. Martin Schiller (Johns Hopkins
University)."
```

ORIGIN

```

Query Match 28.4%; Score 333; DB 1; Length 486;
Best Local Similarity 82.7%; Pred. No. 3.8e-71;
Matches 434; Conservative 0; Mismatches 0; Indels 91; Gaps 1;

QY 647 TGTGCAACCTCGGCCCATGCGCAACCTCTATGCGATGCACCGCGGCTGCGAGCGCAC 706
    |||||
Db 486 TGTGCAACCTCGGCCCATGCGCAACCTCTATGCGATGCACCGCGGCTGCGAGCGCAC 427
    |||||
QY 707 CGCGTCTCTGCACAGGAGTGTGCGAGCCGCGCGGAGCGGAGGAGCGTCCCTC 766
    |||||
Db 426 CGCGTCTCTGCACAGGAGTGTGCGAGCCGCGCGGAGCGGAGGAGCGTCCCTC 367
    |||||
QY 767 AGCCCTCTGAGGAGTGGATCACCTCTGCTGCTGCGCTGATGACCGTCTTTCACATA 826
    |||||
Db 366 AGCCCTCTGAGGAGTGGATCACCTCTGCTGCTGCGCTGATGACCGTCTTTCACATA 307
    |||||
QY 827 TGTGTTCTCTGCCCGTAATTTGTCCTGGAGTCCCGCCCAAGACACCTGGGAGTA 886
    |||||
Db 306 TGTGTTCTCTGCCCGTAATTTGTCCTGGAGTCCCGCCCAAGACACCTGGGAGTA 287
    |||||
QY 887 GGTGAGGCTTGAGGAAACATTTTCACTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCT 946
    |||||
Db 286 -----TATCGCGCT 278
    |||||
QY 947 TACTATGGAGCATTTAAGGATGTCAGGAGAAAACAGAGACCTCTGAAGAACAGAGAC 1006
    |||||
Db 277 TACTATGGAGCATTTAAGGATGTCAGGAGAAAACAGAGACCTCTGAAGAACAGAGAC 218
    |||||
QY 1007 CTCGAGGCTTGGCATTTCTATCTGTGATTTCAATTTGGGACCTTTGGATTTTATCAT 1066
    |||||
Db 217 CTCGAGGCTTGGCATTTCTATCTGTGATTTCAATTTGGGACCTTTGGATTTTATCAT 158
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QY 1067 TTCAGATCTCCAGTATTTCCGATATTTTTCACAAAGATTTTTCATTAGACCTCTTAGGTAC 1126
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Db 157 TTCAGATCTCCAGTATTTCCGATATTTTTCACAAAGATTTTTCATTAGACCTCTTAGGTAC 98
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QY 1127 AGGAGCCGCTGCGCAATTTCCACTAACATGGAATCCAGTCTGTGA 1171
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Db 97 AGGAGCCGCTGCGCAATTTCCACTAACATGGAATCCAGTCTGTGA 53
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RESULT 8

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LOCUS AA105532 520 bp mRNA linear EST 30-OCT-1996
DEFINITION mos7a09.r1 Life Tech mouse embryo 8 5dpc 10664019 Mus musculus CDNA
clone IMAGE:557656 5' similar to TR:G57719 G57719 PROTAGLANDIN D
RECEPTOR ;, mRNA sequence.

```

```

ACCESSION AA105532
VERSION AA105532.1 GI:1654672
KEYWORDS EST.
SOURCE Mus musculus (house mouse)

```

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ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

```

```

REFERENCE 1 (bases 1 to 520)
AUTHORS Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,

```

Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
Waterston, R.

TITLE JOURNAL COMMENT

The WashU-HHMI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810

Email: mouseest@wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.

MGI:338448
Seq primer: -28M13 rev1 from Amersham
High quality sequence stop: 475.

FEATURES source

Location/Qualifiers
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/db_xref="taxon:10090"
/clone="IMAGE:557656"
/issue_type="embryo"
/dev_stage="8.5dpc embryos"
/lab_host="DH10B"
/clone_lib="Life Tech mouse embryo 8 5dpc 10664019"
/note="Organ: whole embryo; Vector: pCMV-SPORT2; Site: 1;
SalI; Site 2: NotI; Cloned unidirectionally. Primer:
Oligo dt. 8.5dpc embryos. pCMV-SPORT2 vector."

ORIGIN

Query Match 28.4%; Score 333; DB 1; Length 520;
Best Local Similarity 78.7%; Pred. No. 3.9e-71;
Matches 410; Conservative 0; Mismatches 110; Indels 1; Gaps 1;
QY 40 GTGGAAGGCAACTCGCGGTGTATGGCGGGTGTCTTTCAGCACCGGCTCTCTGGGC 99
DB 1 GTGGAAGGCGTCTCGCGGAGATGGCGGTGTCTCTCGTGGCGGGTCTCTGGGC 60
QY 100 AACCTGTGGCCCTGGGGCTGTGGCGGCTGTGGGGCTGGGGTGTGTCTGGCGGCTCA 159
DB 61 AATCTTCTGGCGTGTGTCTGGCGGCTGTGGGCTGTGGGCTGTGGCGGCGGCA 120
QY 160 CTGGCGCGCTGCCCTCGGTCTTACATGTGTGTGTGGCTGACGCTCACCACCTTG 219
DB 121 CTACACCGCGCGCTCGGTCTTTTATGTGTGTGTGTGGCTTACGCTCACCACCTTG 180
QY 220 CTGGGCAAGTGTCTTAAAGCCGGTGTGTGGCTGTGGCTTACGCTCAGAACCGGAGTCTG 279
DB 181 CTGGGCAAGTGTGTATCAGCCCGATGTCTGTGGCTGTGGCTTACGCGCAACAGAGCTA 240
QY 280 CGGGTGTGGCCCGGCAATGGACAACTGTTGTGCCAAGCTTCGCCCTTCTTCATGTCC 339
DB 241 AAGGAACCTGCTGCTGCCTCAG-GAATCAGTTATGCAAACTTCGCTTCCTGATGCC 299
QY 340 TTCTTTGGGCTCTCTCGACATGCAATCTCTGGCCATGGCACTGAGTGTGGCTCTCC 399
DB 300 TTCTTTGGGCTAGCTCGACCTTACAGCTGTGTGGTATGGCGGTGGAGTGTGGCTGTCT 359
QY 400 CTAGGGCACTTCTTCTTACCGAGCGGACATCACCCTGCGCTGGCGGCACTGTGGCC 459
DB 360 CTGGGACACCTTCTTCTTACCAAGGACAGTCACTTGGCGCGGGAGTGTGGTGGCA 419
QY 460 CGGGTGTGGAGCGCTTCTCCCTGGCTTCTCGCGGCTTACCTTTCATGGGCTTCGGGAAG 519
DB 420 CGGGTGTGGCGGCTCTGCTGTGGCTTCTGTGGCTTCTGTGGCTTCTGTGGTGGGAG 479
QY 520 TTCGTGCAGTACTGCCCCGGGCACTGGTCTTTATCCAGAT 560
DB 480 TTCGTGCAGTACTGCCCCGGGCACTGGTGTTCATCCAGAT 520

RESULT 9 BB622854

LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE AUTHORS

TITLE JOURNAL COMMENT

BB622854 632 bp mRNA linear EST 26-OCT-2001
BB622854 RIKEN full-length enriched, adult male olfactory brain Mus
musculus cDNA clone 6430566C09 5', mRNA sequence.
BB622854
EST.
Mus musculus (house mouse)
Mus musculus
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 632)
Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T.,
Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J.,
Konno, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K.,
Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K.,
Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,
Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F.,
Takeda, Y., Tanaka, T., Toya, T., Muramatsu, M. and Hayashizaki, Y.
RIKEN Mouse ESTs (Arakawa, T., et al. 2001)
Unpublished (2001)
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E.,
Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T.,
Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A.
and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P.,
Sugahara, Y. and Hayashizaki, Y.
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanaka, I.,
Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and
Hayashizaki, Y.
Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.
e mouse tissues.

FEATURES source

Location/Qualifiers
1..632
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
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/sex="male"
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/dev_stage="adult"
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olfactory brain"
/note="Site 1: SalI; Site 2: BamHI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN, Division of Experimental Animal Research in Riken

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CLONTECH
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: <http://www-shgc.stanford.edu>
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAL Plate: 36 Row: 1 Column: 5
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 4506262
This clone has the following problem: retained intron.

FEATURES
source
1..1038
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ORIGIN
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Best Local Similarity 61.6%; Pred. No. 4.5e-39;
Matches 381; Conservative 0; Mismatches 226; Indels 12; Gaps 3;
QY 98 GCAACCTGTCGGCCCTCGCGCGCTCGGGGCTGGGGTGGTCTCGCGCGCTC 157
DB 112 GCACCTGATGTTCTGGCGCGTGTGGGCAACGGGCTGGCCCTGGCATCCTGAGCG 171
QY 158 CACTGGCC---CGTGGCCCTGGTCTTCTACATGCTGGTGTGGCTGACGGTCAACGG 214
DB 172 CACGGCGACCGCGCGCCCTCGCGCTTGGCGTGTGGTACCGGACTGGCGGCGCACGG 231
QY 215 ACTTGTGGGCAAGTCCCTTAAGCCGGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGG 274
DB 232 ACCCTGTGGGCAACGCTTCTGAGCGCGCGCTGTGGTGTGGTGTGGTGTGGTGTGGTGTGG 291
QY 275 GTCTGGGCTGTGGCGCGCATTTGCAACACTCGTTGTGCAAGCTTTCGCTTCTTCA 334
DB 292 CCTGTGGGCT---GGCGGAGGCGCGCCGCTGTGGATGCTTGGCTTGGCTTGGCA 348
QY 335 TGTCTCTTTTGGGCTCTCTCGACACTGCAACTCTGTGGCCATGGCACTGGAGTGTGCTGC 394
DB 349 TGACCTTCTTGGCGTGGCGTCACTGCTCATCTCTTTGCCATGGCGGTGGAGCGCTGCG 408
QY 395 TCTCCCTAGGCGACCTTCTTCTACCGAGCGCAATCACTTGGCGCTGGCGGCGCACTGG 454
DB 409 TGGCGTGAAGCACCCCTACCTCTAGCGCAGCTGGAACGGCGCGCGCTGGCGCGCGCTGG 468
QY 455 TGGCGCGGTGTGAGCGCTTCTCCCTGGCTTCTGCGCGCTTCTGCGCGCTTCTGCGCGCTTGG 514
DB 469 CGTGGCAGCCATCTAGGCTTCTGGTCTCTTCTGCGCGCTTCTGCGCGCTTCTGCGCGCTGG 528
QY 515 GGAAGTTCGTGAGTACTGCGCGGCACTGTGTCTTATCCAGATGTGTCCACGAGGAGG 574
DB 529 GCCAACACACGAGTACTGCGCGGCGAGCTGGTGTCTTCTCGCGCATGCGC-----TGGG 582
QY 575 GCTCGCTGTGGTGTGGGCTACTGTGTCTTCTACTCCAGCTTCTGCGGCTGTGCTGCTGC 634
DB 583 CCAGCGGCGCGCGCGCTTCTGCTGGCGCTTCTGCTGGCGCTTCTGCTGGCGCTTCTGCTGG 642
QY 635 TCGCCACGCTGTGTGCAACCTCGGCGCATTCGCAACCTCTATGCGATGACCGCGCGCG 694
DB 643 CTGGCATCTTCTTGTGCAACGGCTGGTCACTTCTGCGCATGTACCGCATGTACCGCGCG 702

QY 695 TGCAGGCGCACCGCGCTC 713
DB 703 AGAAGCGCCACCGCGCTC 721

RESULT 13
LOCUS CR601077 2020 bp mRNA linear HTC 21-JUL-2004
DEFINITION full-length cDNA clone CSODI069YD07 of Placenta Cot 25-normalized of Homo sapiens (human).
ACCESSION CR601077
VERSION CR601077.1 GI:50481884
KEYWORDS HTC; CNSLT_cDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2020)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
REMARK Contact : Feng Liang Email : fliang@lifetech.com URL : <http://fulllength.invitrogen.com/> Invitrogen Corporation 1600 Paraday Avenue
REFERENCE 2 (bases 1 to 2020)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
COMMENT - Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.
FEATURES
source
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/mol_type="mRNA"
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/clone="CSODI069YD07"
/tissue_type="Placenta Cot 25-normalized"
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ORIGIN
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Best Local Similarity 61.6%; Pred. No. 5.2e-39;
Matches 381; Conservative 0; Mismatches 226; Indels 12; Gaps 3;
QY 98 GCAACCTGTCGGCCCTGGGCTGTGGCGCGCTCGGGGCTGGGGTGGTGTCTCGCGCGCTC 157
DB 135 GCACCTGATGTTCTGGCGCGTGTGGGCAACGGGCTGGCCCTGGGCATCCTGAGCG 194
QY 158 CACTGGCC---CGTGGCCCTGGTCTTCTACATGCTGGTGTGGCTTGGCTTGGCTTGGCTTGG 214
DB 195 CACGGCGACCGCGCGCGCCCTCGCGCTTGGCGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGG 254
QY 215 ACTTGTGGGCAAGTCCCTTAAGCCGGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGG 274
DB 255 ACCTGTGGGCAACGAGCTTCTGAGCGCGCGCTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGG 314
QY 275 GTCTGGGCGGTGTGGCGCGCATTTGGCAACTGCTGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGG 334
DB 315 CCCTGTGGGCT---GGCGCGAGCGCGCGCGCTGTGGCATGCTTGGCTTGGCTTGGCA 371
QY 335 TGTCTCTTTTGGGCTCTCTCGACACTTCTGCGCACTCTGCGCATGCACTGGAGTGTCTGCG 394
DB 372 TGACCTTCTTGGCGCTGGCGTCCATGCTCTCTTTGCCATGGCCGCTGGAGCGCTGCG 431
QY 395 TCTCCCTAGGCGCACCTTCTTCTTACCGAGCGCAATCACTTGGCGCTTGGCGCGCACTGG 454
DB 432 TGGCGCTGAGCGACCCCTACCTTACGCGGAGCTGGAACGGCGCGCGCTGGCGCGCGCTGG 491

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 22, 2005, 17:53:08 ; Search time 54.229 Seconds
(without alignments)
2111.067 Million cell updates/sec

Title: US-10-689-861-2

Perfect score: 1541

Sequence: 1 MKSPYRCQNTTSVEKNSA.....CSLPVIAFVGVPKTPGSR 296

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: Geneseqp1980s:*
- 2: Geneseqp1990s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003as:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1467	95.2	359	2	Aaw03516 Prostagla
2	1467	95.2	359	4	Aam79009 Human pro
3	1467	95.2	359	6	Abp81901 Human pro
4	1467	95.2	359	7	Ad448182 Human pro
5	1467	95.2	359	8	Ado29614 Human GPC
6	1467	95.2	369	3	Aay94346 Human cel
7	1467	95.2	399	4	Abb12000 Human pro
8	1467	95.2	399	4	Aam79993 Human pro
9	1467	95.2	399	7	Ado09040 Novel pro
10	1467	95.2	424	7	Ado07993 Novel pro
11	1125	73.0	357	7	Ad448180 Rat Prote
12	1100	71.4	357	8	Ado29615 Mouse GPC
13	1099	71.3	357	2	Aar84708 Prostagla
14	595.5	38.6	362	8	Ado29619 Mouse GPC
15	586	38.0	358	6	Abp81903 Human pro
16	586	38.0	358	7	Ad448180 Human pro
17	586	38.0	358	7	Adx52578 Hematolog
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19	586	38.0	358	8	Adri4091 Human NF-
20	586	38.0	358	8	Adr43385 Prostagla
21	586	38.0	358	2	Aay41279 Fusion pr
22	585	38.0	358	2	Aaw44246 Human HP4
23	585	38.0	358	5	Abg30499 Human HP4
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RESULT 1
Aaw03516
ID Aaw03516 standard; protein; 359 AA.

XX AC Aaw03516;

XX DT 11-MAR-1997 (first entry)

XX DE Prostaglandin DP receptor.

XX KW Prostaglandin DP receptor; human; prostanoid receptor; blood platelet;
XX KW smooth muscle; nervous tissue; G protein-coupled receptor; modulator;
XX KW mouse; prostaglandin-related disease; therapy.

XX OS Homo sapiens.

XX PN WO9623066-A2.

XX PD 01-AUG-1996.

XX PF 23-JAN-1996; 96WO-CA0000047.

XX PR 26-JAN-1995; 95US-00378682.

XX (MERI) MERCK FROSST CANADA INC.

XX PI Abramovitz M, Boie Y, Metters K, Sawyer N, Slipetz DM;

XX DR WPI, 1996-362690/36.

XX DR N-PSDB; AAT37402.

XX Human prostaglandin DP receptor and related DNA - used to identify

XX receptor modulators to treat prostaglandin-related diseases.

XX Claim 2; Page 41; 49pp; English.

XX This sequence represents the human prostaglandin DP receptor. The DP
CC receptor is the least ubiquitous and least abundant of the prostanoid
CC receptors. The DP receptors are thought to be distributed mainly in blood
CC platelets, smooth muscle of various tissues, and nervous tissue
CC (including the central nervous system). However, many of the actions and
CC G protein-coupled receptor which can specifically bind prostaglandin
CC molecules. The DNA encoding this sequence was isolated using primers (see
CC AAT37403 and AAT37404) based on the N-terminal sequence, and an internal
CC sequence from purified mouse DP. The human prostaglandin DP receptor can
CC be used to identify modulators of the receptor. The identified modulators
CC can then be used to treat prostaglandin-related diseases, and for

ALIGNMENTS

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CC modulating the effects of prostaglandins on the DP receptor
XX
SQ Sequence 359 AA;
Query Match 95.2%; Score 1467; DB 2; Length 359;
Best Local Similarity 100.0%; Pred. No. 1.6e-147;
Matches 282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MKSPYRCQNTTSVEKGNNAVGGVLFSTGLGNLALGLLARSGLGWCRRPLPLPSV 60
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DB 61 FYMLVCGLTVTDLGKCLLSPVLAAYQNRSLRVLAPALDNSLCOAFPMFFGLSST 120
QY 121 LQLLMALECWLSLGHPPFFRRHITRLGALVAPVVSFAFSLAFALPFGFGKFFVQYCPG 180
DB 121 LQLLMALECWLSLGHPPFFRRHITRLGALVAPVVSFAFSLAFALPFGFGKFFVQYCPG 180
QY 181 TWCFTQMVHEEGSLVGLSVLYSSIMALLVLTATVLCNLGAMRNLYAMHRLQRHRSCT 240
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RESULT 2
AAW79009
ID AAW79009 standard; protein; 359 AA.
XX
AC AAW79009;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human protein SEQ ID NO 1671.
XX
KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorder; arthritis; inflammation.
XX
OS Homo sapiens.
XX
XX WO200157190-A2.
XX
PD 09-AUG-2001.
XX
PF 05-FEB-2001; 2001WO-US004098.
XX
PR 03-FEB-2000; 2000US-00496914.
PR 27-APR-2000; 2000US-00560875.
PR 20-JUN-2000; 2000US-00598075.
PR 19-JUL-2000; 2000US-00620325.
PR 01-SEP-2000; 2000US-00654936.
PR 15-SEP-2000; 2000US-00663561.
PR 20-OCT-2000; 2000US-00693325.
PR 30-NOV-2000; 2000US-00728422.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y;
PI Ma Y, Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;
XX
DR WPI: 2001-476283/51.
DR N-PSDB; AAK52142.
XX
PT Nucleic acids encoding polypeptides with cytokine-like activities, useful
PT in diagnosis and gene therapy.
XX
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PS
XX
CC The invention relates to polynucleotides (AAK51456-AAK53435) and the
CC encoded polypeptides (AAW78323-AAW80302) that exhibit activity elating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111
CC (AAK52582) and 3666 (AAW80020) are omitted as the relevant pages from the
CC sequence listing were missing at the time of publication
XX
SQ Sequence 359 AA;
Query Match 95.2%; Score 1467; DB 4; Length 359;
Best Local Similarity 100.0%; Pred. No. 1.6e-147;
Matches 282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MKSPYRCQNTTSVEKGNNAVGGVLFSTGLGNLALGLLARSGLGWCRRPLPLPSV 60
DB 1 MKSPYRCQNTTSVEKGNNAVGGVLFSTGLGNLALGLLARSGLGWCRRPLPLPSV 60
QY 61 FYMLVCGLTVTDLGKCLLSPVLAAYQNRSLRVLAPALDNSLCOAFPMFFGLSST 120
DB 61 FYMLVCGLTVTDLGKCLLSPVLAAYQNRSLRVLAPALDNSLCOAFPMFFGLSST 120
QY 121 LQLLMALECWLSLGHPPFFRRHITRLGALVAPVVSFAFSLAFALPFGFGKFFVQYCPG 180
DB 121 LQLLMALECWLSLGHPPFFRRHITRLGALVAPVVSFAFSLAFALPFGFGKFFVQYCPG 180
QY 181 TWCFTQMVHEEGSLVGLSVLYSSIMALLVLTATVLCNLGAMRNLYAMHRLQRHRSCT 240
DB 181 TWCFTQMVHEEGSLVGLSVLYSSIMALLVLTATVLCNLGAMRNLYAMHRLQRHRSCT 240
QY 241 RDCAEPRADGREASPOPLELDHLLALMTVLTFTMCSLPVI 282
DB 241 RDCAEPRADGREASPOPLELDHLLALMTVLTFTMCSLPVI 282
RESULT 3
ABP81901
ID ABP81901 standard; protein; 359 AA.
XX
AC ABP81901;
XX
DT 04-MAR-2003 (first entry)
XX
DE Human prostaglandin D2 receptor protein SEQ ID NO:287.
XX
KW G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
KW G protein-coupled receptor modulator; antibody; immune-related disease;
KW growth-related disease; cell regeneration-related disease; AIDS; cancer;
KW immunological-related cell proliferative disease; autoimmune disease;
KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;
KW osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;
KW graft versus host disease; Parkinson's disease; multiple sclerosis; pain;
KW psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
KW hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
KW ulcer.
XX
OS Homo sapiens.
XX
XX WO200261087-A2.
XX
PD 08-AUG-2002.
XX
PF 19-DEC-2001; 2001WO-US050107.
XX
```


Db 1 MKSPFYRCQNTTSVEKNSAVMGVLFSTGLGNLLALGLLARSGLGWCSSRRPLRPLPSV 60
 QY 61 FYMLVCGLTVDLLGKCLLSPVLAAYQNRSLRVLPALDNLSCQAFPMSPFGLSST 120
 Db 61 FYMLVCGLTVDLLGKCLLSPVLAAYQNRSLRVLPALDNLSCQAFPMSPFGLSST 120
 QY 121 LQLLAMALECWLGLGHPFFRRHITRLGALVAPVVSFAFLAFALPFGFKFVQYCPG 180
 Db 121 LQLLAMALECWLGLGHPFFRRHITRLGALVAPVVSFAFLAFALPFGFKFVQYCPG 180
 QY 181 TWCFIQMVHEGSLSVLGYSVLYSSLMALLVATVLCNLGAMRNLYAMHRLQRHPRST 240
 Db 181 TWCFIQMVHEGSLSVLGYSVLYSSLMALLVATVLCNLGAMRNLYAMHRLQRHPRST 240
 QY 241 RDCAPRADGREASPOPLELDHLLALLMTVLTWCSLPVI 282
 Db 241 RDCAPRADGREASPOPLELDHLLALLMTVLTWCSLPVI 282

RESULT 5

ADO29614
 ID ADO29614 standard; protein; 359 AA.

XX ADO29614;

XX 29-JUL-2004 (first entry)

XX Human GPCR PTGDR, SEQ ID NO:716.

KW G protein-coupled receptor; GPCR; drug screening; diagnosis;
 KW transgenic mouse; neurological disorder; adrenal gland disorder;
 KW colon disorder; intestinal disorder; cardiovascular disorder;
 KW muscular disorder; blood disorder; immune disorder; bone disorder;
 KW joint disorder; metabolic disorder; nutritive disorder; cancer;
 KW kidney disorder; liver disorder; lung disorder; breast disorder;
 KW ovary disorder; uterus disorder; prostate disorder; testis disorder;
 KW skin disorder; stomach disorder; pancreas disorder; spleen disorder;
 KW thymus disorder; thyroid disorder; antiparkinsonian; antitumor;
 KW cytostatic; antiinflammatory; vasotropic; antiangiogenic; antiarrhythmic;
 KW CNS; central nervous system; respiratory; antidiarrhoeic; antidiabetic;
 KW virucide; hepatotropic; antibacterial; antianaemic; antiseborrhoeic;
 KW dermatological; antitumor; antithyroid; antiallergic; anorectic;
 KW immunosuppressive; nephrotropic; gene therapy; GPCR modulator; human;
 KW receptor.

XX Homo sapiens.

XX WO2004040000-A2.

XX 13-MAY-2004.

XX 09-SEP-2003; 2003WO-US028226.

XX 09-SEP-2002; 2002US-0409303P.

XX 09-APR-2003; 2003US-0461329P.

XX (PRIM-) PRIMAL INC.

XX Gaitanaris GA, Bergmann JE, Gragerov A, Hohmann J, Li F;
 PI Madisen L, McGilwain KL, Pavlova MN, Vassilatis D, Zeng H;

XX WPI; 2004-390329/36.

XX N-PSDB; ADO30026.

XX Novel mammalian G protein coupled receptors, useful for identifying
 PT compounds that modulates diagnosing and treating disease condition
 PT associated with GPCR dysfunction e.g. autoimmune diseases, angina
 PT pectoris, Parkinson's disease.

XX Claim 151; SEQ ID NO 716; 542pp; English.

XX The invention relates to human and mouse G protein-coupled receptors
 CC (GPCRs) and nucleic acids encoding them. The invention also relates to

CC sequences at least 90% identical to the GPCR proteins and nucleic acids
 CC of the invention; methods of treating, preventing or diagnosing diseases
 CC associated with GPCRs of the invention; methods of screening for
 CC compounds useful in the treatment of GPCR-related diseases; a transgenic
 CC mouse comprising a GPCR gene of the invention; a mouse comprising a
 CC mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived
 CC from the transgenic mice; kits comprising several mice, each of which has
 CC a mutation in a different GPCR gene of the invention; and kits comprising
 CC probes which hybridise to GPCR polynucleotides of the invention. The
 CC invention further discloses variants of the GPCR polypeptides and vectors
 CC comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may
 CC be used in the diagnosis, treatment or prevention of a wide variety of
 CC diseases including neurological disorders (e.g., Alzheimer's disease,
 CC depression, diabetic neuropathy, Parkinson's disease or schizophrenia);
 CC disorders of the adrenal gland; disorders of the colon or intestine
 CC (e.g., Crohn's disease, diarrhoea, food poisoning or irritable bowel
 CC syndrome); cardiovascular disorders (e.g., angina, cardiac arrhythmia or
 CC myocardial infarction); muscular disorders; blood disorders (e.g.,
 CC anaemia or leukaemia); immune disorders (e.g., autoimmune disorders or
 CC AIDS); bone and joint disorders (e.g., osteoarthritis, rheumatoid
 CC arthritis, gout or osteoporosis); metabolic or nutritive disorders (e.g.,
 CC obesity, enzyme deficiency-related diseases or vitamin deficiency-related
 CC diseases); and disorders of the kidney, liver, lung, breast, ovary,
 CC uterus, prostate, testis, skin, stomach, pancreas, spleen, thymus and
 CC thyroid (e.g., cancers). The present sequence represents a GPCR of the
 CC invention. Note: The full sequence data for this patent did not form part
 CC of the printed specification; those sequences not shown were obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 359 AA;

Query Match 95.2%; Score 1467; DB 8; Length 359;

Best Local Similarity 100.0%; Pred. No. 1.6e-147; Mismatches 0; Gaps 0;

Matches 282; Conservative 0; Indels 0;

QY 1 MKSPFYRCQNTTSVEKNSAVMGVLFSTGLGNLLALGLLARSGLGWCSSRRPLRPLPSV 60

Db 1 MKSPFYRCQNTTSVEKNSAVMGVLFSTGLGNLLALGLLARSGLGWCSSRRPLRPLPSV 60

QY 61 FYMLVCGLTVDLLGKCLLSPVLAAYQNRSLRVLPALDNLSCQAFPMSPFGLSST 120

Db 61 FYMLVCGLTVDLLGKCLLSPVLAAYQNRSLRVLPALDNLSCQAFPMSPFGLSST 120

QY 121 LQLLAMALECWLGLGHPFFRRHITRLGALVAPVVSFAFLAFALPFGFKFVQYCPG 180

Db 121 LQLLAMALECWLGLGHPFFRRHITRLGALVAPVVSFAFLAFALPFGFKFVQYCPG 180

QY 181 TWCFIQMVHEGSLSVLGYSVLYSSLMALLVATVLCNLGAMRNLYAMHRLQRHPRST 240

Db 181 TWCFIQMVHEGSLSVLGYSVLYSSLMALLVATVLCNLGAMRNLYAMHRLQRHPRST 240

QY 241 RDCAPRADGREASPOPLELDHLLALLMTVLTWCSLPVI 282

Db 241 RDCAPRADGREASPOPLELDHLLALLMTVLTWCSLPVI 282

RESULT 6

AA94346

ID AA94346 standard; protein; 369 AA.

XX AA94346;

XX 22-AUG-2000 (first entry)

XX Human cell surface receptor protein #13.

XX Human; HCSR; cytostatic; antiarthritic; antirheumatic; antiasthmatic;
 KW immunosuppressive; antiarteriosclerotic; antibacterial; antiparasitic;
 KW neuroprotective; nootropic; anticonvulsant; cancer; leukaemia; melanoma;
 KW rheumatoid arthritis; asthma; atherosclerosis; akathesia;
 KW Alzheimer's diseases; multiple sclerosis; epilepsy.

OS Homo sapiens.
XX Key Location/Qualifiers
FH Peptide 1. .47
FT /label= Signal_peptide
FT Region 6. .20
FT /note= "Prostaglandin D receptor"
FT Region 10. .57
FT /note= "2 Poly-Immunoglobulin receptor"
FT Region 10
FT /note= "potential glycosylation site"
FT Region 11. .58
FT /note= "2 Poly-Immunoglobulin receptor"
FT Region 12
FT /note= "potential phosphorylation site"
FT Region 33. .280
FT /note= "7 Transmembrane receptor"
FT Region 41. .58
FT /note= "Prostaglandin D receptor"
FT Protein 48. .369
FT /label= HCSR-13
FT Region 50
FT /note= "potential phosphorylation site"
FT Region 52. .99
FT /note= "2 Poly-Immunoglobulin receptor"
FT Region 69
FT /note= "potential phosphorylation site"
FT Region 90
FT /note= "potential glycosylation site"
FT Region 92
FT /note= "potential phosphorylation site"
FT Region 93. .104
FT /note= "Prostaglandin D receptor"
FT Domain 144. .161
FT /label= Transmembrane_domain
FT Region 145
FT /note= "potential phosphorylation site"
FT Region 185. .200
FT /note= "Prostaglandin D receptor"
FT Region 195. .225
FT /note= "2 Poly-Immunoglobulin receptor"
FT Domain 196. .219
FT /label= Transmembrane_domain
FT Region 236. .259
FT /note= "Prostaglandin D receptor"
FT Domain 264. .283
FT /label= Transmembrane_domain
FT Region 280. .291
FT /note= "Prostaglandin D receptor"
FT Region 297
FT /note= "potential glycosylation site"
FT Region 299
FT /note= "potential phosphorylation site"
FT Region 312
FT /note= "potential phosphorylation site"
FT Region 330
FT /note= "potential phosphorylation site"
FT Region 346
FT /note= "potential phosphorylation site"
FT Region 346
FT /note= "potential phosphorylation site"
XX WO200028032-A2.
XX
XX 18-MAY-2000.
XX
XX 12-NOV-1999; 99WO-US026742.
XX
XX 12-NOV-1998; 98US-00191280.
PR 07-DEC-1998; 98US-00206647.
PR 08-MAR-1999; 99US-0123404P.
XX (INCY-) INCYTE PHARM INC.
XX
XX Tang YT, Corley NC, Guegler KJ, Yue H, Baughn MR, Lal P;

PI Hillman JL, Bandman O, Azimzai Y, Au-Young J;
XX WPI; 2000-376546/32.
DR N-PSDB; AAA27056.
XX
XX New human cell surface receptor protein and polynucleotide useful for
PT diagnosis, prevention and treatment of cancer, immune disorders,
PT infection and neuronal disorders.
XX
XX Claim 1; Page 87-88; 97pp; English.
XX
XX The present sequence is a novel human cell surface receptor protein
CC (HCSR-13) designated HCSR-13. The nucleotide sequence was identified in
CC Incyte Clone 3576503 from the CDNA library BRONN0101, which was made from
CC RNA isolated from bronchial tissue. A number of Incyte Clones were used
CC to assemble the consensus sequence. BLAST analysis showed that the
CC sequence is homologous to DR prostanoil receptor g940379. HCSR-13 and its
CC antagonist are useful for preventing or treating disorders associated
CC with decreased or increased expression or activity of HCSR-13. Such
CC disorders include cancers such as leukaemia and melanoma, immune
CC disorders such as rheumatoid arthritis, asthma and atherosclerosis,
CC bacterial and parasitic infections and neuronal disorders such as
CC akathisia, Alzheimer's disease, multiple sclerosis and epilepsy.
CC Polynucleotides encoding HCSR-13 may be used as hybridisation probes to
CC diagnose these conditions. Anti-HCSR-13 antibodies may be used as
CC antagonists, as a targeting or delivery mechanism for bringing
CC pharmaceutical agents into contact with cells or tissues expressing HCSR-13
CC and for diagnosis of HCSR-13-related disorders. HCSR-13 and its catalytic or
CC immunogenic fragments are useful for drug screening using libraries of
CC compounds
XX
SQ Sequence 369 AA;
Query Match 95.2%; Score 1467; DB 3; Length 369;
Best Local Similarity 100.0%; Pred. No. 1.7e-147;
Matches 282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MKSPFYRCQNTTSVEKGN SAVMGVLFSTGLGNLLALGLLARSGLGWCRRPLRLPSV 60
DB 1 MKSPFYRCQNTTSVEKGN SAVMGVLFSTGLGNLLALGLLARSGLGWCRRPLRLPSV 60
QY 61 FYMLVCGLTVTDLGKCLLSPVVLAAYQNRSLRVLPALDNLSCQAFNFFSFGLSST 120
DB 61 FYMLVCGLTVTDLGKCLLSPVVLAAYQNRSLRVLPALDNLSCQAFNFFSFGLSST 120
QY 121 LOLLAMALECMLSLGHPPFYRRHITRLGALVAVPVVSFAFLAFALPFGMGFKVQYCPG 180
DB 121 LOLLAMALECMLSLGHPPFYRRHITRLGALVAVPVVSFAFLAFALPFGMGFKVQYCPG 180
QY 181 TWCFTQMVHEGSLSVLGYSVLYSSLMALLVATVLCNLGAMRNLYAMHRRILQRHPRST 240
DB 181 TWCFTQMVHEGSLSVLGYSVLYSSLMALLVATVLCNLGAMRNLYAMHRRILQRHPRST 240
QY 241 RDCAEPRADGREGASPOPLEELDHLHLLALMTVLTMCSLPVI 282
DB 241 RDCAEPRADGREGASPOPLEELDHLHLLALMTVLTMCSLPVI 282
RESULT 7
ABB12000
ID ABB12000 standard; peptide; 399 AA.
XX
XX ABB12000;
XX
XX 11-JAN-2002 (first entry)
XX
XX Human prostaglandin DP receptor homologue, SEQ ID NO:2370.
DE
XX Human; cytokine; cell proliferation; cell differentiation; growth factor;
KW haematopoiesis regulation; tissue growth; immunomodulator; activin;
KW inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis;
KW proliferation; metastasis; cancer; tumour; haematopoietic disorder;
KW myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;

chronic inflammatory condition; proliferative retinopathy;
atherosclerosis; coronary heart disease; arterial ischaemia;
bone disorder; osteoporosis; vascular growth disorder;
tissue regeneration; wound healing; infection; immune disorder;
cell culture; drug screening; gene therapy; antiinflammatory;
antiaesthetic; antiarthritis; haemostatic; antiarteriosclerotic;
cytostatic; osteopathic; vasotropic; cardiant; virucide; antibacterial;
antifungal; vulnerary; antiulcer.

OS Homo sapiens.
XX WO200157188-A2.
XX 09-AUG-2001.
XX 05-FEB-2001; 2001WO-US003800.
XX 03-FEB-2000; 2000US-00496914.
XX 27-APR-2000; 2000US-00560875.
XX (HYSE-) HYSEQ INC.
XX Tang YT, Liu C, Drmanac RT;
XX WPI; 2001-457740/49.
XX N-PSDB; ABA09244.
XX Human proteins and DNA encoding sequences useful for preventing, treating
XX or ameliorating a medical condition in a mammalian subject e.g. arthritis
XX and cancer.
XX Claim 20; Page 294; 1963pp; English.
XX Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and
XX sequences ABA08225-ABA09574 represent nucleic acids encoding them. The
XX invention also relates to vectors and recombinant host cells comprising a
XX nucleotide of the invention, methods of producing the novel polypeptides,
XX antibodies against the polypeptides, methods of detecting the nucleotides
XX or polypeptides in a sample, and methods of identifying compounds which
XX bind to polypeptides of the invention. Although novel, many of the
XX polypeptides of the invention have homology to known proteins, thereby
XX giving an insight into their probable biological activities, and hence
XX potential therapeutic applications. The polypeptides of the invention may
XX have various activities, including cytokine, cell proliferation or cell
XX differentiation activities; stem cell growth factor activity;
XX haematopoiesis regulatory activity; tissue growth activity;
XX immunomodulatory activity; activin- or inhibin-related activities;
XX chemotactic or chemokinetic activities; haemostatic, thrombotic or
XX thrombolytic activities; receptor or ligand activities; or may be
XX involved in oncogenesis, cancer cell proliferation or metastasis.
XX Depending on their biological activities, polypeptides and nucleotides of
XX the invention are useful for preventing, treating or ameliorating medical
XX conditions, e.g., by protein or gene therapy. Such conditions include
XX cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell
XX disorders), chronic inflammatory conditions (e.g., asthma or arthritis),
XX proliferative retinopathy, atherosclerosis, coronary heart disease,
XX arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal
XX vascular growth. Polypeptides involved with tissue regeneration and
XX repair (or nucleic acids encoding them) may be used to promote wound
XX healing (e.g., of burns, incisions and ulcers), while those with
XX immunomodulatory activities may be used in the treatment of viral,
XX bacterial and fungal infections in addition to immune disorders.
XX Polypeptides with growth factor activity may be used in cell cultures to
XX promote cell growth. For example, such polypeptides may be used to
XX manipulate stem cells in culture to give rise to neuroepithelial cells
XX that can be used to augment or replace cells damaged by illness,
XX autoimmune disease or accidental damage. The polypeptides and nucleotides
XX may also be used in the diagnosis of the above conditions, and in drug
XX screening techniques. The present sequence represents a novel human
XX polypeptide of the invention

Sequence 399 AA;

Query Match 95.2%; Score 1467; DB 4; Length 399;
Best Local Similarity 100.0%; Pred. No. 1.9e-147;
Matches 282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MKSPYRCQNTTSVEKGNKSNVGVLFSTGLLGNLLALGLLARSGLGWCRRPLRLPLPSV 60
DB 41 MKSPYRCQNTTSVEKGNKSNVGVLFSTGLLGNLLALGLLARSGLGWCRRPLRLPLPSV 100
QY 61 FYMLVCGLTVDLLGKCLLSPVLLAAYQNRSLRVLAPALDNLSCQAFPMFFSFFGLSST 120
DB 101 FYMLVCGLTVDLLGKCLLSPVLLAAYQNRSLRVLAPALDNLSCQAFPMFFSFFGLSST 160
QY 121 LQLLMALECMWLSLGHPPFFYRRHITRLGALVAPVVSFAFALCPMFGKFFVQYCPG 180
DB 161 LQLLMALECMWLSLGHPPFFYRRHITRLGALVAPVVSFAFALCPMFGKFFVQYCPG 220
QY 181 TWCFTQMVHEEGSLSVLYGYSVLYSSIMALLVATVLCNIGMRNLYAMHRLQRHPRSC 240
DB 221 TWCFTQMVHEEGSLSVLYGYSVLYSSIMALLVATVLCNIGMRNLYAMHRLQRHPRSC 280
QY 241 RDCAEPRADGREASPOPLEELDHLHLLMTVLTFTMCSLPVI 282
DB 281 RDCAEPRADGREASPOPLEELDHLHLLMTVLTFTMCSLPVI 322

RESULT 8
AAM79993
ID AAM79993 standard; protein; 399 AA.
AC AAM79993;
XX 06-NOV-2001 (first entry)
XX Human protein SEQ ID NO 3639.
DE Human; cytokine; cell proliferation; cell differentiation; gene therapy;
XX vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorder; arthritis; inflammation.
XX Homo sapiens.
XX WO200157190-A2.
XX 09-AUG-2001.
XX 05-FEB-2001; 2001WO-US004098.
XX 03-FEB-2000; 2000US-00496914.
XX 27-APR-2000; 2000US-00560875.
XX 20-JUN-2000; 2000US-00598075.
XX 19-JUL-2000; 2000US-00620325.
XX 01-SEP-2000; 2000US-00654936.
XX 15-SEP-2000; 2000US-00663561.
XX 20-OCT-2000; 2000US-00693325.
XX 30-NOV-2000; 2000US-00728422.
XX (HYSE-) HYSEQ INC.
XX Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y;
XX Ma Y, Zhao Q, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
XX Xue AJ, Yang Y, Wejhrman T, Goodrich R;
XX WPI; 2001-476283/51.
XX N-PSDB; AAK53126.
XX Nucleic acids encoding polypeptides with cytokine-like activities, useful
XX in diagnosis and gene therapy.
XX Claim 20; Page 403-404; 6221pp; English.
XX The invention relates to polynucleotides (AAK51456-AAK53435) and the
XX encoded polypeptides (AAM78323-AAAM80302) that exhibit activity elating to

CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111
CC (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the
CC sequence listing were missing at the time of publication
XX
XX Sequence 399 AA;

Query Match 95.2%; Score 1467; DB 4; Length 399;
Best Local Similarity 100.0%; Pred. No. 1.9e-147;
Matches 282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKSPFYRCQNTTSVEKNSAVMGVLFSTGLGNLALGLLARSGLGWCSSRRRLPLPSV 60
DB 41 MKSPFYRCQNTTSVEKNSAVMGVLFSTGLGNLALGLLARSGLGWCSSRRRLPLPSV 100
QY 61 FYMLVGLTDTLLGKCLLSPVLAAYQNRSLRVLPALDNLSCQAFAPFMSFFGLSST 120
DB 101 FYMLVGLTDTLLGKCLLSPVLAAYQNRSLRVLPALDNLSCQAFAPFMSFFGLSST 160
QY 121 LQLLMALECNLSLGHPPFYRRHITLRLGALVAPVVSFAFLAFALPFMGFGKVFQYCPG 180
DB 161 LQLLMALECNLSLGHPPFYRRHITLRLGALVAPVVSFAFLAFALPFMGFGKVFQYCPG 220
QY 181 TWCFIQMVHEGSLVGLSYSLYSSIMALLVTLATVLCNLGAMRNLYAMHRRRLQHRPSCT 240
DB 221 TWCFIQMVHEGSLVGLSYSLYSSIMALLVTLATVLCNLGAMRNLYAMHRRRLQHRPSCT 280
QY 241 RDCAEPRADGREGASQPLELDHLLALLMTVLTWCPSLPVI 282
DB 281 RDCAEPRADGREGASQPLELDHLLALLMTVLTWCPSLPVI 322

RESULT 9
ADE09040
ID ADE09040 standard; protein; 399 AA.
XX
AC ADE09040;
XX
DT 29-JAN-2004 (first entry)
XX
DE Novel protein-related contig polypeptide sequence #106.
XX
KW novel gene; novel protein; tissue marker; molecular weight marker;
KW chromosome marker; genetic disorder; contig.
XX
OS Unidentified.

XX WO2003054152-A2.
XX
XX 03-JUL-2003.
XX
XX 10-DEC-2002; 2002WO-US039555.
XX
XX 10-DEC-2001; 2001US-0339739P.
PR 11-DEC-2001; 2001US-0339453P.
PR 14-MAR-2002; 2002US-0365091P.
PR 14-MAR-2002; 2002US-0365384P.
PR 12-APR-2002; 2002US-0372381P.
PR 12-APR-2002; 2002US-0372615P.
PR 22-APR-2002; 2002US-00128558.
PR 24-APR-2002; 2002US-0376045P.
XX (HYSE-) HYSEQ INC.
XX
XX Tang YT, Asundi V, Goodrich RW, Ren F, Zhang J, Zhao QA, Wang J;
PI Ghosh M, Xue AJ, Wehrman T, Weng G, Zhou P, Drmanac RT, Wang Z;

PI Ma Y, Wang D, Chen R, Xu C, Boyle BJ;
XX
XX WPI; 2003-569235/53.

XX New polynucleotides, useful for expressing recombinant proteins for
PT analysis, characterization or therapeutic use, or as markers for tissues
PT in which the corresponding protein is preferentially expressed.

XX Disclosure; SEQ ID NO 2584; 1177pp; English.

XX The invention comprises the amino acid and coding sequences of novel
CC proteins. The DNA and protein sequences of the invention are useful as:
CC markers for tissues in which the corresponding protein is preferentially
CC expressed; as molecular weight markers on gels; as chromosome markers or
CC tags; to identify chromosomes or to map related gene positions; and to
CC compare with endogenous DNA sequences in patients to identify potential
CC genetic disorders. The present amino acid sequence was used in the
CC exemplification of the invention.

XX Sequence 399 AA;

Query Match 95.2%; Score 1467; DB 7; Length 399;
Best Local Similarity 100.0%; Pred. No. 1.9e-147;
Matches 282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKSPFYRCQNTTSVEKNSAVMGVLFSTGLGNLALGLLARSGLGWCSSRRRLPLPSV 60
DB 41 MKSPFYRCQNTTSVEKNSAVMGVLFSTGLGNLALGLLARSGLGWCSSRRRLPLPSV 100
QY 61 FYMLVGLTDTLLGKCLLSPVLAAYQNRSLRVLPALDNLSCQAFAPFMSFFGLSST 120
DB 101 FYMLVGLTDTLLGKCLLSPVLAAYQNRSLRVLPALDNLSCQAFAPFMSFFGLSST 160
QY 121 LQLLMALECNLSLGHPPFYRRHITLRLGALVAPVVSFAFLAFALPFMGFGKVFQYCPG 180
DB 161 LQLLMALECNLSLGHPPFYRRHITLRLGALVAPVVSFAFLAFALPFMGFGKVFQYCPG 220
QY 181 TWCFIQMVHEGSLVGLSYSLYSSIMALLVTLATVLCNLGAMRNLYAMHRRRLQHRPSCT 240
DB 221 TWCFIQMVHEGSLVGLSYSLYSSIMALLVTLATVLCNLGAMRNLYAMHRRRLQHRPSCT 280
QY 241 RDCAEPRADGREGASQPLELDHLLALLMTVLTWCPSLPVI 282
DB 281 RDCAEPRADGREGASQPLELDHLLALLMTVLTWCPSLPVI 322

RESULT 10
ADE07993
ID ADE07993 standard; protein; 424 AA.
XX
AC ADE07993;
XX
DT 29-JAN-2004 (first entry)
XX
DE Novel protein (useful for identifying genetic disorders) #148.
XX
KW novel gene; novel protein; tissue marker; molecular weight marker;
KW chromosome marker; genetic disorder.
XX
OS Unidentified.

XX WO2003054152-A2.
XX
XX 03-JUL-2003.
XX
XX 10-DEC-2002; 2002WO-US039555.
XX
XX 10-DEC-2001; 2001US-0339739P.
PR 11-DEC-2001; 2001US-0339453P.
PR 14-MAR-2002; 2002US-0365091P.
PR 14-MAR-2002; 2002US-0365384P.
PR 12-APR-2002; 2002US-0372381P.
PR 12-APR-2002; 2002US-0372615P.

PR 22-APR-2002; 2002US-00128558.
PR 24-APR-2002; 2002US-0376045P.
PR (HYSE-) HYSEQ INC.
PI Tang YT, Asundi V, Goodrich RW, Ren F, Zhang J, Zhao QA, Wang J;
PI Ghosh M, Xue AJ, Wehrman T, Weng G, Zhou P, Drmanac RT, Wang Z;
PI Ma Y, Wang D, Chen R, Xu C, Boyle BJ;
XX WPI: 2003-569235/53.
DR N-PSDB; ADE07082.
XX
PT New polynucleotides, useful for expressing recombinant proteins for
PT analysis, characterization or therapeutic use, or as markers for tissues
PT in which the corresponding protein is preferentially expressed.
XX
PS Claim 20; SEQ ID NO 1059; 1177pp; English.
XX
CC The invention comprises the amino acid and coding sequences of novel
CC proteins. The DNA and protein sequences of the invention are useful as:
CC markers for tissues in which the corresponding protein is preferentially
CC expressed; as molecular weight markers on gels; as chromosome markers or
CC tags; to identify chromosomes or to map related gene positions; and to
CC compare with endogenous DNA sequences in patients to identify potential
CC genetic disorders. The present amino acid sequence represents a protein
CC of the invention.
XX
SQ Sequence 424 AA;

Query Match 95.2%; Score 1467; DB 7; Length 424;
Best Local Similarity 100.0%; Pred. No. 2e-147;
Matches 282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKSPFYRCNTTSVEKGSNVMGCVLFSTGLGNLLALGLLARSGLWCRRPLPLPSV 60
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1 MKSPFYRCNTTSVEKGSNVMGCVLFSTGLGNLLALGLLARSGLWCRRPLPLPSV 60

QY 61 FYMLVCGLTVTDLGKCLLSPVLAAYQNRSLRVLPALDNLSCQAFAPFMSFFGLSST 120
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
61 FYMLVCGLTVTDLGKCLLSPVLAAYQNRSLRVLPALDNLSCQAFAPFMSFFGLSST 120

QY 121 LQLLAMALECWLGLGHPFFYRRHITRLGALVAPVVSAPSLAFPCALPFMGFGKVCYCPG 180
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
121 LQLLAMALECWLGLGHPFFYRRHITRLGALVAPVVSAPSLAFPCALPFMGFGKVCYCPG 180

QY 181 TWCFTQWHEEGSLVGLGYSLYSLLMALLVLTATVLCNIGAMRNLYAMHRRLQRPSC 240
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
181 TWCFTQWHEEGSLVGLGYSLYSLLMALLVLTATVLCNIGAMRNLYAMHRRLQRPSC 240

QY 241 RDCAEPRADGRASPOPLEEDHLLLLALMTVLTFTMCSLPVI 282
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
241 RDCAEPRADGRASPOPLEEDHLLLLALMTVLTFTMCSLPVI 282

RESULT 11
ADD48180
ID ADD48180 standard; protein; 357 AA.
XX
AC ADD48180;
XX
DT 02-DEC-2004 (revised)
DT 29-JAN-2004 (first entry)
XX
DE Rat Protein AAB71762, SEQ ID NO 13978.
XX
KW Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
KW chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
XX
OS Rattus norvegicus.
OS Unidentified.
XX
PN WO2003016475-A2.
XX

PD 27-FEB-2003.
XX
PF 14-AUG-2002; 2002WO-US025765.
XX
PR 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333447P.
XX
PA (GEO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX
PI Woolf C, D'urso D, Befort K, Costigan M;
XX
DR WPI: 2003-268312/26.
DR GENBANK; AAB71762.
XX
PT New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX
PS Example 1; Page; 1017pp; English.
XX
CC The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a rat protein (described in Table 3
CC of the specification) which is differentially expressed during pain.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 357 AA;

Query Match 73.0%; Score 1125; DB 7; Length 357;
Best Local Similarity 78.0%; Pred. No. 5.2e-111;
Matches 216; Conservative 21; Mismatches 40; Indels 0; Gaps 0;

QY 6 YRCQNTTSVEKGSNVMGCVLFSTGLGNLLALGLLARSGLWCRRPLPLPSVFMV 65
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
5 YRCQATWVERGSSATMGVLFSTGLGNLLALGLLARSGLWCRRPLPLPSVFMV 64

QY 66 CGLTVDLLGKCLLSPVLAAYQNRSLRVLPALDNLSCQAFAPFMSFFGLSSTLQLLA 125
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
65 CGLTVDLLGKCLLSPVLAAYQNRSLKELLPASGNQLCEAFALMSFFGLASTLQLLA 124

QY 126 WALECWLISLGHPPFFYRRHITRLGALVAPVVSAPSLAFPCALPFMGFGKVCYCPGTC 185
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
125 WALECWLISLGHPPFFYRRHITARRGVLPVAPVAGAFALFALFAGFGKVCYCPGTC 184

QY 186 QMVHEEGSLVGLGYSLYSLLMALLVLTATVLCNIGAMRNLYAMHRRLQRPSC 245
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
185 QMHHKRSFSGVLSVLSLLMALLVLTATVLCNIGAMRNLYAMHRRQRRHPRCSRDR 244

QY 246 PRADGRASPOPLEEDHLLLLALMTVLTFTMCSLPVI 282
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
246 PRADGRASPOPLEEDHLLLLALMTVLTFTMCSLPVI 282

CC This sequence represents the murine prostaglandin D receptor. The
CC encoding sequence was obtained through reverse transcription PCR (using
CC the primers represented by AAT05173-705176). The full length DNA sequence
CC can be used in a vector to transform cells to produce this sequence. This
CC sequence can be used as an agent for the prevention and treatment of
CC diseases caused by excessive production of PGD-2, such as an immune
CC activator and an inhibitor of bleeding
XX
XX
SQ Sequence 357 AA;

Query Match 71.3%; Score 1099; DB 2; Length 357;
Best Local Similarity 75.8%; Pred. No. 3.1e-108;
Matches 210; Conservative 26; Mismatches 41; Indels 0; Gaps 0;
QY 6 YRCQNTTSVEKNSAVMGVLFSTGLGNLLALGLLARSGLGWCRRPLRLPLSPVFMV 65
DB 5 YRCQNTTSVEKNSAVMGVLFSTGLGNLLALGLLARSGLGWCRRPLRLPLSPVFMV 64
QY 66 CGLTVDLLGKLLSPVLAAYQNRSLRVLPALDNLSCQAFPMSPFGLSSTLQLLA 125
DB 65 CGLTVDLLGKLLSPVLAAYQNRSLRVLPALDNLSCQAFPMSPFGLSSTLQLLA 124
QY 126 MALECWLSLGHFFYRRHITLRLGALVAVPVVSAFSLAFPCALPFMGFGKVCPTWCPI 185
DB 125 MALECWLSLGHFFYRRHITLRLGALVAVPVVSAFSLAFPCALPFMGFGKVCPTWCPI 184
QY 186 QMVHEGSLSVLGYSLVYSSLMALLVATVLCNGLGAMRNLYAMHRLQHPHRSCTRDCAE 245
DB 185 QMVHEGSLSVLGYSLVYSSLMALLVATVLCNGLGAMRNLYAMHRLQHPHRSCTRDCAE 244
QY 246 PRADG---REASPOPLELDHLLALMTVLTFTMCSLPV 282
DB 245 SGGDYRHGSLHLELDHFLVLLALMTVLTFTMCSLP 281

RESULT 14
ADO29619
ID ADO29619 standard; protein; 362 AA.
XX ADO29619;
XX
XX 29-JUL-2004 (first entry)
XX
XX Mouse GPCR PTGER2, SEQ ID NO:721.
XX
XX G protein-coupled receptor; GPCR; drug screening; diagnosis;
XX transgenic mouse; neurological disorder; adrenal gland disorder;
XX colon disorder; intestinal disorder; cardiovascular disorder;
XX muscular disorder; blood disorder; immune disorder; bone disorder;
XX joint disorder; metabolic disorder; nutritive disorder; cancer;
XX kidney disorder; liver disorder; lung disorder; breast disorder;
XX ovary disorder; uterus disorder; prostate disorder; testis disorder;
XX skin disorder; stomach disorder; pancreas disorder; spleen disorder;
XX thymus disorder; thyroid disorder; antiparkinsonian; antimanic;
XX cytostatic; antiinflammatory; vasotropic; antianginal; antiarrhythmic;
XX CNS; central nervous system; respiratory; antidiarrhoeic; antidiabetic;
XX virucide; hepatotropic; antibacterial; antianaemic; antiseborrhoeic;
XX dermatological; antitumor; antithyroid; antiallergic; anorectic;
XX immunosuppressive; nephrotropic; gene therapy; GPCR modulator; mouse;
XX murine; receptor.
XX
XX Mus musculus.
XX
XX WO2004040000-A2.
XX
XX 13-MAY-2004.
XX
XX 09-SEP-2003; 2003WO-US028226.
XX
XX 09-SEP-2002; 2002US-0409303P.
XX 09-APR-2003; 2003US-0461329P.
XX
XX (PRIM-) PRIMAL INC.

XX
PI Gaitanaris GA, Bergmann JE, Gragerov A, Hohmann J, Li F;
PI Madisen L, McIlwain KL, Pavlova MN, Vassilatis D, Zeng H;
XX
XX WPI; 2004-390329/36.
DR N-PSDB; ADO30318.
XX
XX Novel mammalian G protein coupled receptors, useful for identifying
XX compounds that modulates diagnosing and treating disease condition
XX associated with GPCR dysfunction e.g. autoimmune diseases, angina
XX pectoris, Parkinson's disease.
XX
XX Claim 151; SEQ ID NO 721; 542pp; English.

XX The invention relates to human and mouse G protein-coupled receptors
XX (GPCRs) and nucleic acids encoding them. The invention also relates to
XX sequences at least 90% identical to the GPCR proteins and nucleic acids
XX of the invention; methods of treating, preventing or diagnosing diseases
XX associated with GPCRs of the invention; methods of screening for
XX compounds useful in the treatment of GPCR-related diseases; a transgenic
XX mouse comprising a GPCR gene of the invention; a mouse comprising a
XX mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived
XX from the transgenic mice; kits comprising several mice, each of which has
XX a mutation in a different GPCR gene of the invention; and kits comprising
XX probes which hybridise to GPCR polynucleotides of the invention. The
XX invention further discloses variants of the GPCR polypeptides and vectors
XX comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may
XX be used in the diagnosis, treatment or prevention of a wide variety of
XX diseases including neurological disorders (e.g., Alzheimer's disease,
XX depression, diabetic neuropathy, Parkinson's disease or schizophrenia);
XX disorders of the adrenal gland; disorders of the colon or intestine
XX (e.g., Crohn's disease, diarrhoea, food poisoning or irritable bowel
XX syndrome); cardiovascular disorders (e.g., angina, cardiac arrhythmia or
XX myocardial infarction); muscular disorders; blood disorders (e.g.,
XX anaemia or leukaemia); immune disorders (e.g., autoimmune disorders or
XX AIDS); bone and joint disorders (e.g., osteoarthritis, rheumatoid
XX arthritis, gout or osteoporosis); metabolic or nutritive disorders (e.g.,
XX obesity, enzyme deficiency-related diseases or vitamin deficiency-related
XX diseases); and disorders of the kidney, liver, lung, breast, ovary,
XX uterus, prostate, testis, skin, stomach, pancreas, spleen, thymus and
XX thyroid (e.g., cancers). The present sequence represents a GPCR of the
XX invention. Note: The full sequence data for this patent did not form part
XX of the printed specification; those sequences not shown were obtained in
XX electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 362 AA;
Query Match 38.6%; Score 595.5; DB 8; Length 362;
Best Local Similarity 45.4%; Pred. No. 1.7e-54;
Matches 128; Conservative 50; Mismatches 87; Indels 17; Gaps 7;
QY 8 CONTTSVEKNSAVMGVLFSTGLGNLLALGLLARSGLG--WCRRPLRLPLSPVFMV 65
DB 14 CKSRQWLLSGSPATSSVYMFAGVLGNLIALALLARRWRGDTGCSAGS-RTSISLPHV 72
QY 66 CGLTVDLLGKLLSPVLAAYQNRSLRVLPALDNLSCQAFPMSPFGLSSTLQLLA 125
DB 73 TELVUTDLGTLCLISPVVLAASYSRMTLVALAP--ESHACTYFATMTFFSLATMLLEA 130
QY 126 MALECWLSLGHFFYRRHITLRLGALVAVPVVSAFSLAFPCALPFMGFGKVCPTWCPI 185
DB 131 MALERYLSIGVYFYRRHLSRRGLAVLFVYAGASLLFCSLPLLYGVEYVQVCPGTWCFI 190
QY 186 QMVHEGSLSVLGYSLVYSSLMALLVATVLCNGLGAMRNLYAMHRLQHPHRSCTRDCAE 245
DB 191 R--HGR-----TAYLQLYATVMTLLLVAVLACNISVILNIRMHRSRR--SRCGLSGSS 241
QY 246 PRADG---REASPOPLELDHLLALMTVLTFTMCSLPV 284
DB 242 LRPGSRRRGERTSMAETDHLILALMTVLTFTMCSLP 283

RESULT 15

ABP81903
 ID ABP81903 standard; protein; 358 AA.
 AC ABP81903;
 XX
 DT 04-MAR-2003 (first entry)
 XX
 DE Human prostaglandin E receptor EP2 protein SEQ ID NO:291.
 XX
 KW G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
 KW G protein-coupled receptor modulator; antibody; immune-related disease;
 KW growth-related disease; cell regeneration-related disease; AIDS; cancer;
 KW immunological-related cell proliferative disease; autoimmune disease;
 KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;
 KW osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;
 KW graft versus host disease; Parkinson's disease; multiple sclerosis; pain;
 KW psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
 KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
 KW hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
 KW ulcer.

Homo sapiens.

WO200261087-A2.

08-AUG-2002.

19-DEC-2001; 2001WO-US050107.

19-DEC-2000; 2000US-0257144P.

(LIFE-) LIFESPAN BIOSCIENCES INC.

Burner GC, Roush CL, Brown JP;

WPI; 2003-046718/04.

N-PSDB; AB242750.

New isolated antigenic peptides e.g., for G protein-coupled receptors (GPCR), useful for diagnosing and designing drugs for treating conditions in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or autoimmune diseases.

Disclosure; Fig 1; 523pp; English.

The present invention describes antigenic peptides (I) comprising: (a) any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino acids. Also described: (1) an assay for the detection of a particular G protein-coupled receptor (GPCR) or a candidate polypeptide in a sample; and (2) an isolated antibody having high specificity and high affinity or avidity for a particular GPCR. (I) can be used as GPCR modulators and in gene therapy. The antigenic peptides for GPCRs are useful in detecting an antibody against a particular GPCR, and in the production of specific antibodies. The peptides and antibodies are also useful for detecting the presence or absence of corresponding GPCRs. The antigenic peptides for GPCRs and antibodies are useful for diagnosing and designing drugs for treating immune-related diseases, growth-related diseases, cell regeneration-related disease, immunological-related cell proliferative diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease, atherosclerosis, bacterial, fungal, protozoan or viral infections, osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute inflammation, allergies, Crohn's disease, diabetes, graft versus host disease, Parkinson's disease, multiple sclerosis, pain, psoriasis, anxiety, depression, schizophrenia, dementia, mental retardation, memory loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension, hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or any other disorder in which GPCRs are involved. The antibodies may be used in immunoassays and immunodiagnosis. AB242523 to AB242869 encode GPCR proteins given in ABP81675 to ABP82018, which are used in the exemplification of the present invention

Sequence 358 AA;

Query Match 38.0%; Score 586; DB 6; Length 358;
 Best Local Similarity 45.2%; Pred. No. 1.8e-53;
 Matches 128; Conservative 45; Mismatches 92; Indels 18; Gaps 7;
 QY 8 QNTTSVEKGN SAVMGVLFSTGLGNLALGLARSGLG--WCRRPLRPLPSVFMVLV 65
 DB 13 CETRWLPFGESPAISSVMFSGVLGNLTALARRWRGDCSAGRSSL-SLPHVLV 71
 QY 66 CGLTVTDLIGKCLLSPVLAAYQNRSLRVLAPALDNLSCQAFAPFMSFFGLSSTLQLLA 125
 DB 72 TELVFTDLLGTCLISPVVLASVARNQTLVALAP--ESRACTYFAFANTFSLATMLMFA 129
 QY 126 MALECWLSLGHFFFYRRHITLRLGALVAPVVSFAFLAFCALPFMGKFKVQYCPGTWCFT 185
 DB 130 MALERYLSIGHFYFYQRRVSASGLAVLPVIYAVSLLFCSLPLLDYQVYQYCPGTWCFT 189
 QY 186 QMVEEGSLSLVGLSYSLMALVLAIVLNLGAMRNLYAMHRELQRPSCRTDCAE 245
 DB 190 R--HGR-----TAYLQLYATLTLILIVSLACNFSVILNLRHRRSR--SRCGPSLGS 240
 QY 246 ----PRADGREASPOPLELDHLLLLALMTVLFTMCSLPVIAP 284
 DB 241 GRGFCARRRGERSVMAEETHLILLAINITITFAVCSLEPTIF 283

Search completed: April 22, 2005, 21:27:23
 Job time : 57.229 secs

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OM protein - protein search, using sw model

Run on: April 22, 2005, 21:00:43 ; Search time 17.6244 Seconds
(without alignments)
1253.721 Million cell updates/sec

Title: US-10-689-861-2
Perfect score: 1541
Sequence: 1 MKSPYRCQNTTSVEKNSA.....CSLPVIAFVPGVPAKTPGSR 296

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
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2: /cgn2_6/prodata/1/1aa/5B COMB.pep:*
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4: /cgn2_6/prodata/1/1aa/6B COMB.pep:*
5: /cgn2_6/prodata/1/1aa/PCTUS COMB.pep:*
6: /cgn2_6/prodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1467	95.2	359	2 US-08-812-203-3	Sequence 3, Appli
2	1467	95.2	359	3 US-09-300-864-3	Sequence 3, Appli
3	1467	95.2	359	3 US-09-598-418-3	Sequence 3, Appli
4	585	38.0	358	1 US-08-239-431A-4	Sequence 4, Appli
5	585	38.0	358	1 US-09-267-423-4	Sequence 4, Appli
6	580	37.6	358	4 US-09-826-509-559	Sequence 559, App
7	564	36.6	358	2 US-08-463-0818-6	Sequence 6, Appli
8	564	36.6	358	2 US-08-461-378A-6	Sequence 6, Appli
9	564	36.6	358	2 US-08-462-390B-6	Sequence 6, Appli
10	564	36.6	358	2 US-08-463-074B-6	Sequence 6, Appli
11	564	36.6	358	3 US-08-465-585C-6	Sequence 6, Appli
12	564	36.6	358	3 US-08-652-446-6	Sequence 6, Appli
13	518.5	33.6	386	1 US-08-134-012-3	Sequence 3, Appli
14	518.5	33.6	386	1 US-08-520-513-3	Sequence 3, Appli
15	518.5	33.6	386	3 US-09-039-798-3	Sequence 3, Appli
16	389	25.2	513	1 US-08-390-162-6	Sequence 6, Appli
17	389	25.2	513	1 US-08-685-945B-6	Sequence 6, Appli
18	364.5	23.7	488	1 US-08-115-365-2	Sequence 2, Appli
19	364.5	23.7	488	1 US-08-586-897-2	Sequence 2, Appli
20	361.5	23.5	488	4 US-09-826-509-561	Sequence 561, App
21	261.5	17.0	361	1 US-08-390-162-4	Sequence 4, Appli
22	261.5	17.0	361	1 US-08-685-945B-4	Sequence 4, Appli
23	261.5	17.0	365	1 US-08-390-162-2	Sequence 2, Appli
24	261.5	17.0	365	1 US-08-685-945B-2	Sequence 2, Appli
25	256	16.6	385	1 US-08-416-758A-3	Sequence 3, Appli
26	256	16.6	385	4 US-08-880-865-3	Sequence 3, Appli
27	250.5	16.3	343	4 US-09-054-272-6	Sequence 6, Appli

28 244.5 15.9 365 3 US-08-155-005A-8 Sequence 8, Appli
29 244.5 15.9 365 3 US-09-363-783-8 Sequence 8, Appli
30 244.5 15.9 365 4 US-09-661-758A-8 Sequence 8, Appli
31 244.5 15.9 388 3 US-08-155-005A-6 Sequence 6, Appli
32 244.5 15.9 388 3 US-09-363-783-6 Sequence 6, Appli
33 244.5 15.9 388 4 US-09-661-758A-6 Sequence 6, Appli
34 244.5 15.9 390 3 US-08-155-005A-4 Sequence 4, Appli
35 244.5 15.9 390 3 US-08-155-005A-17 Sequence 17, Appli
36 244.5 15.9 390 3 US-09-363-783-4 Sequence 4, Appli
37 244.5 15.9 390 3 US-09-363-783-17 Sequence 17, Appli
38 244.5 15.9 390 4 US-09-661-758A-4 Sequence 4, Appli
39 244.5 15.9 390 4 US-09-661-758A-17 Sequence 17, Appli
40 225.5 14.6 378 1 US-08-416-758A-4 Sequence 4, Appli
41 225.5 14.6 378 4 US-08-880-865-4 Sequence 4, Appli
42 219.5 14.2 402 2 US-08-068-729-4 Sequence 4, Appli
43 219.5 14.2 402 3 US-09-255-671-4 Sequence 4, Appli
44 219.5 14.2 402 4 US-09-395-366-4 Sequence 4, Appli
45 219.5 14.2 402 4 US-09-826-509-557 Sequence 557, App

ALIGNMENTS

RESULT 1
US-08-812-203-3
; Sequence 3, Application US/08812203
; Patent No. 5958723
; GENERAL INFORMATION:
; APPLICANT: ABRAMOVITZ, MARK
; APPLICANT: BOIE, YVES
; APPLICANT: SAWYER, NICOLE
; APPLICANT: METTERS, KATHLEEN
; APPLICANT: SLIPETZ, DEBORAH
; TITLE OF INVENTION: DNA ENCODING PROSTAGLANDIN RECEPTOR DP
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: JOHN W. WALLEN, III
; STREET: 126 E. LINCOLN AVE., P.O. BOX 2000
; CITY: RAHWAY
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065-0900

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/812,203
FILING DATE: 06-MAR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/378,682
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: WALLEN III, JOHN W.
REGISTRATION NUMBER: 35,403
REFERENCE/DOCKET NUMBER: MRL 94/185
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908)594-3905
TELEX: (908)594-4720
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 359 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-812-203-3

Query Match 95.2%; Score 1467; DB 2; Length 359;
Best Local Similarity 100.0%; Pred. No. 6.2e-131;
Matches 282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKSPFYRCQNTTTSVEKGN SAVMGVLFSTGLGNLLALGLLARSGLGWCRRPLRLPSV 60
DB 1 MKSPFYRCQNTTTSVEKGN SAVMGVLFSTGLGNLLALGLLARSGLGWCRRPLRLPSV 60
QY 61 FYMLVCGLTVDLLGKCLLSPVLAAYAQNRSLRVLPALDNLSCQAFAFMSFFGLSST 120
DB 61 FYMLVCGLTVDLLGKCLLSPVLAAYAQNRSLRVLPALDNLSCQAFAFMSFFGLSST 120
QY 121 LQLLAMALECWLGLGHPFFYRRHITLRIGALVAPVVSFAFLAFALPFMGFGKFVQYCPG 180
DB 121 LQLLAMALECWLGLGHPFFYRRHITLRIGALVAPVVSFAFLAFALPFMGFGKFVQYCPG 180
QY 181 TWCFTQMVHEGSLSVLGYSVLYSSIMALLVATVLCNIGAMRNLYAMHRRILQRHPRST 240
DB 181 TWCFTQMVHEGSLSVLGYSVLYSSIMALLVATVLCNIGAMRNLYAMHRRILQRHPRST 240
QY 241 RDCAPRADGREASPOPLEELDHLLALLMTVLTFTMCSLPVI 282
DB 241 RDCAPRADGREASPOPLEELDHLLALLMTVLTFTMCSLPVI 282

RESULT 2

US-09-300-864-3
; Sequence 3, Application US/09300864
; Patent No. 6214972
; GENERAL INFORMATION:
; APPLICANT: ABRAMOVITZ, MARK
; APPLICANT: BOIE, YVES
; APPLICANT: SAWYER, NICOLE
; APPLICANT: METTERS, KATHLEEN
; APPLICANT: SLIPETZ, DEBORAH
; TITLE OF INVENTION: DNA ENCODING PROSTAGLANDIN RECEPTOR DP
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: JOHN W. WALLEN, III
; STREET: 126 E. LINCOLN AVE., P.O. BOX 2000
; CITY: RAHWAY
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065-0900
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/300,864
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/378,682
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: WALLEN III, JOHN W.
; REGISTRATION NUMBER: 35,403
; REFERENCE/DOCKET NUMBER: MRL 94/185
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908)594-3905
; TELEX: (908)594-4720
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 359 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-300-864-3

Query Match 95.2%; Score 1467; DB 3; Length 359;
Best Local Similarity 100.0%; Pred. No. 6.2e-131;
Matches 282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKSPFYRCQNTTTSVEKGN SAVMGVLFSTGLGNLLALGLLARSGLGWCRRPLRLPSV 60
DB 1 MKSPFYRCQNTTTSVEKGN SAVMGVLFSTGLGNLLALGLLARSGLGWCRRPLRLPSV 60
QY 61 FYMLVCGLTVDLLGKCLLSPVLAAYAQNRSLRVLPALDNLSCQAFAFMSFFGLSST 120
DB 61 FYMLVCGLTVDLLGKCLLSPVLAAYAQNRSLRVLPALDNLSCQAFAFMSFFGLSST 120
QY 121 LQLLAMALECWLGLGHPFFYRRHITLRIGALVAPVVSFAFLAFALPFMGFGKFVQYCPG 180
DB 121 LQLLAMALECWLGLGHPFFYRRHITLRIGALVAPVVSFAFLAFALPFMGFGKFVQYCPG 180
QY 181 TWCFTQMVHEGSLSVLGYSVLYSSIMALLVATVLCNIGAMRNLYAMHRRILQRHPRST 240
DB 181 TWCFTQMVHEGSLSVLGYSVLYSSIMALLVATVLCNIGAMRNLYAMHRRILQRHPRST 240
QY 241 RDCAPRADGREASPOPLEELDHLLALLMTVLTFTMCSLPVI 282
DB 241 RDCAPRADGREASPOPLEELDHLLALLMTVLTFTMCSLPVI 282

RESULT 3

US-09-598-418-3
; Sequence 3, Application US/09598418
; Patent No. 6395499
; GENERAL INFORMATION:
; APPLICANT: ABRAMOVITZ, MARK
; APPLICANT: BOIE, YVES
; APPLICANT: SAWYER, NICOLE
; APPLICANT: METTERS, KATHLEEN
; APPLICANT: SLIPETZ, DEBORAH
; TITLE OF INVENTION: DNA ENCODING PROSTAGLANDIN RECEPTOR DP
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: JOHN W. WALLEN, III
; STREET: 126 E. LINCOLN AVE., P.O. BOX 2000
; CITY: RAHWAY
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065-0900
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/598,418
; FILING DATE: 20-Jun-2000
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: WALLEN III, JOHN W.
; REGISTRATION NUMBER: 35,403
; REFERENCE/DOCKET NUMBER: MRL 94/185
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908)594-3905
; TELEX: (908)594-4720
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 359 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-598-418-3

Query Match 95.2%; Score 1467; DB 3; Length 359;
Best Local Similarity 100.0%; Pred. No. 6.2e-131;
Matches 282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKSPFYRCQNTTTSVEKGN SAVMGVLFSTGLGNLLALGLLARSGLGWCRRPLRLPSV 60
DB 1 MKSPFYRCQNTTTSVEKGN SAVMGVLFSTGLGNLLALGLLARSGLGWCRRPLRLPSV 60

QY 61 FYMLVCGLTVDLLGKCLLSPVLAAYQNRSLRVLPALDLSLCOAFAPFMSFFGLSST 120
DB |||||
QY 61 FYMLVCGLTVDLLGKCLLSPVLAAYQNRSLRVLPALDLSLCOAFAPFMSFFGLSST 120
DB |||||
QY 121 LOLLAMALECWLGLGHPFFYRRHITLRLGALVAPVVSFAFALCPFMGFGKFGVQYCPG 180
DB |||||
QY 121 LOLLAMALECWLGLGHPFFYRRHITLRLGALVAPVVSFAFALCPFMGFGKFGVQYCPG 180
DB |||||
QY 181 TWCFFIQMHVEEGSLSVLGYSVLYSSLMALLVATVLCNIGAMRNLYAMHRRLQHRPSRCT 240
DB |||||
QY 181 TWCFFIQMHVEEGSLSVLGYSVLYSSLMALLVATVLCNIGAMRNLYAMHRRLQHRPSRCT 240
DB |||||
QY 241 RDCASPRADGREASPOPLEBHDHLLALLMTVLTWCSSLPVI 282
DB |||||
QY 241 RDCASPRADGREASPOPLEBHDHLLALLMTVLTWCSSLPVI 282
DB |||||

RESULT 4

US-08-239-431A-4
; Sequence 4, Application US/08239431A
; Patent No. 5716835
; GENERAL INFORMATION:
; APPLICANT: Regan, John W.
; APPLICANT: Gil, Daniel W.
; TITLE OF INVENTION: NOVEL HUMAN EP PROTAGLANDIN RECEPTOR
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson and Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: USA
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/239,431A
; FILING DATE: 05-MAY-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Israelien, Ned A
; REGISTRATION NUMBER: 29,655
; REFERENCE/DOCKET NUMBER: ALRGN.053A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-235-8550
; TELEFAX: 619-235-0176
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 358 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
US-08-239-431A-4

Query Match 38.0%; Score 585; DB 1; Length 358;
Best Local Similarity 45.2%; Pred. No. 2.2e-47;
Matches 128; Conservative 45; Mismatches 92; Indels 18; Gaps 7;

QY 8 CONTTSVEKGSANVGGVLFSTGLLGNLLALGLLARSGLG--WCRRRLPRLPSPVFMV 65

DB 13 CETROWLPPGESPAISSVMFSGVLGNLTALALLARRWRGDCVCCSAGRSSL-SLPHVLV 71
QY |||||
DB 66 CGLTVTDLLGKCLLSPVLAAYQNRSLRVLPALDLSLCOAFAPFMSFFGLSSTLQLLA 125
QY |||||
DB 72 TELVFTDLLGKCLLSPVLAAYQNRSLRVLPALDLSLCOAFAPFMSFFGLSSTLQLLA 129
QY |||||
DB 126 MALECWLSLGHPPFFYRRHITLRLGALVAPVVSFAFALCPFMGFGKFGVQYCPGTCFI 185
DB |||||
QY 130 MALERYLSIGHPPFYQRRVSRSGGLAVLPVIYAVSLLCFSLPLLDYGOVYQVCPGTCFI 189
QY |||||
DB 186 QMVHEEGSLSVLGYSVLYSSLMALLVATVLCNIGAMRNLYAMHRRLQHRPSRCTDCAE 245
DB |||||
QY 190 R--HGR-----TAYLQLYATLTLIVSVLACNFVILNLRMHRSSR--SRCGSPSLGS 240
QY |||||
DB 246 ----PRADGREASPOPLEBHDHLLALLMTVLTWCSSLPVI 284
QY |||||
DB 241 GRGGPGARRRGERSVMAEETHLILLAITITFAVCSLPFTTIF 283
QY |||||

RESULT 5

US-09-267-423-4
; Sequence 4, Application US/09267423
; Patent No. 6395878
; GENERAL INFORMATION:
; APPLICANT: Regan, John W.
; APPLICANT: Gil, Daniel W.
; APPLICANT: Woodward, David F.
; TITLE OF INVENTION: No. 6395878el Human Prostaglandin Ep Receptor
; FILE REFERENCE: 17023 DIV CIP
; CURRENT APPLICATION NUMBER: US/09/267,423
; CURRENT FILING DATE: 1999-03-12
; EARLIER APPLICATION NUMBER: 09/019,393
; EARLIER FILING DATE: 1998-02-05
; EARLIER APPLICATION NUMBER: 08/239,431
; EARLIER FILING DATE: 1994-05-05
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 358
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-267-423-4

Query Match 38.0%; Score 585; DB 3; Length 358;
Best Local Similarity 45.2%; Pred. No. 2.2e-47;
Matches 128; Conservative 45; Mismatches 92; Indels 18; Gaps 7;

QY 8 CONTTSVEKGSANVGGVLFSTGLLGNLLALGLLARSGLG--WCRRRLPRLPSPVFMV 65
DB |||||
QY 13 CETROWLPPGESPAISSVMFSGVLGNLTALALLARRWRGDCVCCSAGRSSL-SLPHVLV 71
DB |||||
QY 66 CGLTVTDLLGKCLLSPVLAAYQNRSLRVLPALDLSLCOAFAPFMSFFGLSSTLQLLA 125
DB |||||
QY 72 TELVFTDLLGKCLLSPVLAAYQNRSLRVLPALDLSLCOAFAPFMSFFGLSSTLQLLA 129
QY |||||
QY 126 MALECWLSLGHPPFFYRRHITLRLGALVAPVVSFAFALCPFMGFGKFGVQYCPGTCFI 185
DB |||||
QY 130 MALERYLSIGHPPFYQRRVSRSGGLAVLPVIYAVSLLCFSLPLLDYGOVYQVCPGTCFI 189
QY |||||
QY 186 QMVHEEGSLSVLGYSVLYSSLMALLVATVLCNIGAMRNLYAMHRRLQHRPSRCTDCAE 245
DB |||||
QY 190 R--HGR-----TAYLQLYATLTLIVSVLACNFVILNLRMHRSSR--SRCGSPSLGS 240
QY |||||
QY 246 ----PRADGREASPOPLEBHDHLLALLMTVLTWCSSLPVI 284
DB |||||
QY 241 GRGGPGARRRGERSVMAEETHLILLAITITFAVCSLPFTTIF 283
QY |||||

RESULT 6

US-09-826-509-559
; Sequence 559, Application US/09826509
; Patent No. 6806054

```
; GENERAL INFORMATION:
; APPLICANT: Lehmann-Brunnsma, Karin
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: No. 6806054-Endogenous, Constitutively Activated Known G
; FILE REFERENCE: AREN-207
; CURRENT APPLICATION NUMBER: US/09/826,509
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/195,747
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 589
; SOFTWARE: PatentIn Version 2.1
; SEQ ID NO 559
; LENGTH: 358
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-826-509-559

Query Match      37.6%; Score 580; DB 4; Length 358;
Best Local Similarity 44.9%; Pred. No. 6.5e-47;
Matches 127; Conservative 45; Mismatches 93; Indels 18; Gaps 7;

QY      8  CONTTSVEKGSAAVMGGVLFSTGLIGNLLALGLLARSGLG--WCSRRRLRLPLPSVYVMLV 65
Db      13  CETRWLPFGSPALSSVWFSAGVIGNLIALALLARRWGDVGCAGRRSSL-SLFHVLV 71
QY      66  CGLTVTDLLGKCLLSPVVLAAYAQNRSLRVLPALDNLSCQAFPMFSGFGLSSTLQLLA 125
Db      72  TELVFTDLGLTCLISPVVLAAYARNQTLVALAP--ESRACTVFAFAMTFFSLATMLMFA 129
QY      126  MALECWLSLGHPPFRRHITLRLGALVAPVVSASFALCALPFMGFGKVFQVCPGTWCFI 185
Db      130  MALERYLSIGHFYQRRVSAGGLAVLPVIYAVSLFCSLPLLDYGOYVQVCPGTWCFI 189
QY      186  QMVHEEGSLVGLSVLYSSLMALLVATVLCNLGAMNLYAMHRRRLQRPSCSTRDCAE 245
Db      190  R--HGR-----TAYLQLVATLILLIVSVLACNFVSILNLRMHRRSR--SRCGPSLGS 240
QY      246  ----PRADGRASQPLBELDHLHLLALMTVLTWCSPVIAF 284
Db      241  GRGGPGARRRGERSMAETDHKILLAIWITTFVAVCSLPFTIF 283

RESULT 7
US-08-463-081B-6
; Sequence 6, Application US/08463081B
; Patent No. 5871960
; Patent No. 5871960 5837487
; GENERAL INFORMATION:
; APPLICANT: Smith, Kendall A. & Beadling, Carol
; TITLE OF INVENTION: Nucleic Acids Encoding CR5 Polypeptide,
; TITLE OF INVENTION: Vector and Transformed Cell Thereof, and Expression Thereof
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PRETTY, SCHROEDER & POPLAWSKI
; STREET: 444 South Flower St. - Suite 1900
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0,
; SOFTWARE: Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/463,081B
; FILING DATE: 5-JUN-1995
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION NUMBER: US/08/463,081B
```

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; APPLICATION NUMBER: US 08/104,736
; FILING DATE: 10-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/796,066
; FILING DATE: 20-NOV-91
; ATTORNEY/AGENT INFORMATION:
; NAME: Viviana Amzel, Ph. D.
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: P66 38150 (DART-060)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 622-7700
; TELEFAX: (213) 489-4210
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 358 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-463-081B-6

Query Match      36.6%; Score 564; DB 2; Length 358;
Best Local Similarity 44.2%; Pred. No. 2.1e-45;
Matches 125; Conservative 44; Mismatches 96; Indels 18; Gaps 7;

QY      8  CONTTSVEKGSAAVMGGVLFSTGLIGNLLALGLLARSGLG--WCSRRRLRLPLPSVYVMLV 65
Db      13  CETRWLPFGSPALSSVWFSAGVIGNLIALALLARRWGDVGCAGRRSSL-SLFHVLV 71
QY      66  CGLTVTDLLGKCLLSPVVLAAYAQNRSLRVLPALDNLSCQAFPMFSGFGLSSTLQLLA 125
Db      72  TELVFTDLGLTCLISPVVLAAYARNQTLVALAP--ESRACTVFAFAMTFFSLATMLMFT 129
QY      126  MALECWLSLGHPPFRRHITLRLGALVAPVVSASFALCALPFMGFGKVFQVCPGTWCFI 185
Db      130  MALERYLSIGHFYQRRVSAGGLAVLPVIYAVSLFCSLPLLDYGOYVQVCPGTWCFI 189
QY      186  QMVHEEGSLVGLSVLYSSLMALLVATVLCNLGAMNLYAMHRRRLQRPSCSTRDCAE 245
Db      190  R--HGR-----TAYLQLVATLILLIVSVLACNFVSILNLRMHRRSR--SRCGPSLGS 240
QY      246  ----PRADGRASQPLBELDHLHLLALMTVLTWCSPVIAF 284
Db      241  GRGGPGARRRGERSMAETDHKILLAIWITTFVAVCSLPFTIF 283

RESULT 8
US-08-461-379A-6
; Sequence 6, Application US/08461379A
; Patent No. 5871961
; GENERAL INFORMATION:
; APPLICANT: Smith, Kendall A. & Beadling, Carol
; TITLE OF INVENTION: Nucleic Acids Encoding CR5 Polypeptide,
; TITLE OF INVENTION: Vector and Transformed Cell Thereof, and
; TITLE OF INVENTION: Expression Thereof
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ratner & Prestia
; CITY: Valley Forge
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0,
; SOFTWARE: Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/461,379A
; FILING DATE: 5-JUNE-1995
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION NUMBER: USSN 08/330,108; 08/104,736
```

APPLICATION NUMBER: 07/796,066
FILING DATE: 27-OCT-1994; 10-AUG-1993 & 20-NOV-91
ATTORNEY/AGENT INFORMATION:
NAME: Viviana Amzel, Ph. D.
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: DART-070
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610)470-0700
TELEFAX: (610)470-0701
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 358 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-461-379A-6

Query Match 36.6%; Score 564; DB 2; Length 358;
Best Local Similarity 44.2%; Pred. No. 2.1e-45;
Matches 125; Conservative 44; Mismatches 96; Indels 18; Gaps 7;
QY 8 CQNTTSVERKNSAVMGVLFSTGLLGNLALGLLARSGLG--WCSRRPLRPLPSVFMVLV 65
DB 13 CTRQWFPFGESPAISVMFSAGVLNLIETALLARRWQDVCCSAGRSSL-SLPHVLV 71
QY 66 CGLTVTDLGKLLSPVLAAYAQNRSLRVLPALDNSLCOAFAPFMSFGLSSTLQLLA 125
DB 72 TELVFTDLGTLCLISPVVLASYARNQTLVALAP--ESRSTYFAPFAMTFFSLATMLMLFT 129
QY 126 MALECWLSLGHFFYRRHTLRGALVAPVVSFAFLAFALPFGMGKFKVQCPGTWCPI 185
DB 130 MALERYLSIGHFYQRRVSRSGGLAVLPIYAVLSLLFCSLPLLDYGQVQVQCPGTWCPI 189
QY 186 QMVHEEGSLVGLSYSLMALIVLATVLCNIGAMRNLYAMHRLQRHPRSCTRDCAE 245
DB 190 R--HGR-----TAYLQLYATLILLVSVLACNFSVILNIRHRRSR--SRCGSPSLGS 240
QY 246 ----PRADGREASPOPLELDHLLALMTVLFTMCSLPIAF 284
DB 241 GRGGPGARRGRVSMABETHLLAILMTITFAVCSLPFTIF 283

RESULT 9

US-08-462-390B-6
Sequence 6, Application US/08462390B
Patent No. 5832894
GENERAL INFORMATION:
APPLICANT: Smith, K. A., & Beadling, C.
TITLE OF INVENTION: Nucleic Acids Encoding CR8 Polypeptide, Vector and
TITLE OF INVENTION: Transformed Cell Thereof, and Expression Thereof
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ratner & Prestia
CITY: Valley Forge
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19482
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,390B
FILING DATE: 5-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/330,108
FILING DATE: 27-OCT-1994
APPLICATION NUMBER: USSN 08/104,736
FILING DATE: 10-AUG-1993
APPLICATION NUMBER: USSN 07/796,066
FILING DATE: 20-NOV-91

ATTORNEY/AGENT INFORMATION:
NAME: Viviana Amzel, Ph. D.
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: DART-040
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610)407-0700
TELEFAX: (610)407-0701
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 358 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-462-390B-6

Query Match 36.6%; Score 564; DB 2; Length 358;
Best Local Similarity 44.2%; Pred. No. 2.1e-45;
Matches 125; Conservative 44; Mismatches 96; Indels 18; Gaps 7;
QY 8 CQNTTSVERKNSAVMGVLFSTGLLGNLALGLLARSGLG--WCSRRPLRPLPSVFMVLV 65
DB 13 CTRQWFPFGESPAISVMFSAGVLNLIETALLARRWQDVCCSAGRSSL-SLPHVLV 71
QY 66 CGLTVTDLGKLLSPVLAAYAQNRSLRVLPALDNSLCOAFAPFMSFGLSSTLQLLA 125
DB 72 TELVFTDLGTLCLISPVVLASYARNQTLVALAP--ESRSTYFAPFAMTFFSLATMLMLFT 129
QY 126 MALECWLSLGHFFYRRHTLRGALVAPVVSFAFLAFALPFGMGKFKVQCPGTWCPI 185
DB 130 MALERYLSIGHFYQRRVSRSGGLAVLPIYAVLSLLFCSLPLLDYGQVQVQCPGTWCPI 189
QY 186 QMVHEEGSLVGLSYSLMALIVLATVLCNIGAMRNLYAMHRLQRHPRSCTRDCAE 245
DB 190 R--HGR-----TAYLQLYATLILLVSVLACNFSVILNIRHRRSR--SRCGSPSLGS 240
QY 246 ----PRADGREASPOPLELDHLLALMTVLFTMCSLPIAF 284
DB 241 GRGGPGARRGRVSMABETHLLAILMTITFAVCSLPFTIF 283

RESULT 10

US-08-463-074B-6
Sequence 6, Application US/08463074B
Patent No. 6020155
GENERAL INFORMATION:
APPLICANT: Smith, Kendall A. & Beadling, Carol
TITLE OF INVENTION: Nucleic Acids Encoding CR1 Fusion Protein, Vector an
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: PRETTY, SCHROEDER & POPLAWSKI
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0,
SOFTWARE: Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,074B
FILING DATE: 5-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/104,736
FILING DATE: 10-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/796,066
FILING DATE: 20-NOV-91
ATTORNEY/AGENT INFORMATION:
NAME: Viviana Amzel, Ph. D.
REGISTRATION NUMBER: 30,930

444 South Flower St. - Suite 1900

REFERENCE/DOCKET NUMBER: P66 38143 (DART-020)
TELEPHONE: (213) 622-7700
TELEFAX: (213) 489-4210
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 358 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-463-074B-6

Query Match 36.6%; Score 564; DB 3; Length 358;
Best Local Similarity 44.2%; Pred. No. 2.1e-45;
Matches 125; Conservative 44; Mismatches 96; Indels 18; Gaps 7;
QY 8 QNTTSVEKGN SAVMGVLFSTGLGNLALGLLARSGLG--WCRRRLRLPLPSVYMLV 65
Db 13 CETQWFPFGSPAISSVMFSGVLGNLTIELALLARRWQGVGCSAGRSSL-SLFHVLV 71
QY 66 CGLTVTDLLGKLLSPVLAAYQNRSLRVLPALDNLSCQAFAPFMSFFGLSSTLQLLA 125
Db 72 TELVFTDLGLTCLISPVVLASVARNQTLVALAP--ESRASTVFAPAMTFFSLATMLFT 129
QY 126 MALECWLSLGHFPFRRHITRLGALVAPVVSFAFALCALPFGKFGVQVCPGTWCFI 185
Db 130 MALERYLSIGHFYFYQRRVRSRGGGLAVLPVIYAVSLFLFCSLPDDYQVQVCPGTWCFI 189
QY 186 QMVHEGSLVGLSVLYSSLMALLVATVLCNGLAMRNLYAMHRLQRHPRSCTRDCAE 245
Db 190 R--HGR-----TAYLQLYATLTLILVSVLACNFSVILNLMHRRSR--SRCGPGSLGS 240
QY 246 ----PRADGREASPOPLELDHLLALMTVLTWCSSLPIAF 284
Db 241 GRGGGARRRGERSVMAETDHLILLAIMTITFAVCSLPFTIF 283

RESULT 11
US-08-465-585C-6
Sequence 6, Application US/084655585C
Patent No. 6027914
GENERAL INFORMATION:
APPLICANT: Smith, K. A., & Beadling, C.
TITLE OF INVENTION: Nucleic Acids Encoding CR6 Polypeptide, Vecto
TITLE OF INVENTION: Transformed Cell Thereof, and Expression Thereof
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: PRETTY, SCHROEDER & POPLAWSKI
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 900071
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 5-JUNE-1995
PRIOR APPLICATION NUMBER: US/08/465,585C
APPLICATION NUMBER: USSN 08/330,108
FILING DATE: 27-OCT-1994
APPLICATION NUMBER: USSN 08/104,736
FILING DATE: 10-AUG-1993
APPLICATION NUMBER: USSN 07/796,066
FILING DATE: 20-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: Viviana Anzel, Ph.D.
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: P66 38149 (DART-050)
TELECOMMUNICATION INFORMATION:
444 South Flower St. - Suite 1900

TELEPHONE: (213) 622-7700
TELEFAX: (213) 4894210
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 358 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-465-585C-6
Query Match 36.6%; Score 564; DB 3; Length 358;
Best Local Similarity 44.2%; Pred. No. 2.1e-45;
Matches 125; Conservative 44; Mismatches 96; Indels 18; Gaps 7;
QY 8 QNTTSVEKGN SAVMGVLFSTGLGNLALGLLARSGLG--WCRRRLRLPLPSVYMLV 65
Db 13 CETQWFPFGSPAISSVMFSGVLGNLTIELALLARRWQGVGCSAGRSSL-SLFHVLV 71
QY 66 CGLTVTDLLGKLLSPVLAAYQNRSLRVLPALDNLSCQAFAPFMSFFGLSSTLQLLA 125
Db 72 TELVFTDLGLTCLISPVVLASVARNQTLVALAP--ESRASTVFAPAMTFFSLATMLFT 129
QY 126 MALECWLSLGHFPFRRHITRLGALVAPVVSFAFALCALPFGKFGVQVCPGTWCFI 185
Db 130 MALERYLSIGHFYFYQRRVRSRGGGLAVLPVIYAVSLFLFCSLPDDYQVQVCPGTWCFI 189
QY 186 QMVHEGSLVGLSVLYSSLMALLVATVLCNGLAMRNLYAMHRLQRHPRSCTRDCAE 245
Db 190 R--HGR-----TAYLQLYATLTLILVSVLACNFSVILNLMHRRSR--SRCGPGSLGS 240
QY 246 ----PRADGREASPOPLELDHLLALMTVLTWCSSLPIAF 284
Db 241 GRGGGARRRGERSVMAETDHLILLAIMTITFAVCSLPFTIF 283

RESULT 12
US-08-652-446-6
Sequence 6, Application US/08652446
Patent No. 6057427
GENERAL INFORMATION:
APPLICANT: Smith, Kendall A. & Beadling, Carol
TITLE OF INVENTION: Nucleic Acids Encoding CRS
TITLE OF INVENTION: Polypeptide, Vector and Transformed Cell Thereof, and
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: PRETTY, SCHROEDER & POPLAWSKI
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0,
SOFTWARE: Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: US/08/652,446
PRIOR APPLICATION NUMBER: EP App. # 96921319.8
FILING DATE: 5-JAN-1998
APPLICATION NUMBER: PCT/US/96/09194
FILING DATE: 5-JUN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,108
FILING DATE: 27-OCT-1994
APPLICATION NUMBER: 08/463,074
FILING DATE: 5-JUN-1995
PRIOR APPLICATION DATA:
444 South Flower St. - Suite 1900

APPLICATION NUMBER: 08/462,337
FILING DATE: 5-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/462,390
FILING DATE: 5-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/465,585
FILING DATE: 5-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/463,081
FILING DATE: 5-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/461,379
FILING DATE: 5-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/739,523
FILING DATE: 29-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Viviana Anzel, Ph. D.
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: FP66 40035
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 622-7700
TELEFAX: (213) 489-4210
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 358 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-652-446-6

Query Match 36.6%; Score 564; DB 3; Length 358;

Best Local Similarity 44.2%; Pred. No. 2.1e-45;

Matches 125; Conservative 44; Mismatches 96; Indels 18; Gaps 7;

QY 8 QNTTSVEKGSNAVMGVLFSTGLGNLALGLLARSGLG--WCSRRPLRLPSVYMLV 65
DB 13 CETROFFPGESEPAISVNFSAVLGNLIELALLARRWQGVGCSAGRSSL-SLFHVLV 71
QY 66 CGLTVTDLGKCLSPVLLAAVNAONSLRVLAPALDNLSCQAFAPFMSFFGLSSTLQLLA 125
DB 72 TELVFTDLGTCILSPVLLASTARNLILVALAP--ESRASTVPAPMTFFSLATMLMLFT 129
QY 126 MALECWLSLGHPPFYRRHITRLGALVAPVWSAFSLAFALCPFMGFKFVQYCPGTWCFI 185
DB 130 MALERYLSIGHPPFYQRRYSRSGSLAVLPVIVAVSLFLCSLPLLDYQYVQYCPGTWCFI 189
QY 186 QMVHEGSLVGLSYVLSLMAVLLVATVLCNLGAMRNLYAMHRLQRHPRSCRTDCAE 245
DB 190 R--HGR-----TAYLQVATLILLITVSVLACNFSVILNLRHRSR--SRCGPSLGS 240
QY 246 ----PRADGREASPOPLELDHLLALMTVLTMCSLPVIAP 284
DB 241 GRGGGARRRGERSVMAEETHLLAILMTITFAVCSLPFTIP 283

RESULT 13

US-08-134-012-3

Sequence 3, Application US/08134012

Patent No. 5516652

GENERAL INFORMATION:

APPLICANT: Abramovitz, Mark

APPLICANT: Boie, Yves

APPLICANT: Grygorczyk, Richard

APPLICANT: Metters, Kathleen

APPLICANT: Rushmore, Thomas H.

APPLICANT: Slipetz, Deborah M.

TITLE OF INVENTION: DNA ENCODING PROSTAGLANDIN RECEPTOR IP

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSEE: John Wallen

STREET: 126 E. Lincoln Avenue

CITY: Rahway

STATE: New Jersey

COUNTRY: USA

ZIP: 07065-0907

CITY: Rahway
STATE: New Jersey
COUNTRY: USA
ZIP: 07065
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/134,012
FILING DATE: 06-OCT-1993
CLASSIFICATION: S30
ATTORNEY/AGENT INFORMATION:
NAME: Wallen, John W
REGISTRATION NUMBER: 35,403
REFERENCE/DOCKET NUMBER: 19098
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-3905
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 386 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-134-012-3

Query Match 33.6%; Score 518.5; DB 1; Length 386;

Best Local Similarity 43.3%; Pred. No. 4.7e-41;

Matches 122; Conservative 39; Mismatches 82; Indels 39; Gaps 8;

QY 8 QNTTSVEKGSNAVMGVLFSTGLGNLALGLLARSGLGWSRRPLRLPSVYMLVCG 67
DB 5 CRNLTVRSGVGPATSTLMFVAGVGVNGLAIGLS-----ARRPAR--PSAFAVLVTG 55
QY 68 LVTDLGKCLSPVLLAAVNAONSLRVLVLA---PALDNLSCQAFAPFMSFFGLSSTLQLL 124
DB 56 LAATDLGTSFSPVAVFVAYARNSSLGLARGGPA---LCDAFAPAMTFFGLASMLILF 111
QY 125 ANALECWLSLGHPPFYRRHITRLGALVAPVWSAFSLAFALCPFMGFKFVQYCPGTWCF 184
DB 112 ANAVERCIALSPYLYAQDGPFCARLALPATYAFCVLFCALPLGLGQHQYCPGWSWCF 171
QY 185 IQM--VHEEGSLVGLSYVLSLMAVLLVATVLCNLGAMRNLYAMHRLQRHPRSCRTD 242
DB 172 LRMWQAQPGA---AFSLAYAGVALLVAAIFLCNGSVTLSCRMVROQKRHQS---- 223
QY 243 CAEPRADGREASPOPL---EELDHLILLALMTVLTMCSLPV 281
DB 224 -----LQPRPRTGDEVDHLLILALMTVVMVAVCSLPL 255

RESULT 14

US-08-520-519-3

Sequence 3, Application US/08520519

Patent No. 5728808

GENERAL INFORMATION:

APPLICANT: Abramovitz, Mark

APPLICANT: Boie, Yves

APPLICANT: Grygorczyk, Richard

APPLICANT: Metters, Kathleen

APPLICANT: Rushmore, Thomas H.

APPLICANT: Slipetz, Deborah M.

TITLE OF INVENTION: DNA ENCODING PROSTAGLANDIN RECEPTOR IP

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSEE: Jack L. Tribble

STREET: 126 E. Lincoln Avenue

CITY: Rahway

STATE: New Jersey

COUNTRY: USA

ZIP: 07065-0907

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/520,519
FILING DATE: 29-AUG-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Tribble, Jack L.
REGISTRATION NUMBER: 32,633
REFERENCE/DOCKET NUMBER: 19098DA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-5321
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 386 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-520-519-3

Query Match      33.6%; Score 518.5; DB 1; Length 386;
Best Local Similarity 43.3%; Pred. No. 4.7e-41;
Matches 122; Conservative 39; Mismatches 82; Indels 39; Gaps 8;

QY 8 CONTTSVEKGNNAVGVLFSTGLGNLALGLLARSGLGWCRRPLPLPSVFMVLVCG 67
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 5 CRNLTYVRGSGVPATSTLMFVAGVVGNGLGALGILS-----ARRPAR--PSAFVAVLTG 55

QY 68 LTVTDLLGKCLLSPVLAAYAQNRSLRVL---PALDNSLCOAFAPFMSFFGLSSTLQLL 124
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 56 LAATDLLGTSLSPAVFVAYARNSSLGLARGGPA-----LCDAFAPAMTFFGLASMLILF 111

QY 125 AMALECWLSLGHPPFYRRHITLRGLAVPVVVSFAFSLAFALPFMGFKFVQYCPGTWCF 184
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Db 112 AMAVERCLALSHPLYAQLDGPRCARLALPAIYAFCVLFCALPLLLGLGQHQYCPGSMCF 171

QY 185 IQM--VHEGSLSVLGYSVLYSSLMALLVATVLCNLGAMRNLYAMHRLQRHPRSCRTD 242
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Db 172 LRMRWAQPGGA-----AFSLAYAGLVALLVAIFLCNGSVTTLSCRMRYQQRKHOGS---- 223

QY 243 CAEPRADGREASPOPL---EELDHLILLALMTVLTMCSLPV 281
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RESULT 15
US-09-039-798-3
Sequence 3, Application US/09039798
Patent No. 6385360
GENERAL INFORMATION:
APPLICANT: Abramovitz, Mark
APPLICANT: Boie, Yves
APPLICANT: Grygorczyk, Richard
APPLICANT: Metters, Kathleen
APPLICANT: Rushmore, Thomas H.
APPLICANT: Slipetz, Deborah M.
TITLE OF INVENTION: DNA ENCODING PROSTAGLANDIN RECEPTOR IP
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: J. Mark Hand
STREET: 126 E. Lincoln Avenue
CITY: Rahway
STATE: New Jersey
COUNTRY: USA
ZIP: 07065-0907
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/039,798
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/520,519
FILING DATE: 29-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Hand, J. Mark
REGISTRATION NUMBER: 36,545
REFERENCE/DOCKET NUMBER: 19098DB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (732) 594-3905
TELEFAX: (732) 594-4720
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 386 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-039-798-3

Query Match      33.6%; Score 518.5; DB 3; Length 386;
Best Local Similarity 43.3%; Pred. No. 4.7e-41;
Matches 122; Conservative 39; Mismatches 82; Indels 39; Gaps 8;

QY 8 CONTTSVEKGNNAVGVLFSTGLGNLALGLLARSGLGWCRRPLPLPSVFMVLVCG 67
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 5 CRNLTYVRGSGVPATSTLMFVAGVVGNGLGALGILS-----ARRPAR--PSAFVAVLTG 55

QY 68 LTVTDLLGKCLLSPVLAAYAQNRSLRVL---PALDNSLCOAFAPFMSFFGLSSTLQLL 124
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 56 LAATDLLGTSLSPAVFVAYARNSSLGLARGGPA-----LCDAFAPAMTFFGLASMLILF 111

QY 125 AMALECWLSLGHPPFYRRHITLRGLAVPVVVSFAFSLAFALPFMGFKFVQYCPGTWCF 184
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Db 112 AMAVERCLALSHPLYAQLDGPRCARLALPAIYAFCVLFCALPLLLGLGQHQYCPGSMCF 171

QY 185 IQM--VHEGSLSVLGYSVLYSSLMALLVATVLCNLGAMRNLYAMHRLQRHPRSCRTD 242
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Db 172 LRMRWAQPGGA-----AFSLAYAGLVALLVAIFLCNGSVTTLSCRMRYQQRKHOGS---- 223

QY 243 CAEPRADGREASPOPL---EELDHLILLALMTVLTMCSLPV 281
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Db 224 -----LGPRTGTGEVDHLLILLALMTVVMVAVCSLPL 255
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Search completed: April 22, 2005, 21:30:47
Job time : 19.6244 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 22, 2005, 21:29:33 ; Search time 153.649 Seconds
(without alignments)
641.112 Million cell updates/sec

Title: US-10-689-861-2
Perfect score: 1541
Sequence: 1 MKSPYRCQNTTSVEKNSA.....CSLPVIAFVPGVPKTPGSR 296

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1424015 seqs, 332791073 residues

Total number of hits satisfying chosen parameters: 1424015

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : Published Applications_AA.*
- 1: /cgn2_6/prodata/1/pubpaa/US07_PUBCOMB.pep.*
 - 2: /cgn2_6/prodata/1/pubpaa/PCT_NEW_PUB.pep.*
 - 3: /cgn2_6/prodata/1/pubpaa/US06_NEW_PUB.pep.*
 - 4: /cgn2_6/prodata/1/pubpaa/US06_PUBCOMB.pep.*
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 - 6: /cgn2_6/prodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
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 - 10: /cgn2_6/prodata/1/pubpaa/US09B_PUBCOMB.pep.*
 - 11: /cgn2_6/prodata/1/pubpaa/US09C_PUBCOMB.pep.*
 - 12: /cgn2_6/prodata/1/pubpaa/US09_NEW_PUB.pep.*
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 - 16: /cgn2_6/prodata/1/pubpaa/US10D_PUBCOMB.pep.*
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 - 20: /cgn2_6/prodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1467	95.2	359	14	US-10-225-567A-287
2	1467	95.2	359	15	US-10-276-774-2370
3	586	38.0	358	14	US-10-225-567A-291
4	586	38.0	358	15	US-10-352-684A-36
5	586	38.0	358	15	US-10-366-288-36
6	586	38.0	358	16	US-10-755-889-92
7	585	38.0	358	17	US-10-108-714-4
8	585	38.0	358	17	US-10-684-206-38
9	580	37.6	358	17	US-09-826-509-559
10	580	37.6	358	17	US-10-925-095-559
11	518.5	33.6	289	15	US-10-108-260A-3907
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13	364.5	23.7	488	14	US-10-225-567A-296

14	364.5	23.7	488	14	US-10-320-351-3	Sequence 3, Appli
15	364.5	23.7	488	15	US-10-295-027-1326	Sequence 1326, Ap
16	364.5	23.7	488	16	US-10-755-889-170	Sequence 170, App
17	363.5	23.6	490	14	US-10-243-501-3	Sequence 3, Appli
18	361.5	23.5	488	10	US-09-826-509-561	Sequence 561, App
19	361.5	23.5	488	17	US-10-925-095-561	Sequence 561, App
20	361.5	23.5	490	14	US-10-243-351-2	Sequence 2, Appli
21	250.5	16.3	328	13	US-10-087-192-204	Sequence 204, App
22	250.5	16.3	343	14	US-10-225-567A-448	Sequence 448, App
23	250.5	16.3	343	16	US-10-755-889-596	Sequence 596, App
24	250.5	16.3	369	16	US-10-408-765A-176	Sequence 176, App
25	250.5	16.3	407	14	US-10-198-070-104	Sequence 104, App
26	244.5	15.9	365	14	US-10-060-902-32	Sequence 32, Appl
27	244.5	15.9	365	15	US-10-354-247-32	Sequence 32, Appl
28	244.5	15.9	374	14	US-10-060-902-30	Sequence 30, Appl
29	244.5	15.9	374	15	US-10-354-247-30	Sequence 30, Appl
30	244.5	15.9	388	14	US-10-060-902-16	Sequence 16, Appl
31	244.5	15.9	388	15	US-10-354-247-16	Sequence 16, Appl
32	244.5	15.9	390	14	US-10-060-902-22	Sequence 22, Appl
33	244.5	15.9	390	14	US-10-060-902-24	Sequence 22, Appl
34	244.5	15.9	390	15	US-10-354-247-22	Sequence 22, Appl
35	244.5	15.9	390	15	US-10-354-247-24	Sequence 24, Appl
36	244.5	15.9	393	14	US-10-060-902-28	Sequence 28, Appl
37	244.5	15.9	393	14	US-10-060-902-36	Sequence 36, Appl
38	244.5	15.9	393	15	US-10-354-247-28	Sequence 28, Appl
39	244.5	15.9	393	15	US-10-354-247-36	Sequence 36, Appl
40	244.5	15.9	402	14	US-10-225-567A-294	Sequence 294, App
41	244.5	15.9	402	14	US-10-060-902-34	Sequence 34, Appl
42	244.5	15.9	402	15	US-10-354-247-34	Sequence 34, Appl
43	244.5	15.9	407	14	US-10-060-902-18	Sequence 18, Appl
44	244.5	15.9	407	15	US-10-354-247-18	Sequence 18, Appl
45	244.5	15.9	425	14	US-10-060-902-26	Sequence 26, Appl

ALIGNMENTS

RESULT 1

US-10-225-567A-287
; Sequence 287, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burner, Glenna C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 287
; LENGTH: 359
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-287

Query Match 95.2%; Score 1467; DB 14; Length 359;
Best Local Similarity 100.0%; Pred. No. 5.9e-134;
Matches 282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MKSPYRCQNTTSVEKNSAVMGVLFSTGLGNLALGLLARSGLGWCSPRLPLPSV	60
Db	1	MKSPYRCQNTTSVEKNSAVMGVLFSTGLGNLALGLLARSGLGWCSPRLPLPSV	60
Qy	61	FYMLVCGITVTDLLGKCLLSPVLAAYQNSRLRVLPALDNLQCAFAMFFGLSST	120
Db	61	FYMLVCGITVTDLLGKCLLSPVLAAYQNSRLRVLPALDNLQCAFAMFFGLSST	120
Qy	121	LQLLMALECWLSLGHGHPFFYRRHITRLGALVAPVVSFAFLCALPFMGFKVQYCPG	180

Db 121 LQLLMALECWLSLGHPPFYRRHITLRLGALVAPVVSFAFLAFALPFMGFGKFFVQYCPG 180
QY 181 TWCFTQMVHEEGLSVLGVSVLYSSIMALLVLTATVLCNIGAMRNLYAMHRRRLQRHPRSC 240
Db 181 TWCFTQMVHEEGLSVLGVSVLYSSIMALLVLTATVLCNIGAMRNLYAMHRRRLQRHPRSC 240
QY 241 RDCAEPRADGRASPOPLEEHLHLLALMTVLTWCISLPVI 282
Db 241 RDCAEPRADGRASPOPLEEHLHLLALMTVLTWCISLPVI 282

RESULT 2

US-10-774-2370
; Sequence 2370, Application US/10276774
; Publication No. US20040053245A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; APPLICANT: Tang, Y, Tom et al
; TITLE OF INVENTION: No. US20040053245A1el Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-030
; CURRENT APPLICATION NUMBER: US/10/276,774
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 09/496,914
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 2700
; SOFTWARE: Custom
; SEQ ID NO 2370
; LENGTH: 399
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-276-774-2370

Query Match 95.2%; Score 1467; DB 15; Length 399;
Best Local Similarity 100.0%; Pred. No. 6.7e-134;
Matches 282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MKSPFYRCQNTTSVEKGSNAVGGVLFSTGLGNLLALGLLARSGLGWCRRPLRLPSV 60
Db 41 MKSPFYRCQNTTSVEKGSNAVGGVLFSTGLGNLLALGLLARSGLGWCRRPLRLPSV 100
QY 61 FYMLVGLTVTLGLKCLLSPVLAAYQNRSLRVLAPALDNLSCQAFAPFMSFFGLSST 120
Db 101 FYMLVGLTVTLGLKCLLSPVLAAYQNRSLRVLAPALDNLSCQAFAPFMSFFGLSST 160
QY 121 LQLLMALECWLSLGHPPFYRRHITLRLGALVAPVVSFAFLAFALPFMGFGKFFVQYCPG 180
Db 161 LQLLMALECWLSLGHPPFYRRHITLRLGALVAPVVSFAFLAFALPFMGFGKFFVQYCPG 220
QY 181 TWCFTQMVHEEGLSVLGVSVLYSSIMALLVLTATVLCNIGAMRNLYAMHRRRLQRHPRSC 240
Db 221 TWCFTQMVHEEGLSVLGVSVLYSSIMALLVLTATVLCNIGAMRNLYAMHRRRLQRHPRSC 280
QY 241 RDCAEPRADGRASPOPLEEHLHLLALMTVLTWCISLPVI 282
Db 281 RDCAEPRADGRASPOPLEEHLHLLALMTVLTWCISLPVI 322

RESULT 3

US-10-225-567A-291
; Sequence 291, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burner, Glenna C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19

; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 291
; LENGTH: 358
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-291
Query Match 38.0%; Score 536; DB 14; Length 358;
Best Local Similarity 45.2%; Pred. No. 2.3e-48;
Matches 128; Conservative 45; Mismatches 92; Indels 18; Gaps 7;
QY 8 CONTTSVEKGSNAVGGVLFSTGLGNLLALGLLARSGLG--WCRRPLRLPSVYFMYLV 65
Db 13 CETQWLPPGESPAISSVMFSGVGNLIALLARRWGDVGCAGRRSSL-SLHFVILV 71
QY 66 CGLTVTLGLKCLLSPVLAAYQNRSLRVLAPALDNLSCQAFAPFMSFFGLSSTLQLLA 125
Db 72 TELVPTDLGLTCLLSPVLAAYQNRSLRVLAPALDNLSCQAFAPFMSFFGLSSTLQLLA 129
QY 126 MALECWLSLGHPPFYRRHITLRLGALVAPVVSFAFLAFALPFMGFGKFFVQYCPGTWCFI 185
Db 130 MALECWLSLGHPPFYRRHITLRLGALVAPVVSFAFLAFALPFMGFGKFFVQYCPGTWCFI 189
QY 186 QMVHEEGLSVLGVSVLYSSIMALLVLTATVLCNIGAMRNLYAMHRRRLQRHPRSC 245
Db 190 R--HGR-----TAYLQLYATLTLVSVLACNFSVILNLRMHRRRR--SRCGFSGLS 240
QY 246 ---PRADGRASPOPLEEHLHLLALMTVLTWCISLPVI 284
Db 241 GRGFGARRRGERSVMAEETHLLILLALMTITFAVCSLPFTIF 283

RESULT 4

US-10-352-684A-36
; Sequence 36, Application US/10352684A
; Publication No. US20030215452A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals Inc.
; APPLICANT: Carroll, Joseph M.
; APPLICANT: Healy, Aileen
; APPLICANT: Weich, Nadine S.
; APPLICANT: Kelly, Louise M.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: HEMATOLOGICAL DISORDERS USING 131, 148, 199, 12303, 13906,
; TITLE OF INVENTION: 15513, 17822, 302, 5677, 194, 14393, 28059, 7366, 12212,
; TITLE OF INVENTION: 1981, 261, 12416, 270, 1410, 137, 1871, 13051, 1847, 1849,
; TITLE OF INVENTION: 15402, 340, 10217, 837, 1761, 8990 OR 13249 MOLECULES
; FILE REFERENCE: MP102-019P1RNMNIM
; CURRENT APPLICATION NUMBER: US/10/352,684A
; CURRENT FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: US 60/354,333
; PRIOR FILING DATE: 2002-02-04
; PRIOR APPLICATION NUMBER: US 60/360,258
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/364,476
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: US 60/375,626
; PRIOR FILING DATE: 2002-04-26
; PRIOR APPLICATION NUMBER: US 60/386,494
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/390,965
; PRIOR FILING DATE: 2002-06-24
; PRIOR APPLICATION NUMBER: US 60/392,480
; PRIOR FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: US 60/394,128
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 60/399,783
; PRIOR FILING DATE: 2002-07-31
; PRIOR APPLICATION NUMBER: US 60/403,221
; PRIOR FILING DATE: 2002-08-13

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 62
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 36
LENGTH: 358
TYPE: PRT
ORGANISM: Homo Sapiens
US-10-352-684A-36

Query Match 38.0%; Score 586; DB 15; Length 358;
Best Local Similarity 45.2%; Pred. No. 2.3e-48;
Matches 128; Conservative 45; Mismatches 92; Indels 18; Gaps 7;
QY 8 CQNTTSVEKGN SAVMGVLFSTGLLGNLALGILLARSGLG--WCSRRLPLPLPSVFMVLV 65
DB 13 CETRWLPPGESPAISSVMFSGVGLNLIALLARRWGDVCCSAGRSSL-SLFHVLV 71
QY 66 CGLTVTDLLGKCLLSPVLAAYQNRSLRVLPALDNLSCQAFAPFMSFGLSSTLQLLA 125
DB 72 TELVFTDLLGTCLISPVVLAAYARNQTLVALAP--ESRACTYFAFAMTFFSLATMLMFA 129
QY 126 MALECWLSLGHPPFYRRHITLRLGALVAPVVSFAFALCPMGFKFVQYCPGTWCFFI 185
DB 130 MALERYLSIGHPPFYQRRVSASGLAVLPVIYAVSLFLFCSLPDLDYQYVQYCPGTWCFFI 189
QY 186 QMVHEEGSLVGLGYSVLVYSSLMALLVLTVCNLGAMRNLYAMHRLQHRPRSCTRDCAE 245
DB 190 R--HGR-----TAYLQLYATLILLIVSVLACNFSVILNIRMHRSRR--SRCGPSLGS 240
QY 246 ----PRADGREASPOPLELDHLLALLAMTVLFTWCSSLPIVAF 284
DB 241 GRGGPGARRRGRVSMAEETHLILLAIMTITFAVCSLPFTIF 283

RESULT 5
US-10-366-288-36
Sequence 36, Application US/10366288
Publication No. US20030216288A1
GENERAL INFORMATION:
APPLICANT: Powell, Douglas S.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
TITLE OF INVENTION: AIDS AND HIV-RELATED DISORDERS USING 1414, 1481, 1553,
TITLE OF INVENTION: 34021, 1720, 1683, 1552, 1682, 1675, 12825, 9952, 5816,
TITLE OF INVENTION: 10002, 1611, 1371, 14324, 126, 270, 312, 167, 326, 18926,
TITLE OF INVENTION: 6747, 1793, 1784 OR 2045 MOLECULES
FILE REFERENCE: MPI02-025PIRNOWMIM
CURRENT APPLICATION NUMBER: US/10/366,288
PRIOR FILING DATE: 2003-02-13
PRIOR APPLICATION NUMBER: 60/357,391
PRIOR FILING DATE: 2002-02-15
PRIOR APPLICATION NUMBER: 60/380,249
PRIOR FILING DATE: 2002-05-13
PRIOR APPLICATION NUMBER: 60/391,306
PRIOR FILING DATE: 2002-06-25
PRIOR APPLICATION NUMBER: 60/406,297
PRIOR FILING DATE: 2002-08-27
PRIOR APPLICATION NUMBER: 60/412,007
PRIOR FILING DATE: 2002-09-19
PRIOR APPLICATION NUMBER: 60/417,508
PRIOR FILING DATE: 2002-10-10
PRIOR APPLICATION NUMBER: 60/432,318
PRIOR FILING DATE: 2002-12-10
NUMBER OF SEQ ID NOS: 52
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 36
LENGTH: 358
TYPE: PRT
ORGANISM: Homo Sapien
US-10-366-288-36

Query Match 38.0%; Score 586; DB 15; Length 358;
Best Local Similarity 45.2%; Pred. No. 2.3e-48;

Matches 128; Conservative 45; Mismatches 92; Indels 18; Gaps 7;
QY 8 CQNTTSVEKGN SAVMGVLFSTGLLGNLALGILLARSGLG--WCSRRLPLPLPSVFMVLV 65
DB 13 CETRWLPPGESPAISSVMFSGVGLNLIALLARRWGDVCCSAGRSSL-SLFHVLV 71
QY 66 CGLTVTDLLGKCLLSPVLAAYQNRSLRVLPALDNLSCQAFAPFMSFGLSSTLQLLA 125
DB 72 TELVFTDLLGTCLISPVVLAAYARNQTLVALAP--ESRACTYFAFAMTFFSLATMLMFA 129
QY 126 MALECWLSLGHPPFYRRHITLRLGALVAPVVSFAFALCPMGFKFVQYCPGTWCFFI 185
DB 130 MALERYLSIGHPPFYQRRVSASGLAVLPVIYAVSLFLFCSLPDLDYQYVQYCPGTWCFFI 189
QY 186 QMVHEEGSLVGLGYSVLVYSSLMALLVLTVCNLGAMRNLYAMHRLQHRPRSCTRDCAE 245
DB 190 R--HGR-----TAYLQLYATLILLIVSVLACNFSVILNIRMHRSRR--SRCGPSLGS 240
QY 246 ----PRADGREASPOPLELDHLLALLAMTVLFTWCSSLPIVAF 284
DB 241 GRGGPGARRRGRVSMAEETHLILLAIMTITFAVCSLPFTIF 283

RESULT 6
US-10-755-889-92
Sequence 92, Application US/10755889
Publication No. US20040171823A1
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ASSOCIATED WITH THE NF-kB
FILE OF INVENTION: PATHWAY
FILE REFERENCE: D0284 NP
CURRENT APPLICATION NUMBER: US/10/755,889
CURRENT FILING DATE: 2004-01-13
PRIOR APPLICATION NUMBER: U.S. 60/440,068
PRIOR FILING DATE: 2003-01-14
PRIOR APPLICATION NUMBER: U.S. 60/469,757
PRIOR FILING DATE: 2003-05-12
NUMBER OF SEQ ID NOS: 823
SOFTWARE: PatentIn version 3.2
SEQ ID NO 92
LENGTH: 358
TYPE: PRT
ORGANISM: Homo sapiens
US-10-755-889-92

Query Match 38.0%; Score 586; DB 16; Length 358;
Best Local Similarity 45.2%; Pred. No. 2.3e-48;
Matches 128; Conservative 45; Mismatches 92; Indels 18; Gaps 7;
QY 8 CQNTTSVEKGN SAVMGVLFSTGLLGNLALGILLARSGLG--WCSRRLPLPLPSVFMVLV 65
DB 13 CETRWLPPGESPAISSVMFSGVGLNLIALLARRWGDVCCSAGRSSL-SLFHVLV 71
QY 66 CGLTVTDLLGKCLLSPVLAAYQNRSLRVLPALDNLSCQAFAPFMSFGLSSTLQLLA 125
DB 72 TELVFTDLLGTCLISPVVLAAYARNQTLVALAP--ESRACTYFAFAMTFFSLATMLMFA 129
QY 126 MALECWLSLGHPPFYRRHITLRLGALVAPVVSFAFALCPMGFKFVQYCPGTWCFFI 185
DB 130 MALERYLSIGHPPFYQRRVSASGLAVLPVIYAVSLFLFCSLPDLDYQYVQYCPGTWCFFI 189
QY 186 QMVHEEGSLVGLGYSVLVYSSLMALLVLTVCNLGAMRNLYAMHRLQHRPRSCTRDCAE 245
DB 190 R--HGR-----TAYLQLYATLILLIVSVLACNFSVILNIRMHRSRR--SRCGPSLGS 240
QY 246 ----PRADGREASPOPLELDHLLALLAMTVLFTWCSSLPIVAF 284
DB 241 GRGGPGARRRGRVSMAEETHLILLAIMTITFAVCSLPFTIF 283

RESULT 7
US-10-108-714-4

```
; Sequence 4, Application US/10108714
; Publication No. US20020128445A1
; GENERAL INFORMATION:
; APPLICANT: Regan, John W.
; APPLICANT: Gil, Daniel W.
; APPLICANT: Woodward, David F.
; TITLE OF INVENTION: No. US20020128445A1el Human Prostaglandin EP Receptor
; FILE REFERENCE: 17023 DIV CIP
; CURRENT APPLICATION NUMBER: US/10/108,714
; CURRENT FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/267,423
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/239,431
; PRIOR FILING DATE: EARLIER FILING DATE: 1994-05-05
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 358
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-108-714-4

Query Match 38.0%; Score 585; DB 13; Length 358;
Best Local Similarity 45.2%; Pred. No. 2.9e-48;
Matches 128; Conservative 45; Mismatches 92; Indels 18; Gaps 7;

QY 8 QNTTSVEKGN SAVMGVLFSTGLGNLLALGLLARSGLG--WCRRRLPLPLPSVYFMYLV 65
DB 13 CETROWLPPEGSPAISSVMFSGVLGNLIALALLARRWRGDVGCAGRRSSL-SLFHVLV 71
QY 66 CGLTVDLLGKCLLSPVLAAYQNRSLRVLAPALDNLSCQAFAFMFSPFGLSSTLQLIA 125
DB 72 TELVFTDLLGTCLISPVVLASVARNQTLVALAP--ESRACTYFAFAMTFFSLATMLMFA 129
QY 126 MALECWLSLGHPPFFYRRHITLRLGALVAPVVSFAFSLAFCAFPFMGFGKVFQVCPGTWCFI 185
DB 130 MALERYLSIGHYPFYQRRVSRSGGLAVLPVIYAVSLLFCSLPLLDYGVQVQCPGTWCFI 189
QY 186 QMVHEEGSLVGLGYSLVSSLMALLVATVLCNLGAMNLYAMHRLQRPSCSTRDCAE 245
DB 190 R--HGR-----TAYLQLYATLULLLVSVLACNFSVILNLRHRRSRR--SRCGFSLGS 240
QY 246 ----PRADGREASPOPLELDHLLIALMTVLFTMCSLPVIAF 284
DB 241 GRGGFGARRGERVSMAEETHLLAILMTITFAVCSLPFTIF 283

RESULT 8
US-10-684-206-38
; Sequence 38, Application US/10684206
; Publication No. US20050032725A1
; GENERAL INFORMATION:
; APPLICANT: Rao, Patricia
; APPLICANT: Szymanska, Grazyna
; TITLE OF INVENTION: Molecules Associated With Regulatory T
; TITLE OF INVENTION: Cells and Methods of Their Use
; FILE REFERENCE: TLN-021CP
; CURRENT APPLICATION NUMBER: US/10/684,206
; CURRENT FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: US 60/417102
; PRIOR FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US 60/417103
; PRIOR FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US 60/417243
; PRIOR FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US 60/419575
; PRIOR FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: US 60/424777
; PRIOR FILING DATE: 2002-11-08
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 358

QY 8 QNTTSVEKGN SAVMGVLFSTGLGNLLALGLLARSGLG--WCRRRLPLPLPSVYFMYLV 65
DB 13 CETROWLPPEGSPAISSVMFSGVLGNLIALALLARRWRGDVGCAGRRSSL-SLFHVLV 71
QY 66 CGLTVDLLGKCLLSPVLAAYQNRSLRVLAPALDNLSCQAFAFMFSPFGLSSTLQLIA 125
DB 72 TELVFTDLLGTCLISPVVLASVARNQTLVALAP--ESRACTYFAFAMTFFSLATMLMFA 129
QY 126 MALECWLSLGHPPFFYRRHITLRLGALVAPVVSFAFSLAFCAFPFMGFGKVFQVCPGTWCFI 185
DB 130 MALERYLSIGHYPFYQRRVSRSGGLAVLPVIYAVSLLFCSLPLLDYGVQVQCPGTWCFI 189
QY 186 QMVHEEGSLVGLGYSLVSSLMALLVATVLCNLGAMNLYAMHRLQRPSCSTRDCAE 245
DB 190 R--HGR-----TAYLQLYATLULLLVSVLACNFSVILNLRHRRSRR--SRCGFSLGS 240
QY 246 ----PRADGREASPOPLELDHLLIALMTVLFTMCSLPVIAF 284
DB 241 GRGGFGARRGERVSMAEETHLLAILMTITFAVCSLPFTIF 283
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; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-684-206-38

Query Match 38.0%; Score 585; DB 17; Length 358;
Best Local Similarity 45.2%; Pred. No. 2.9e-48;
Matches 128; Conservative 45; Mismatches 92; Indels 18; Gaps 7;

QY 8 QNTTSVEKGN SAVMGVLFSTGLGNLLALGLLARSGLG--WCRRRLPLPLPSVYFMYLV 65
DB 13 CETROWLPPEGSPAISSVMFSGVLGNLIALALLARRWRGDVGCAGRRSSL-SLFHVLV 71
QY 66 CGLTVDLLGKCLLSPVLAAYQNRSLRVLAPALDNLSCQAFAFMFSPFGLSSTLQLIA 125
DB 72 TELVFTDLLGTCLISPVVLASVARNQTLVALAP--ESRACTYFAFAMTFFSLATMLMFA 129
QY 126 MALECWLSLGHPPFFYRRHITLRLGALVAPVVSFAFSLAFCAFPFMGFGKVFQVCPGTWCFI 185
DB 130 MALERYLSIGHYPFYQRRVSRSGGLAVLPVIYAVSLLFCSLPLLDYGVQVQCPGTWCFI 189
QY 186 QMVHEEGSLVGLGYSLVSSLMALLVATVLCNLGAMNLYAMHRLQRPSCSTRDCAE 245
DB 190 R--HGR-----TAYLQLYATLULLLVSVLACNFSVILNLRHRRSRR--SRCGFSLGS 240
QY 246 ----PRADGREASPOPLELDHLLIALMTVLFTMCSLPVIAF 284
DB 241 GRGGFGARRGERVSMAEETHLLAILMTITFAVCSLPFTIF 283

RESULT 9
US-09-826-509-559
; Sequence 559, Application US/09826509
; Publication No. US20030204073A1
; GENERAL INFORMATION:
; APPLICANT: Lehmann-Bruinsma, Karin
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: No. US20030204073A1-Endogenous, Constitutively Activated Known G
; FILE REFERENCE: AREN-207
; CURRENT APPLICATION NUMBER: US/09/826,509
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/195,747
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 589
; SOFTWARE: Patent In Version 2.1
; SEQ ID NO 559
; LENGTH: 358
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-826-509-559

Query Match 37.6%; Score 580; DB 10; Length 358;
Best Local Similarity 44.9%; Pred. No. 8.9e-48;
Matches 127; Conservative 45; Mismatches 93; Indels 18; Gaps 7;

QY 8 QNTTSVEKGN SAVMGVLFSTGLGNLLALGLLARSGLG--WCRRRLPLPLPSVYFMYLV 65
DB 13 CETROWLPPEGSPAISSVMFSGVLGNLIALALLARRWRGDVGCAGRRSSL-SLFHVLV 71
QY 66 CGLTVDLLGKCLLSPVLAAYQNRSLRVLAPALDNLSCQAFAFMFSPFGLSSTLQLIA 125
DB 72 TELVFTDLLGTCLISPVVLASVARNQTLVALAP--ESRACTYFAFAMTFFSLATMLMFA 129
QY 126 MALECWLSLGHPPFFYRRHITLRLGALVAPVVSFAFSLAFCAFPFMGFGKVFQVCPGTWCFI 185
DB 130 MALERYLSIGHYPFYQRRVSRSGGLAVLPVIYAVSLLFCSLPLLDYGVQVQCPGTWCFI 189
QY 186 QMVHEEGSLVGLGYSLVSSLMALLVATVLCNLGAMNLYAMHRLQRPSCSTRDCAE 245
DB 190 R--HGR-----TAYLQLYATLULLLVSVLACNFSVILNLRHRRSRR--SRCGFSLGS 240
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QY 246 ----PRADGREGASPOPLELDHLLALLMTVLFTWCSLPVIAF 284
Db 241 GRGGPGARRRGRVSNABETHKILLAINITFAVCSLPFTTIF 283

RESULT 10
US-10-925-095-559
; Sequence 559, Application US/10925095
; Publication No. US20050019840A1
; GENERAL INFORMATION:
; APPLICANT: Lehmann-Bruinsma, Karin
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: Non-Endogenous, Constitutively Activated Known G
; FILE OF INVENTION: Protein-Coupled Receptors
; FILE REFERENCE: AREN-207
; CURRENT APPLICATION NUMBER: US/10/925,095
; CURRENT FILING DATE: 2004-08-24
; PRIOR APPLICATION NUMBER: US/09/826,509
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/195,747
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 589
; SOFTWARE: Patent In Version 2.1
; SEQ ID NO 559
; LENGTH: 358
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-925-095-559

Query Match 37.6%; Score 580; DB 17; Length 358;
Best Local Similarity 44.9%; Pred. No. 8.9e-48;
Matches 127; Conservative 45; Mismatches 93; Indels 18; Gaps 7;

QY 8 CONTTSVEKGSANVGGVLFSTGLGNLLALGLLARSGLG--WCRRRLPLRPLPSVFMVLV 65
Db 13 CETROWLPGESPAISVNFSGVLGNLTALLARRWRGVDGCSAGRSSL-SLFHLV 71
QY 66 CGLTVDLLGKCLLSPVLAAYANRSLRVLAAPALDNLSCQAFAPFMSFGLSSTLQLL 125
Db 72 TELVFTDGLTCLISPVVLAASARNQTLVALAP--ESRACTYFAFAMTFSLATMLMFA 129
QY 126 MALECWLSLGHPPFYRRHITRLGALVAPVVSFAFSLAFALFPMGFGKFGVQYCPGTWCFI 185
Db 130 MALERYLSIGHPPFYQRRVSAAGSLAVLPVIYAVSLFCSLPDLDYGVQYVQYCPGTWCFI 189
QY 186 QMVHEEGSLVGLSVLYSSLMALLVATVLCNLGAMRNLYAMHRRRLQRHPRSCRTDCAE 245
Db 190 R--HGR-----TAYLQLVATLTLVSVLACNFSVILNLRHRRSR--SRCGPGSLGS 240
QY 246 ----PRADGREGASPOPLELDHLLALLMTVLFTWCSLPVIAF 284
Db 241 GRGGPGARRRGRVSNABETHKILLAINITFAVCSLPFTTIF 283

RESULT 11
US-10-108-260A-3907
; Sequence 3907, Application US/10108260A
; Publication No. US20040005560A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20040005560A1e1 full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/10/108,260A
; CURRENT FILING DATE: 2002-03-27
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 3907
; LENGTH: 289
; TYPE: PRT

```

```

; ORGANISM: Homo sapiens
US-10-108-260A-3907

Query Match 33.6%; Score 518.5; DB 15; Length 289;
Best Local Similarity 43.3%; Pred. No. 6.5e-42;
Matches 122; Conservative 39; Mismatches 82; Indels 39; Gaps 8;

QY 8 CONTTSVEKGSANVGGVLFSTGLGNLLALGLLARSGLGWCRRRLPLRPLPSVFMVLVCG 67
Db 5 CRNLTYVRGSGVPATSTLPMFVAGVVGNGLAGLILS-----ARRPAR--PSAFVLTG 55
QY 68 LTVTDLLGKCLLSPVLAAYANRSLRVLA---PALDNLSCQAFAPFMSFGLSSTLQLL 124
Db 56 LAATDLLGTSLSPAVFVAYARNSSLGLARGGPA----LCDAFAPAMTFGLASMLILF 111
QY 125 AMALECWLSLGHPPFYRRHITRLGALVAPVVSFAFSLAFALFPMGFGKFGVQYCPGTWCF 184
Db 112 AMAVERCLALSHPIYLAQLDGPRCARLALPAIYAFVLCALPLGLGQHQYCPGSMWCF 171
QY 185 IQM--VHEEGSLVGLSVLYSSLMALLVATVLCNLGAMRNLYAMHRRRLQRHPRSCRTD 242
Db 172 LRMRWAQPGGA---AFSLAYAGLVALLVAIFLCNGSVTLSCRMRYRQQRHQS---- 223
QY 243 CAEPRADGREGASPOPL---EELDHLILLALMTVLFTWCSLPV 281
Db 224 -----LGPRTGDEVDHLLALLMTVTVWAVCSLPL 255

RESULT 12
US-10-225-567A-285
; Sequence 285, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burner, Glenna C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 285
; LENGTH: 386
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-285

Query Match 33.6%; Score 518.5; DB 14; Length 386;
Best Local Similarity 43.3%; Pred. No. 9.2e-42;
Matches 122; Conservative 39; Mismatches 82; Indels 39; Gaps 8;

QY 8 CONTTSVEKGSANVGGVLFSTGLGNLLALGLLARSGLGWCRRRLPLRPLPSVFMVLVCG 67
Db 5 CRNLTYVRGSGVPATSTLPMFVAGVVGNGLAGLILS-----ARRPAR--PSAFVLTG 55
QY 68 LTVTDLLGKCLLSPVLAAYANRSLRVLA---PALDNLSCQAFAPFMSFGLSSTLQLL 124
Db 56 LAATDLLGTSLSPAVFVAYARNSSLGLARGGPA----LCDAFAPAMTFGLASMLILF 111
QY 125 AMALECWLSLGHPPFYRRHITRLGALVAPVVSFAFSLAFALFPMGFGKFGVQYCPGTWCF 184
Db 112 AMAVERCLALSHPIYLAQLDGPRCARLALPAIYAFVLCALPLGLGQHQYCPGSMWCF 171
QY 185 IQM--VHEEGSLVGLSVLYSSLMALLVATVLCNLGAMRNLYAMHRRRLQRHPRSCRTD 242
Db 172 LRMRWAQPGGA---AFSLAYAGLVALLVAIFLCNGSVTLSCRMRYRQQRHQS---- 223
QY 243 CAEPRADGREGASPOPL---EELDHLILLALMTVLFTWCSLPV 281

```

Db 224 -----LGRPRGTGDEVDHLILLALMTVMVAVCSLPL 255

RESULT 13

US-10-225-567A-296

; Sequence 296, Application US/10225567A

; Publication No. US20030113798A1

; GENERAL INFORMATION:

; APPLICANT: LifeSpan Biosciences

; APPLICANT: Brown, Joseph P.

; APPLICANT: Burner, Glenna C.

; APPLICANT: Rough, Christine L.

; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS

; FILE REFERENCE: 1920-4-4

; CURRENT APPLICATION NUMBER: US/10/225,567A

; CURRENT FILING DATE: 2001-12-19

; PRIOR APPLICATION NUMBER: 60/257,144

; PRIOR FILING DATE: 2000-12-19

; NUMBER OF SEQ ID NOS: 2292

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 296

; LENGTH: 488

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-225-567A-296

Query Match 23.7%; Score 364.5; DB 14; Length 488;

Best Local Similarity 31.5%; Pred. No. 1.1e-26;

Matches 97; Conservative 51; Mismatches 121; Indels 39; Gaps 8;

QY 1 MKSPFYRCQNTTSVEKGN SAV-MGGVLFSTGLLGNLLALGLLARSGLGWCRRRLRLPLPS 59

Db 1 MSTPGVNSSASLPDLNSPVTIPAVMFIFGVGNLVAIVLCK-----SRKEQK--ET 52

QY 60 VFYMLVCGLTVDLLGKLLSPVLAAYAAQNRSLRVLAPALDNLSCQAFAPFMSFFGLSS 119

Db 53 TFYTLVCGLA VTDLLGLTLLVSPVTIATYMKGQ-----WPG-QGPLCEYSTFILLFFSLG 106

QY 120 TLQLLMALECWLSLGHPPFYRRHITRLGALVAPVVSFAFALCALPMGFGKFVQVCP 179

Db 107 LSIICAMSVERYLAINHAYFYSHYVDYKRLAGLTLFAVYASNVLFCA LPMGLGSSRLQYP 166

QY 180 GTWCFTQMVHEEGSLVGLSVLYSSLMALLVLA TLVCLNGLAMRNLYAMHRLQHRPSC 239

Db 167 DTWCFTDWT--TNVTAHAAYSVMYAGFSFLILATVCLNVLVCGALLRMHROFMERTSLG 224

QY 240 TRD-----CAEPRADGREASPOPL-----EELDHLLLLALMTVLF TMC 277

Db 225 TEQHHAASVSRGHGHPAASPALPRLSDFRRRSFRRIAGAEIQMVILLIATSLVLIC 284

QY 278 SLPVIAFV 285

Db 285 SIPLVVRV 292

RESULT 15

US-10-295-027-1326

; Sequence 1326, Application US/10295027

; Publication No. US20030232350A1

; GENERAL INFORMATION:

; APPLICANT: Afar, Daniel

; APPLICANT: Aziz, Natasha

; APPLICANT: Ginsberg, Wendy M.

; APPLICANT: Gish, Kurt C.

; APPLICANT: Glynn, Richard

; APPLICANT: Hetezi, Peter A.

; APPLICANT: Mack, David H.

; APPLICANT: Murray, Richard

; APPLICANT: Watson, Susan R.

; APPLICANT: Eos Biotechnology, Inc.

; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and

; TITLE OF INVENTION: Methods of Screening for Modulators of Cancer

; FILE REFERENCE: 018501-012500US

; CURRENT APPLICATION NUMBER: US/10/295,027

; CURRENT FILING DATE: 2002-11-13

; PRIOR APPLICATION NUMBER: US 09/663,733

; PRIOR FILING DATE: 2000-09-15

; PRIOR APPLICATION NUMBER: US 60/350,666

; PRIOR FILING DATE: 2001-11-13

; PRIOR APPLICATION NUMBER: US 60/335,394

; PRIOR FILING DATE: 2001-11-15

; PRIOR APPLICATION NUMBER: US 60/332,464

; PRIOR FILING DATE: 2001-11-21

; PRIOR APPLICATION NUMBER: US 60/334,393

; PRIOR FILING DATE: 2001-11-29

; PRIOR APPLICATION NUMBER: US 60/340,376

; PRIOR FILING DATE: 2001-12-14

; PRIOR APPLICATION NUMBER: US 60/347,211

; PRIOR FILING DATE: 2002-01-08

; PRIOR APPLICATION NUMBER: US 60/347,349

; PRIOR FILING DATE: 2002-01-10

; PRIOR APPLICATION NUMBER: US 60/355,250

; PRIOR FILING DATE: 2002-02-08

; PRIOR APPLICATION NUMBER: US 60/356,714

Db 224 -----LGRPRGTGDEVDHLILLALMTVMVAVCSLPL 255

RESULT 13

US-10-225-567A-296

; Sequence 296, Application US/10225567A

; Publication No. US20030113798A1

; GENERAL INFORMATION:

; APPLICANT: LifeSpan Biosciences

; APPLICANT: Brown, Joseph P.

; APPLICANT: Burner, Glenna C.

; APPLICANT: Rough, Christine L.

; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS

; FILE REFERENCE: 1920-4-4

; CURRENT APPLICATION NUMBER: US/10/225,567A

; CURRENT FILING DATE: 2001-12-19

; PRIOR APPLICATION NUMBER: 60/257,144

; PRIOR FILING DATE: 2000-12-19

; NUMBER OF SEQ ID NOS: 2292

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 296

; LENGTH: 488

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-225-567A-296

Query Match 23.7%; Score 364.5; DB 14; Length 488;

Best Local Similarity 31.5%; Pred. No. 1.1e-26;

Matches 97; Conservative 51; Mismatches 121; Indels 39; Gaps 8;

QY 1 MKSPFYRCQNTTSVEKGN SAV-MGGVLFSTGLLGNLLALGLLARSGLGWCRRRLRLPLPS 59

Db 1 MSTPGVNSSASLPDLNSPVTIPAVMFIFGVGNLVAIVLCK-----SRKEQK--ET 52

QY 60 VFYMLVCGLTVDLLGKLLSPVLAAYAAQNRSLRVLAPALDNLSCQAFAPFMSFFGLSS 119

Db 53 TFYTLVCGLA VTDLLGLTLLVSPVTIATYMKGQ-----WPG-QGPLCEYSTFILLFFSLG 106

QY 120 TLQLLMALECWLSLGHPPFYRRHITRLGALVAPVVSFAFALCALPMGFGKFVQVCP 179

Db 107 LSIICAMSVERYLAINHAYFYSHYVDYKRLAGLTLFAVYASNVLFCA LPMGLGSSRLQYP 166

QY 180 GTWCFTQMVHEEGSLVGLSVLYSSLMALLVLA TLVCLNGLAMRNLYAMHRLQHRPSC 239

Db 167 DTWCFTDWT--TNVTAHAAYSVMYAGFSFLILATVCLNVLVCGALLRMHROFMERTSLG 224

QY 240 TRD-----CAEPRADGREASPOPL-----EELDHLLLLALMTVLF TMC 277

Db 225 TEQHHAASVSRGHGHPAASPALPRLSDFRRRSFRRIAGAEIQMVILLIATSLVLIC 284

QY 278 SLPVIAFV 285

Db 285 SIPLVVRV 292

RESULT 14

US-10-320-351-3

; Sequence 3, Application US/10320351

; Publication No. US20030134314A1

; GENERAL INFORMATION:

; APPLICANT: Carroll, Joseph M.

; APPLICANT: Healy, Aileen

; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING

; TITLE OF INVENTION: HEMATOLOGICAL DISORDERS USING 252, 304, 1980, 14717, 9941,

; FILE REFERENCE: 19310 AND 17832

; CURRENT APPLICATION NUMBER: US/10/320,351

; CURRENT FILING DATE: 2002-12-16

; PRIOR APPLICATION NUMBER: 60/341,606

; PRIOR FILING DATE: 2001-12-17

; NUMBER OF SEQ ID NOS: 21

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 3

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OM protein - protein search, using sw model

Run on: April 22, 2005, 20:46:09 ; Search time 14.4611 Seconds
(without alignments)
1969.437 Million cell updates/sec

Title: US-10-689-861-2
Perfect score: 1541
Sequence: 1 MKSPYRCQNTTSVEKGNLSA.....CSLPVIAFVGVPKTPGSR 296
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1467	95.2	359	2 I39153	prostanoid DP rece
2	943	61.2	231	2 I59269	prostaglandin D re
3	595.5	38.6	362	2 S66674	prostaglandin E re
4	586	38.0	358	2 I38920	prostaglandin E2 r
5	585	38.0	358	2 S51312	EP2 prostaglandin
6	519	33.7	417	2 A54416	prostacyclin recep
7	518.5	33.6	386	2 A57066	prostacyclin recep
8	506.5	32.9	416	2 S52078	prostacyclin - rat
9	389	25.2	513	2 A46638	prostaglandin E re
10	383	24.9	488	2 JC2241	prostaglandin E re
11	364.5	23.7	488	2 A53572	prostaglandin E2 r
12	267	17.3	362	2 A58689	prostaglandin E(2)
13	267	17.3	366	2 S51280	EP3-alpha receptor
14	261.5	17.0	361	2 A45211	prostaglandin E re
15	261.5	17.0	364	2 JC2115	prostaglandin E re
16	261.5	17.0	364	2 S65009	prostaglandin E re
17	261.5	17.0	365	2 A42414	prostaglandin E re
18	261.5	17.0	365	2 JN0693	prostaglandin E2 r
19	251.5	16.3	361	2 A53216	prostaglandin E2 r
20	251.5	16.3	411	2 B53216	prostaglandin E2 r
21	250.5	16.3	343	2 A49117	thromboxane A2 rec
22	250.5	16.3	369	2 A53959	thromboxane A-2 re
23	250.5	16.3	407	2 T02670	probable thromboxa
24	244.5	15.9	365	2 I38748	prostaglandin recep
25	244.5	15.9	365	2 S51315	prostaglandin E re
26	244.5	15.9	374	2 I38747	prostaglandin recep
27	244.5	15.9	374	2 S51317	prostaglandin E re
28	244.5	15.9	388	2 S51316	prostaglandin E re
29	244.5	15.9	388	2 I38750	prostaglandin recep

ALIGNMENTS

RESULT 1

I39153
prostanoid DP receptor - human
N:Alternate names: prostaglandin D2 receptor
C:Species: Homo sapiens (man)
C:Date: 09-Mar-1996 #sequence revision 03-May-1996 #text_change 09-Jul-2004
C:Accession: I39153; I39150; I39149
R:Boie, Y.; Sawyer, N.; Slipetz, D.M.; Metters, K.M.; Abramovitz, M.
J. Biol. Chem. 270, 18910-18916, 1995
A:Title: Molecular cloning and characterization of the human prostanoid DP receptor.
A:Reference number: I39149; MUID:95370201; PMID:7642548
A:Accession: I39153
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-282 <RES>
A:Cross-references: UNIPROT:Q13258; EMBL:U31332; NID:G940378; PIDN:AAC50178.1; PID:G940375
A:Accession: I39150
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 216-359 <RE2>
A:Cross-references: EMBL:U31099; NID:G940376; PIDN:AAC50177.1; PID:G940377
A:Accession: I39149
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 283-328 <RE3>
A:Cross-references: EMBL:U31098; NID:G940374; PIDN:AAC50176.1; PID:G940375
C:Genetics: GDB:PTGDR
A:Cross-references: GDB:681159
A:Map position: 10q23-10q23
C:Superfamily: prostaglandin E receptor EP1
C:Keywords: G protein-coupled receptor

Query Match 95.2%; Score 1467; DB 2; Length 359;
Best Local Similarity 100.0%; Pred. No. 9.2e-118;
Matches 282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKSPYRCQNTTSVEKGNLSAVMGVLFSTGLGNLLALGLLARSGLGWCRRPLRLPSV 60
Db 1 MKSPYRCQNTTSVEKGNLSAVMGVLFSTGLGNLLALGLLARSGLGWCRRPLRLPSV 60

Qy 61 FYMLVCGITVTDLLGKCLLSPVVLAAYAQNRSLRVLAIPALDNLSCQAFPMFSGLSST 120
Db 61 FYMLVCGITVTDLLGKCLLSPVVLAAYAQNRSLRVLAIPALDNLSCQAFPMFSGLSST 120

Qy 121 LQLLMALECWLSLGHPPFYRRHITRLGALVAPVWSAFSLAFPCALPMGFGKFPVQYCPG 180
Db 121 LQLLMALECWLSLGHPPFYRRHITRLGALVAPVWSAFSLAFPCALPMGFGKFPVQYCPG 180

Qy 181 TWCFTQWHEGSGLSVLGYSVLYSSLMALLVATVLCNLGAMRNLYAMHRLQHRPRST 240
Db 181 TWCFTQWHEGSGLSVLGYSVLYSSLMALLVATVLCNLGAMRNLYAMHRLQHRPRST 240

```
QY 241 RDCAPRADGRASPOPLEELDHLLALLMTVLFTWCSPV 282
Db 241 RDCAPRADGRASPOPLEELDHLLALLMTVLFTWCSPV 282

RESULT 2
I59269
prostaglandin D receptor (prostanoid DP receptor) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 04-Sep-1998
C:Accession: I59269
R:Hitata, M.; Kakizuka, A.; Aizawa, M.; Ushikubi, F.; Narumiya, S.
Proc. Natl. Acad. Sci. U.S.A. 91, 11192-11196, 1994
A:Title: Molecular characterization of a mouse prostaglandin D receptor and functional e
A:Reference number: I59269; MUID:95062232; PMID:7972033
A:Accession: I59269
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-231 <RES>
A:Cross-references: GB:D29764; NID:g577718; PID:g577719
C:Superfamily: prostaglandin E receptor EPI

Query Match 61.2%; Score 943; DB 2; Length 231;
Best Local Similarity 79.2%; Pred. No. 3.2e-73;
Matches 179; Conservative 19; Mismatches 28; Indels 0; Gaps 0;

QY 6 YRCQNTTSVEKNSAVMGVLFSTGLGNLLALGLLARSGLWCRRRLPRLPSPVYMLV 65
Db 5 YRCQNTTSVEKNSAVMGVLFSTGLGNLLALGLLARSGLWCRRRLPRLPSPVYMLV 64

QY 66 CGLTVTDLLGKCLSPVLAAYQNRSLRVLPALDNLSCQAFAPFMSFFGLSSTLQLLA 125
Db 65 CGLTVTDLLGKCLSPVLAAYQNRSLRVLPALDNLSCQAFAPFMSFFGLSSTLQLLA 124

QY 126 MALECWLISLGHFFYRRHITLRLGALVAPVWSAFSLAFALFPMGFKFVQYCPGTWCFI 185
Db 125 MALECWLISLGHFFYRRHITLRLGALVAPVWSAFSLAFALFPMGFKFVQYCPGTWCFI 184

QY 186 QMVHBEGLSVGLSVYSSLMALLVLAIVLCNIGAMRNLYAMHRR 231
Db 185 QMVHBEGLSVGLSVYSSLMALLVLAIVLCNIGAMRNLYAMHRR 230

RESULT 3
S66674
prostaglandin E receptor EP2 subtype - mouse
C:Species: Mus musculus (house mouse)
C>Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C:Accession: S66674
R:Katsuyama, M.; Nishigaki, N.; Sugimoto, Y.; Morimoto, K.; Negishi, M.; Narumiya, S.; I
FEBS Lett. 372, 151-156, 1995
A:Title: The mouse prostaglandin E receptor EP(2) subtype: cloning, expression, and Nor
A:Reference number: S66674; MUID:96000196; PMID:7556658
A:Accession: S66674
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-362 <NAT>
A:Cross-references: UNIPROT:Q62053; EMBL:D50589; NID:g829048; PID:BAA09137.1; PID:g8290
C:Superfamily: prostaglandin E receptor EPI

Query Match 38.6%; Score 595.5; DB 2; Length 362;
Best Local Similarity 45.4%; Pred. No. 2.2e-43;
Matches 128; Conservative 50; Mismatches 87; Indels 17; Gaps 7;

QY 8 CQNTTSVEKNSAVMGVLFSTGLGNLLALGLLARSGLG--WCSRRRLPRLPSPVYMLV 65
Db 14 CQNTTSVEKNSAVMGVLFSTGLGNLLALGLLARSGLG--WCSRRRLPRLPSPVYMLV 72

QY 66 CGLTVTDLLGKCLSPVLAAYQNRSLRVLPALDNLSCQAFAPFMSFFGLSSTLQLLA 125
Db 73 TELVLTDLGKCLSPVLAAYQNRSLRVLPALDNLSCQAFAPFMSFFGLSSTLQLLA 130
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QY 126 MALECWLISLGHFFYRRHITLRLGALVAPVWSAFSLAFALFPMGFKFVQYCPGTWCFI 185
Db 131 MALECWLISLGHFFYRRHITLRLGALVAPVWSAFSLAFALFPMGFKFVQYCPGTWCFI 190

QY 186 QMVHBEGLSVGLSVYSSLMALLVLAIVLCNIGAMRNLYAMHRRLQRHPRSCSTRDCAE 245
Db 191 R--HGR-----TAYLQLVATVMTLLIVAVLACNIVSLNIRMHRRSR--SRCGLSGSS 241

QY 246 PRADG---REASPOPLEELDHLLALLMTVLFTWCSPVIAF 284
Db 242 LRPGSRRRGERTSMAEETHLLAILMTITFAICSLPFTIF 283

RESULT 4
I38920
prostaglandin E2 receptor - human
C:Species: Homo sapiens (man)
C>Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 09-Jul-2004
C:Accession: I38920
R:Regan, J.W.; Bailey, T.J.; Pepperl, D.J.; Pierce, K.L.; Bogardus, A.M.; Donello, J.E.;
Mol. Pharmacol. 46, 213-220, 1994
A:Title: Cloning of a novel human prostaglandin receptor with characteristics of the pha
A:Reference number: I38920; MUID:94359483; PMID:8078484
A:Accession: I38920
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-358 <RES>
A:Cross-references: UNIPROT:P43116; EMBL:U19487; NID:g639719; PID:AAA61681.1; PID:g63262;
C:Superfamily: prostaglandin E receptor EPI

Query Match 38.0%; Score 586; DB 2; Length 358;
Best Local Similarity 45.2%; Pred. No. 1.4e-42;
Matches 128; Conservative 45; Mismatches 92; Indels 18; Gaps 7;

QY 8 CQNTTSVEKNSAVMGVLFSTGLGNLLALGLLARSGLG--WCSRRRLPRLPSPVYMLV 65
Db 13 CQNTTSVEKNSAVMGVLFSTGLGNLLALGLLARSGLG--WCSRRRLPRLPSPVYMLV 71

QY 66 CGLTVTDLLGKCLSPVLAAYQNRSLRVLPALDNLSCQAFAPFMSFFGLSSTLQLLA 125
Db 72 TELVLTDLGKCLSPVLAAYQNRSLRVLPALDNLSCQAFAPFMSFFGLSSTLQLLA 129

QY 126 MALECWLISLGHFFYRRHITLRLGALVAPVWSAFSLAFALFPMGFKFVQYCPGTWCFI 185
Db 130 MALECWLISLGHFFYRRHITLRLGALVAPVWSAFSLAFALFPMGFKFVQYCPGTWCFI 189

QY 186 QMVHBEGLSVGLSVYSSLMALLVLAIVLCNIGAMRNLYAMHRRLQRHPRSCSTRDCAE 245
Db 190 R--HGR-----TAYLQLVATVMTLLIVAVLACNIVSLNIRMHRRSR--SRCGPGSLGS 240

QY 246 ---PRADGRASPOPLEELDHLLALLMTVLFTWCSPVIAF 284
Db 241 GRGPGARRRGERTSMAEETHLLAILMTITFAVCSLPFTIF 283

RESULT 5
S51312
EP2 prostaglandin receptor - human
C:Species: Homo sapiens (man)
C>Date: 07-May-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004
C:Accession: S51312
R:Oakley, C.J.
submitted to the EMBL Data Library, January 1995
A:Reference number: S51312
A:Accession: S51312
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-358 <OAK>
A:Cross-references: UNIPROT:P43116; EMBL:X83868; NID:g633205; PID:CAA58749.1; PID:g63320
C:Superfamily: prostaglandin E receptor EPI

Query Match 38.0%; Score 585; DB 2; Length 358;
Best Local Similarity 45.2%; Pred. No. 1.7e-42;
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Matches	128;	Conservative	45;	Mismatches	92;	Indels	18;	Gaps	7;
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Qy 8 CONTTSVEKGSANVGVLVFTSTGLGNLALLGLLARSGLG--WCSRRRLPLRPSVFYMLV 65
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 13 CETROWLPGESPAISSVMFSAGVLGNLIATALLARWRGDVGCSSAGRSSL-SLFHLV 71
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Qy 66 CGLTVTDLLGHCKLLSPVLAAYAQNRSLRVLAPALDNLSCQAFAPFMSPFGLSSTQLLMA 125
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 72 TELVPTDLUGTCLISPVVASARNQTILVALP--ESRACTYFAFAMTFFLSATMLMIFA 129
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Qy 126 MALCEWLISLGHPFFVRHHITLRIGALVAVPVVSAPSFLAFCALPFMGFGKFVOYCPTWCFI 185
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 130 MALERYLSIGHYPFYQRVRVSSGGUAVLVPIYAVISLLFCSLPDDYGIVQVCPTWCFI 189
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Qy 186 QMWHEEGSLSVGLSYSSLMALLIATVLCNLAGMENLYAMHRRRLORHPRSCTRDCAE 245
: | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 190 R--HGR-----TAVYLQLYATVLTLLLIVSVLACNFVSILNMHRSSR--SRCGPSLGS 240
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Qy 246 ----PRADGRASPOPLEDHLLLLLAMTVLFTWCSLPVIAP 284
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 241 GRGGPGARRRGERVSMABETDHLILLAIMTIIFAVCSLPFTIF 283
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :

```

RESULT 6
A54416
prostaglyclin receptor - mouse
C:Species: Mus musculus (house mouse)
C>Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 20-Jun-2000
C:Accession: A54416
E:Namba, T.; Oida, H.; Sugimoto, Y.; Kakiuka, A.; Negishi, M.; Ichikawa, A.; Narumiya, J. Biol. Chem. 269, 9986-9992, 1994
A>Title: cDNA cloning of a mouse prostaglyclin receptor. Multiple signaling pathways and
A:Reference number: A54416; PMID:94193694; PMID:7511597
A:Accession: A54416
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-417 <NAME>
A:Cross-references: GB:D26157; NID:g493687; PIDN:BAA05144.1; PID:g493688
C:Superfamily: prostaglandin E receptor EP1
    
```

Query Match 33.7% ; Score 519; DB 2; Length 417;
Best Local Similarity 43.1% ; Pred. No. 8.5e-37;
Matches 125; Conservative 38; Mismatches 101; Indels 26; Gaps 8;

Qy	8	CONTTSVEKGSANVGVLVFTSTGLGNLALLGLLARSGLGWCRRRLPLRPSVFYMLVCG 67
Db	35	CWNITYQDSVGPATSILMFVAGVVNGNALGIIG-----ARR--RSHSAFAVLVTG 85
		: : : : : : : : : : : : : : :
Qy	68	LTVTDLLGKLLSPVLAAYAQNRSLRVLAPALDNLSCQAFAPFMSPFGLSSTQLLAMA 127
Db	86	LAVTDLLGTCLFSPA VFVAYARNSSLGLAHG-GTMLCDTFAFAMTFFLGSTLILFWA 144
		: : : : : : : : : : : : : : :
Qy	128	LECWLISGHPFFYRRHTLRIGALVAVPVVSAPSFLAFCALPFMGFGKFVOYCPTWCFIQM 187
		: : : : : : : : : : : : : : :
Db	145	VERCALSHPLYAQLDGPCRCAREPALPSIYAFCFLCSLPDLLGEHQOQCPGWCFIRM 204
		: : : : : : : : : : : : : : :
Qy	188	VHBEGSLSVGLSYSSLMALLIATVLCNLAGMENLYAMHRRRLORHPRSCTRDCAEPR 247
		: : : : : : : : : : : : : : : :
Db	205	--RSAQGCGCAFSLAYASLMMALLVTSTIFFCNCSVTLSDHYMYROQRHHHSFV-----PT 257
		: : : : : : : : : : : : : : :
Qy	248	ADGREASPQPLEEHDHLLLLLAMTVLFTWCSLPVIAPVPG-VPAKTPEGSR 296
		: : : : : : : : : : : : : : :
Db	258	SRARE-----DEVVHLLIAMTMIVAVCSLPM--IRGFQAIPDSR 299
		: : : : : : : : : : : : : : :

RESULT 7
A57066
prostaglyclin receptor - human
N:Alternate names: prostaglandin I2 receptor; prostanoid IP receptor
C:Species: Homo sapiens (man)
C>Date: 03-Oct-1995 #sequence_revision 03-Oct-1995 #text_change 09-Jul-2004
C:Accession: A57066; A43952; A53587; I52867
R:Odawara, Y.; Tanaka, I.; Inoue, M.; Yoshitake, Y.; Issse, N.; Nakagawa, O.; Usui, T.; Itokura, S.

Genomics 27, 142-148, 1995

A;Title: Structural organization and chromosomal assignment of the human prostacyclin receptor cDNA
A;Reference number: A57066; MUID:95394450; PMID:7665161

A;Accession: A57066

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: DNA

A;Residues: 1-386 <OGA>

A;Cross-references: UNIPROT:P43119; GB:D38127; GB:D38128; NID:g1019364; PIDN:BAA07325.1;
R;Katsuyama, M.; Sugimoto, Y.; Namba, T.; Irie, A.; Negishi, M.; Narumiya, S.; Ichikawa,
FEBS Lett. 344, 74-78, 1994

A;Title: Cloning and expression of a cDNA for the human prostacyclin receptor.

A;Reference number: S43952; MUID:94237286; PMID:7514139

A;Accession: S43952

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-386 <KAT>

A;Cross-references: EMBL:D25418; NID:g467509; PIDN:BAA05008.1; PID:g467510
R;Boie, Y.; Rushmore, T.H.; Darmon-Goodwin, A.; Grygorczyk, R.; Slipetz, D.M.; Metters, F.
J. Biol. Chem. 269, 12173-12178, 1994

A;Title: Cloning and expression of a cDNA for the human prostanoid IP receptor.

A;Reference number: A53587; MUID:94216334; PMID:7512962

A;Accession: A53587

A;Molecule type: mRNA

A;Residues: 1-386 <BOI>

A;Cross-references: GB:L29016; NID:g495042; PIDN:AAA36448.1; PID:g495043
R;Nakagawa, O.; Tanaka, I.; Usui, T.; Harada, M.; Sasaki, Y.; Itoh, H.; Yoshimasa, T.; Ne
Circulation 90, 1643-1647, 1994

A;Title: Molecular cloning of human prostacyclin receptor cDNA and its gene expression in

A;Reference number: I52867; MUID:9508086; PMID:7923647

A;Accession: I52867

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-386 <RES>

A;Cross-references: GB:D29634; NID:g577629; PIDN:BAA06110.1; PID:g577630

C;Genetics:

A;Gene: GDB:PTGIR

A;Cross-references: GDB:373439; OMIM:600022

A;Map position: 19q13.3-19q13.3

C;Superfamily: prostaglandin E receptor EP1

C;Keywords: transmembrane protein

Query Match 33.6%; Score 518.5; DB 2; Length 386;
Best Local Similarity 43.3%; Pred. No. 8.7e-37;
Matches 122; Conservative 39; Mismatches 82; Indels 39; Gaps 8;

Qy 8 CONTTSVEKGNSAVMGVLFSTGLGNLLALGLIARSLGWCSRRLPLRSVFYMLVCG 67
| | | | : : : : | : | : | : | : | : | : | : | : | : | :
Db 5 CRNLTVRGSGPATSTLMFVAGVVGNGLAGILS-----ARRPAR--PSAFVLVTG 55

Qy 68 LTVTDLLGKCLLSPVVLAAYAQNRSLRVLA---PALDNLSCQAFAPFMFSFGLSSTQLL 124
| | | | | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 56 LAATDLLGTSTLSPANFVAARNSSLGLARGGA---LCDAFAPAMTFGLASMLILF 111

Qy 125 AMALECNWLSIGHFFYYRRHTTLRGALVAPVWSAFSLAFCAFPWMGFQYQYCGTWCF 184
| | | | | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 112 AMAVERCLASHPHYLAQLDGPCARLALPAIVAFCVLCALPLLGLGOHQYCPSWCWF 171

Qy 185 IQM--VHEEGSLSVLGYSVLYSSIMALLVLTVCNIGMRNLYAMHRRLOHPRCSTRD 242
| | | | : : : : | : | : | : | : | : | : | : | : | : | :
Db 172 LRMRWAQPGGA----AFSLAYAGLVALLVAAIFLCNGSVTSLSCRMYRQQRHQGS---- 223

Qy 243 CAEPRADGREASPQPL---EELDHLLALLMTVLTFTMCISLPV 281
| | | | : : | : | : | : | : | : | : | : | : | : | :
Db 224 -----LGRPRRTGEVDHILLALTVMVAVCSLPL 255

RESULT 8
S52078
prostacyclin - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 14-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
C;Accession: S52078
R;Sasaki, Y.; Usui, T.; Tanaka, I.; Nakagawa, O.; Sando, T.; Takahashi, T.; Namba, T.;

R:Bastien, L.; Sawyer, N.; Grygorczyk, R.; Metters, K.M.; Adam, M.
 J. Biol. Chem. 269, 11873-11877, 1994
 A:Title: Cloning, functional expression, and characterization of the human prostaglandin
 A:Reference number: A53572; MUID:94216291; PMID:8163486
 A:Accession: A53572
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-488 <BAS>
 R:An, S.; Yang, J.; Xia, M.; Goetzl, E.J.
 Biochem. Biophys. Res. Commun. 197, 263-270, 1993
 A:Title: Cloning and expression of the EP2-subtype of human receptors for prostaglandin
 A:Reference number: I52289; MUID:94071953; PMID:8250933
 A:Accession: I52289
 A>Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: mRNA
 A:Residues: 1-463, 'WAC', 467-488 <ANS>
 A:Cross-references: GB:L25124; NID:9435049; PIDN:AAA36438.1; PID:9435050
 C:Genetics: EP2
 A:Gene: GDB:PTGER2; EP2
 A:Cross-references: GDB:270672; OMIM:176804
 A:Map position: Sp13.1-Sp13.1
 C:Superfamily: vertebrate rhodopsin
 C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 23.7%; Score 364.5; DB 2; Length 488;
 Best Local Similarity 31.5%; Pred. No. 1.5e-23;
 Matches 97; Conservative 51; Mismatches 121; Indels 39; Gaps 8;

QY 1 MKSPFYRCQNTTSVEKGNNAV-MGGVLFSTGLGNLLALGLLARSGLGWCRRPLPLPS 59
 DB 1 MSTPGVNSASLPDRLNSPVTIPAVMTFTFGVGNLVAIVLCK-----SRKEQK--ET 52

QY 60 VFYMLVCGTLVTDLLGKCLLSPVLAAYAQNRSLRVLAFLALDNLSCQAFAPFMSFFGLSG 119
 DB 53 TYTTLVCGLAIVDGLTLVSPVTIATYMKGQ-----WFG-GQPLCEYTFILLFFSLSG 106

QY 120 TLQLLMALECLSLGHPPFYRRHITRLGALVAPVVSFAFSLAFALCPFMGFGKVFQYCP 179
 DB 107 LSIICAMSVRYLAINHAFYSHYVDKRLAGLTLFPAVYASNVLFALCPNMGGLSSRLQYP 166

QY 180 GTWCTIQVHEGSLSVLGYSVLVSSLMALLVATVLCNIGAMRNLYAMHRLQRHPRSC 239
 DB 167 DTWCFIDMT--TNVTAHAAYSIMYAGFSSFLILATVLCNVLVCGALLRHQFMRTSLG 224

QY 240 TRD-----CAEPRADGREASPOPL-----BELDHLHLLALMTVLTFC 277
 DB 225 TQHHAAAAASVASRGRHAPASPALPRLSDFRRRSRFRRTAGAEIQWVILLIATSLVVLIC 284

QY 278 SLPVIAFV 285
 DB 285 SIPLVVRV 292

RESULT 12
 S48689
 prostaglandin E(2) receptor (EP3 beta subtype) - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 15-Jul-1995 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
 C:Accession: S48689; S46934
 R:Neuschaefer-Rube, F.; DeVries, C.; Haenecke, K.; Jungermann, K.; Püeschel, G.P.
 FEBS Lett. 351, 119-122, 1994
 A:Title: Molecular cloning and expression of a prostaglandin E(2) receptor of the EP(3-B
 A:Reference number: S48689; MUID:94357264; PMID:8076679
 A:Accession: S48689
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-362 <NEU>
 A:Cross-references: EMBL:X80133; NID:G514418; PIDN:CAA56432.1; PID:G514419
 C:Superfamily: prostaglandin E receptor EPI

Query Match 17.3%; Score 267; DB 2; Length 362;
 Best Local Similarity 29.5%; Pred. No. 2.4e-15;

Matches 85; Conservative 45; Mismatches 116; Indels 42; Gaps 9;

QY 10 NTTTSVEKGNNAVGG---VLFSTGLGNLLALGLLARSGLGWCRRPLPLPSVFYMLVC 66
 DB 16 NQSSAADGCGSVSVAFPTMTVTFGVGNALMALLVSR-----YRRRESKRKKSFLLCIG 70

QY 67 GLUTVDLLGKCLLSPVLAAYAQNRSLRVLAFLALDNLSCQAFAPFMSFFGLSSTLQLLAM 126
 DB 71 WLALTDLVGQLLTSPPVILVLSQRRWEQLDPS--GRLCCTFFGLTMTVFGLSLLVASAM 128

QY 127 ALECMWLSLGHPPFYRRHITRLGALVAPVVSFAFSLAFALCPFMGFGKVFQYCPGTWCFFI- 185
 DB 129 AVERALATRAPHWYASHMKTRATRVLLGVWLSVLAFLALLPVLGVRYSVQWPGTWCFFIS 188

QY 186 -----QMVEEGSLSVLGYSVLVSSLMALLVATVLCNIGAMRNLYAMHRLQRHPR 237
 DB 189 TGPAGNETDSAREPGSVA---FASAFACLGLLALVVTACNLATIKALVS----- 235

QY 238 SCTRDCAEPRAD---GREASPOPLEELHLLALMTVLTFCVCSLPVI 282
 DB 236 RCRAKAAASQSSAQWGRITTTTAIQ-----LMGIMCVL-SVCWSPLL 276

RESULT 13
 S51280
 EP3-alpha receptor - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 07-May-1995 #sequence_revision 01-Sep-1995 #text_change 23-Jul-1999
 C:Accession: S51280
 R:Neuschaefer-Rube, F.; de Vries, C.; Haenecke, K.; Jungermann, K.; Püeschel, G.P.
 submitted to the EMBL Data Library, January 1995
 A:Reference number: S51280
 A:Accession: S51280
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-366 <NEU>
 A:Cross-references: EMBL:X83855; NID:G633623; PIDN:CAA58735.1; PID:G633624
 C:Superfamily: prostaglandin E receptor EPI

Query Match 17.3%; Score 267; DB 2; Length 366;
 Best Local Similarity 29.5%; Pred. No. 2.4e-15;
 Matches 85; Conservative 45; Mismatches 116; Indels 42; Gaps 9;

QY 10 NTTTSVEKGNNAVGG---VLFSTGLGNLLALGLLARSGLGWCRRPLPLPSVFYMLVC 66
 DB 16 NQSSAADGCGSVSVAFPTMTVTFGVGNALMALLVSR-----YRRRESKRKKSFLLCIG 70

QY 67 GLUTVDLLGKCLLSPVLAAYAQNRSLRVLAFLALDNLSCQAFAPFMSFFGLSSTLQLLAM 126
 DB 71 WLALTDLVGQLLTSPPVILVLSQRRWEQLDPS--GRLCCTFFGLTMTVFGLSLLVASAM 128

QY 127 ALECMWLSLGHPPFYRRHITRLGALVAPVVSFAFSLAFALCPFMGFGKVFQYCPGTWCFFI- 185
 DB 129 AVERALATRAPHWYASHMKTRATRVLLGVWLSVLAFLALLPVLGVRYSVQWPGTWCFFIS 188

QY 186 -----QMVEEGSLSVLGYSVLVSSLMALLVATVLCNIGAMRNLYAMHRLQRHPR 237
 DB 189 TGPAGNETDSAREPGSVA---FASAFACLGLLALVVTACNLATIKALVS----- 235

QY 238 SCTRDCAEPRAD---GREASPOPLEELHLLALMTVLTFCVCSLPVI 282
 DB 236 RCRAKAAASQSSAQWGRITTTTAIQ-----LMGIMCVL-SVCWSPLL 276

RESULT 14
 A45211
 prostaglandin E receptor EP3 beta, PGE receptor EP3 beta (alternatively spliced) - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
 C:Accession: A45211
 R:Sugimoto, Y.; Negishi, M.; Hayashi, Y.; Namba, T.; Honda, A.; Watabe, A.; Hirata, M.; I
 J. Biol. Chem. 268, 2712-2716, 1993
 A:Title: Two isoforms of the EP3 receptor with different carboxyl-terminal domains. Ident

A;Reference number: A45211; MUID:93155085; PMID:8381413

A;Accession: A45211

A;Status: Preliminary; not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 1-361 <SUG>

A;Cross-references: UNIPROT:P30557; GB:D13321; NID:G286108; PIDN:BAA02578.1; PID:G286109

A;Experimental source: mastocytoma P-815

A;Note: sequence extracted from NCBI backbone (NCBIP:124180)

C;Superfamily: prostaglandin E receptor EPI

C;Keywords: G protein-coupled receptor; transmembrane protein

Query Match 17.0%; Score 261.5; DB 2; Length 361;

Best Local Similarity 29.6%; Pred. No. 7e-15;

Matches 85; Conservative 50; Mismatches 107; Indels 47; Gaps 11;

QY 10 NNTSVEKNSAVMGV-LFSTGLLGNLLALGLLARSGLWCRRRLPLPSVFMVLCGL 68

DB 18 SSTTDCGVSVAFFITMTMTGFGNALAMLLVRS-----YRRRESKRKKSFLLCIGWL 72

QY 69 TTTDLGKCLLSPVVLAAVAQNRSRLVLPALDNLSCQAFPMSPFGLSSTLQLLAL 128

DB 73 AUTDLVGQLTSPVILVYLSORRWEQLDPS--GRLCFTFGLTMTVFGLSLLVASAMAV 130

QY 129 ECWLSLGHFFFYRRHITLRLGALVAPV---VSAFSLAFCAFPFMGFGKVFQYCPGTWCFI 185

DB 131 ERALAIRAPHWYASHMKT-----ATPVLGGVLSVLAFAFPVLGVGRYSVQWPGTWCFI 186

QY 186 QM-----VHEGSLSVLGYSVLSMALLVLAIVLCNLGAMRNLYAMHRLQRHP 236

DB 187 STGPAGNETDPAREPGSVA---FASAFACLGILLAVITFACNLATIKALVS----- 234

QY 237 RSCTRDCAEPRAD---GREASQPLELDHLLALLMTVLTMCSLPVI 282

DB 235 -RCRAKAASQSSAOWGRITTTETAIO-----LMGIMCVL-SVCWSPLL 275

RESULT 15

JC2115

Prostaglandin E receptor EP3 subtype rEP3B - rat

N;Contains: prostaglandin E receptor rEP3A

C;Species: Rattus norvegicus (Norway rat)

C;Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 17-Mar-1999

C;Accession: JC2115

R;Takeuchi, K.; Takahashi, N.; Abe, T.; Abe, K.

Biochem. Biophys. Res. Commun. 199; 834-840, 1994

A;Title: Two isoforms of the rat kidney EP3 receptor derived by alternative RNA splicing

A;Reference number: JC2115; MUID:94183265; PMID:8135830

A;Accession: JC2115

A;Molecule type: mRNA

A;Residues: 1-364 <TAK>

A;Note: the authors translated the codon GAT for residue 360 as Val

C;Comment: this protein is co-localized to distal tubules exerting an effect on water an

C;Superfamily: prostaglandin E receptor EPI

C;Keywords: glycoprotein; GTP binding; phosphoprotein; receptor; transmembrane protein

F;1-364/Product: prostaglandin E receptor rEP3B #status predicted <PEC>

F;1-335/Product: prostaglandin E receptor rEP3A #status predicted <PER>

F;31-55/Domain: transmembrane #status predicted <TM1>

F;69-89/Domain: transmembrane #status predicted <TM2>

F;108-130/Domain: transmembrane #status predicted <TM3>

F;152-173/Domain: transmembrane #status predicted <TM4>

F;204-229/Domain: transmembrane #status predicted <TM5>

F;260-283/Domain: transmembrane #status predicted <TM6>

F;304-325/Domain: transmembrane #status predicted <TM7>

F;16.193/Binding site: carbohydrate (Asn) (covalent) #status predicted

F;59.64/Binding site: phosphate (Ser) (covalent) (by CAMP-dependent kinase) #status pred

Query Match

Best Local Similarity 17.0%; Score 261.5; DB 2; Length 364;

Matches 86; Conservative 44; Mismatches 112; Indels 49; Gaps 11;

QY 10 NNTSVEKNSAVMGV---VLFSTGLLGNLLALGLLARSGLWCRRRLPLPSVFMVLC 66

DB 16 NQSSAADCGSVSAFFITMTMTGFGNALAMLLVRS-----YRRRESKRKKSFLLCIG 70

QY 67 GLTVDLLGKCLLSPVVLAAVAQNRSRLVLPALDNLSCQAFPMSPFGLSSTLQLLAL 126

DB 71 WIALTDLVGQLTSPVILVYLSORRWEQLDPS--GRLCFTFGLTMTVFGLSLLVASAM 128

QY 127 ALECWLSLGHFFFYRRHITLRLGALVAPV---VSAFSLAFCAFPFMGFGKVFQYCPGTWC 183

DB 129 AVERALAIRAPHWYASHMKT-----ATPVLGGVLSVLAFAFPVLGVGRYSVQWPGTWC 184

QY 184 FI-----QMWHEGSLSVLGYSVLSMALLVLAIVLCNLGAMRNLYAMHRLQR 234

DB 185 FISTGPAGNETDSAREPGSVA---FASAFACLGILLAVITFACNLATIKALVS----- 234

QY 235 HPRSCTRDCAEPRAD---GREASQPLELDHLLALLMTVLTMCSLPVI 282

DB 235 ---RCRAKAASQSSAOWGRITTTETAIO-----LMGIMCVL-SVCWSPLL 275

Search completed: April 22, 2005, 21:30:02

Job time : 15.4611 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 22, 2005, 18:00:17 ; Search time 52.4214 Seconds
(without alignments)
2891.482 Million cell updates/sec

Title: US-10-689-861-2
Perfect score: 1541
Sequence: 1 MKSPYRCQNTTSVKGNSA.....CSLPVIAFVGVPKTPGSR 296

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 03.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	1467	95.2	359	1	PD2R_HUMAN	Q13258 homo sapien
2	1127	73.1	357	2	Q9R261	Q9R261 rattus norv
3	1125	73.0	357	2	O35932	O35932 rattus norv
4	1100	71.4	357	1	PD2R_MOUSE	P70263 mus musculu
5	1095	71.1	357	2	O8CCM3	O8CCM3 mus musculu
6	802	39.1	361	1	PD22_CANFA	Q9X822 canis famil
7	595.5	38.6	362	1	PE22_MOUSE	Q62053 mus musculu
8	593.5	38.5	308	2	Q8B275	Q8B275 mus musculu
9	585	38.0	358	1	PE22_HUMAN	P43116 homo sapien
10	569	36.9	361	2	Q8HY57	Q8HY57 oryctolagus
11	569	36.9	371	2	Q6NZ15	Q6NZ15 xenopus lae
12	565.5	36.7	357	1	PE22_RAT	Q62928 rattus norv
13	556	36.1	352	2	Q8MJ09	Q8MJ09 bos taurus
14	549	35.6	385	1	PI2R_BOVIN	P79393 bos taurus
15	519	33.7	415	1	PI2R_MOUSE	P43252 mus musculu
16	518.5	33.6	386	1	PI2R_HUMAN	P43119 homo sapien
17	506.5	32.9	416	1	PI2R_RAT	P43253 rattus norv
18	493.5	32.0	281	2	Q6PFT8	Q6PFT8 brachydanio
19	393	25.5	292	2	Q7TSX4	Q7TSX4 rattus norv
20	389	25.2	488	2	Q91VE4	Q91VE4 mus musculu
21	389	25.2	513	1	PE24_MOUSE	P32240 mus musculu
22	383	24.9	488	1	PE24_RAT	P43114 rattus norv
23	372.5	24.2	492	2	Q9TUL6	Q9TUL6 canis famil
24	372	24.1	492	2	Q8MJ08	Q8MJ08 bos taurus
25	364.5	23.7	488	1	PE24_HUMAN	P35408 homo sapien
26	363.5	23.6	490	2	Q95J39	P32240 macaca fasc
27	363.5	23.6	490	1	PE24_RABIT	Q7JGJ7 papio hamad
28	363	23.6	488	1	PE24_RABIT	Q28691 oryctolagus
29	361.5	23.5	490	1	PE24_PANTR	Q95KZ0 pan troglod
30	316.5	20.5	154	2	Q7TSX3	Q7TSX3 mus musculu
31	300.5	19.5	168	2	Q95M50	Q95M50 bos taurus

32	277.5	18.0	133	2	Q95M51	Q95M51 bos taurus
33	266	17.3	362	2	Q6PDF2	Q6PDF2 mus musculu
34	261.5	17.0	360	2	Q99PG3	Q99PG3 rattus norv
35	261.5	17.0	365	1	PE23_MOUSE	P30557 mus musculu
36	261.5	17.0	365	1	PE23_RAT	P34980 rattus norv
37	255.5	16.6	370	2	Q6VPS4	Q6VPS4 canis famil
38	255.5	16.6	416	2	Q6VPS5	Q6VPS5 canis famil
39	251.5	16.3	411	1	PE23_RABIT	P46069 oryctolagus
40	250.5	16.3	369	1	TA2R_HUMAN	P21731 homo sapien
41	250.5	16.3	407	2	O75228	O75228 homo sapien
42	244.5	15.9	366	2	O6TTN3	O6TTN3 homo sapien
43	244.5	15.9	390	1	PE23_HUMAN	P43115 homo sapien
44	244.5	15.9	393	2	O00326	O00326 homo sapien
45	244.5	15.9	402	2	O00325	O00325 homo sapien

ALIGNMENTS

RESULT 1
PD2R_HUMAN
ID PD2R_HUMAN STANDARD; PRT; 359 AA.
AC Q13258; Q13250; Q13251;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE 25-OCT-2004 (Rel. 45, Last annotation update)
DE Prostaglandin D2 receptor (Prostanoid DP receptor) (PGD receptor).
GN Name=PTGDR;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A.
RP MEDLINE=95370201; PubMed=7642548; DOI=10.1074/jbc.270.32.18910;
RX Boie Y., Sawyer N., Slipetz D.M., Metters K.M., Abramovitz M.;
RA "Molecular cloning and characterization of the human prostanoid DP
receptor.";
RL J. Biol. Chem. 270:18910-18916 (1995).
RN [2]
SEQUENCE FROM N.A.
RP
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heich F.,
RA Diatchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting J., Madao A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
CC -!- FUNCTION: Receptor for prostaglandin D2 (PGD2). The activity of
this receptor is mainly mediated by G(s) proteins that stimulate
adenylate cyclase, resulting in an elevation of intracellular
cAMP. A mobilization of calcium is also observed, but without
formation of inositol 1,4,5-trisphosphate.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: Expressed in retina and small intestine.
CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
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CC or send an email to license@isb-sib.ch).

ENBL; U31332; AAC50178.1; -
DR DR
ENBL; U31098; AAC50176.1; -
DR DR
ENBL; U31099; AAC50177.1; -
DR DR
ENBL; BC040968; AAH40968.1; -
DR DR
PIR; I39153; I39153.
DR DR
Genew; HGNC:9591; PTGDR.
DR DR

RESULT 2
Q9R261

ID	Q9R361	PRELIMINARY;	PRT;	357 AA.
AC	Q9R361;			
DT	01-MAY-2000	(TrEMBLrel. 13, Created)		
DT	01-MAY-2000	(TrEMBLrel. 13, Last sequence update)		
DT	01-OCT-2003	(TrEMBLrel. 25, Last annotation update)		
DE	Prostaglandin D2 receptor.			
OS	Rattus norvegicus (Rat).			
DE	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
OX	NCBI_TaxID=10116;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=Sprague-Dawley;			
RC	MEDLINE=99376163; PubMed=10489933; DOI=10.1016/S0014-2999(99)00358-1;			
RT	Wright D.H., Nantel F., Metters K.M., Ford-Hutchinson A.W.;			
RA	"A novel biological role for prostaglandin D2 is suggested by			
RL	distribution studies of the rat Dp prostanoïd receptor.";			
RL	Eur. J. Pharmacol. 377:101-115(1999).			

RESULT 3
035932

035932	PRELIMINARY;	PRT;	357 AA.
AC	O35932;		
DT	01-JAN-1998	(TREMBLrel. 05,	Created)
DT	01-JAN-1998	(TREMBLrel. 05,	Last sequence update)
DT	01-OCT-2003	(TREMBLrel. 25,	Last annotation update)
DE	Prostaglandin D2 receptor.		
OS	Rattus norvegicus (Rat).		

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=101116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Retina;
RX MEDLINE=98387174; PubMed=9721719; Kanaoka Y., Eguchi N., Gordon W.C.,
RA Gershenenko D., Beuckmann C.T., Kanaoka Y., Eguchi N., Gordon W.C.,
RA Urade Y., Bazan N.G., Hayaishi O.;
RT "Dominant expression of rat prostanoïd DP receptor mRNA in
RT leptomeninges, inner segments of photoreceptor cells, iris epithelium,
RT and ciliary processes."
RL J. Neurochem. 71:937-945(1998).
DR EMBL; U92289; AAB7162.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004956; F:prostaglandin D receptor activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0004960; F:thromboxane receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . ; IEA.
DR InterPro; IPR000276; GPCR Rhodopsin.
DR InterPro; IPR000376; GPCR Rhodopsin.
DR InterPro; IPR008365; Prostanoidrecept.
DR InterPro; IPR001105; Thbox_receptor.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PRO1788; PROSTANOIDR.
DR PRINTS; PRO0854; PRSTNOIDDR.
DR PRINTS; PRO0429; THROMBOXANER.
DR PROSITE; PS0262; G_PROTEIN_RECEP_FL_2; 1.
KW Receptor.
SQ SEQUENCE 357 AA; 39802 MW; DB966276DD68184C CRC64;

Query Match 73.0%; Score 1125; DB 2; Length 357;
Best Local Similarity 78.0%; Pred. No. 7.6e-80;
Matches 216; Conservative 21; Mismatches 40; Indels 0; Gaps 0;

QY 6 YRCQNTTSVEKNSAVMGVLFSTGLGNLLALGALLARSGLGWCRRRLPLPSVPMVLV 65
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
5 YRCQATWVERGSSATMGVLFSTGLGNLLALGALLARSGLGWCRRRLPLPSVPMVLV 64
QY 66 CGLTVDLLGKCLLSPVLAAYQNRSLRVLPALDNLSCQAFAPFMSFGLSSTLQLLA 125
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
65 CGLTVDLLGKCLLSPVLAAYQNRSLRVLPALDNLSCQAFAPFMSFGLSSTLQLLA 124
QY 126 MALECWLSLGHPPFFYRRHITLRLGALVAPVSAFSLAFALCPFMGKGVQCPGTWCFI 185
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
125 MALECWLSLGHPPFFYRRHITLRLGALVAPVSAFSLAFALCPFMGKGVQCPGTWCFI 184

QY 186 QMVBEGSLVGLYSSLMALLVATVLCNIGAMRNLYAMHRLQRHPRSCRTDCAE 245
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
185 QMIKKRSFVIGFVLYSSLMALLVATVLCNIGAMRNLYAMHRLQRHPRSCRTDCAE 244
QY 246 PRADGREGASPOPLELDHLLALMTVLTMCSLPVI 282
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
245 SGSDYRHGSPNPLELDHFPVLLATVLTMCSLPLI 281

RESULT 4
PD2R MOUSE
ID PD2R MOUSE STANDARD; PRT; 357 AA.
AC P70263;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Prostaglandin D2 receptor (Prostanoid DP receptor) (PGD receptor).
GN Name=PgdR;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SV; TISSUE=Lung;

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RX MEDLINE=95062232; PubMed=7972033;
RA Hirata M., Kakizuka A., Aizawa M., Ushikubi F., Narumiya S.;
RT "Molecular characterization of a mouse prostaglandin D receptor and
RT functional expression of the cloned gene."
RL Proc. Natl. Acad. Sci. U.S.A. 91:11192-11196(1994).
CC -!- FUNCTION: Receptor for prostaglandin D2 (PGD2). The activity of
CC this receptor is mainly mediated by G(s) proteins that stimulate
CC adenylyl cyclase, resulting in an elevation of intracellular
CC CAMP. A mobilization of calcium is also observed, but without
CC formation of inositol 1,4,5-trisphosphate.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: Most abundantly expressed in the ileum,
CC followed by lung, stomach and uterus.
CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@sib-sib.ch)
CC -----
DR EMBL; D29765; BAA06168.1; -.
DR EMBL; D29764; BAA06168.1; JOINED.
DR MGD; MGI:102966; Ptdgr.
DR GO; GO:0004956; F:prostaglandin D receptor activity; IEA.
DR GO; GO:0001785; F:prostaglandin J receptor activity; IEA.
DR InterPro; IPR000276; GPCR Rhodopsin.
DR InterPro; IPR000376; GPCR Rhodopsin.
DR InterPro; IPR008365; Prostanoidrecept.
DR InterPro; IPR001105; Thbox_receptor.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PRO1788; PROSTANOIDR.
DR PRINTS; PRO0429; THROMBOXANER.
DR PROSITE; PS00237; G_PROTEIN_RECEP_FL_1; FALSE_NEG.
DR PROSITE; PS0262; G_PROTEIN_RECEP_FL_2; 1.
KW G-protein coupled receptor; Glycoprotein; Transmembrane.
KW DOMAIN 1 20 Extracellular (Potential).
FT TRANSMEM 21 41 1 (Potential).
FT DOMAIN 42 58 Cytoplasmic (Potential).
FT TRANSMEM 59 79 2 (Potential).
FT DOMAIN 80 106 Extracellular (Potential).
FT TRANSMEM 107 127 3 (Potential).
FT DOMAIN 128 149 Cytoplasmic (Potential).
FT TRANSMEM 150 170 4 (Potential).
FT DOMAIN 171 194 Extracellular (Potential).
FT TRANSMEM 195 215 5 (Potential).
FT DOMAIN 216 261 Cytoplasmic (Potential).
FT TRANSMEM 262 282 6 (Potential).
FT DOMAIN 283 306 Extracellular (Potential).
FT TRANSMEM 307 327 7 (Potential).
FT DOMAIN 328 357 Cytoplasmic (Potential).
FT DISULFID 104 182 By similarity.
FT CARBOHYD 2 2 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 89 89 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 357 AA; 40005 MW; 91CBFF7A5936EB05 CRC64;

Query Match 71.4%; Score 1100; DB 1; Length 357;
Best Local Similarity 75.8%; Pred. No. 6.8e-78;
Matches 210; Conservative 26; Mismatches 41; Indels 0; Gaps 0;

QY 6 YRCQNTTSVEKNSAVMGVLFSTGLGNLLALGALLARSGLGWCRRRLPLPSVPMVLV 65
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
5 YRCQSTWVERGSSATMGVLFSTGLGNLLALGALLARSGLGWCRRRLPLPSVPMVLV 64
QY 66 CGLTVDLLGKCLLSPVLAAYQNRSLRVLPALDNLSCQAFAPFMSFGLSSTLQLLA 125
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
65 CGLTVDLLGKCLLSPVLAAYQNRSLRVLPALDNLSCQAFAPFMSFGLSSTLQLLA 124
QY 126 MALECWLSLGHPPFFYRRHITLRLGALVAPVSAFSLAFALCPFMGKGVQCPGTWCFI 185
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
125 MALECWLSLGHPPFFYRRHITLRLGALVAPVSAFSLAFALCPFMGKGVQCPGTWCFI 184

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QY 186 QMWHEEGSLVGYSLVYSSLMALLVLTATVLCNIGAMRNLYAMHRLQHRPSCRTDCAE 245
 DB 195 QMIHKERSFVIGFVSVLSLALLVLTATVLCNIGAMRNLYAMHRLQHRPSCRTDCAE 244

QY 246 PRADGREASPOPLELDHLLALLMTVLTFTWCSLPVI 282
 DB 245 SGSDYRHGSLHPLLELDHFLVLLALMTVLTFTWCSLPVI 281

RESULT 5
 ID Q8CCM3 PRELIMINARY; PRT; 357 AA.
 AC Q8CCM3;
 DT 01-MAR-2003 (TReMBLrel. 23, Created)
 DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
 DE Mus musculus adult male olfactory brain cDNA, RIKEN full-length
 DE enriched library, clone:643056C09 product:prostaglandin D receptor,
 DE full insert sequence.
 GN Name=PtGdr;
 OS Eus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Olfactory brain;
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning";
 RL Meth. Enzymol. 303:19-44(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Olfactory brain;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA RIKEN FANTOM Consortium;
 RT "Functional annotation of a full-length mouse cDNA collection";
 RL Nature 409:685-690(2001).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Olfactory brain;
 RA The FANTOM Consortium;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs";
 RL Nature 420:563-573(2002).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Olfactory brain;
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes";
 RL Genome Res. 10:1617-1630(2000).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Olfactory brain;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
 RA Sumi N., Tahii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer";
 RL Genome Res. 10:1757-1771(2000).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Olfactory brain;

RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno M., Hanaoka T., Hara A., Hashizume W.,
 RA Hayashida K., Hayatsu N., Hirakami K., Hiraoka T., Hirozane T.,
 RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
 RA Kato H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Takahashi F., Takaku-Akaiura S., Takeda Y., Tanaka M.,
 RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AK032488; BAC27895.1;
 DR MGD; MGI:102966; PtGdr.
 DR GO; GO:0016021; C: integral to membrane; TAS.
 DR GO; GO:0004956; F: prostaglandin D receptor activity; IDA.
 DR GO; GO:0001785; F: prostaglandin J receptor activity; IDA.
 DR InterPro; IPR000376; GPCR_Rhodpsn.
 DR InterPro; IPR000376; Pglndnd_receptor.
 DR InterPro; IPR008365; Prostanoidrecept.
 DR InterPro; IPR001105; Tbox_receptor.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR01788; PROSTANOIDR.
 DR PRINTS; PR00854; PRSTNOIDDR.
 DR PRINTS; PR00429; THROMBOXANER.
 DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
 KW Receptor.
 SQ SEQUENCE 357 AA; 39990 MW; A0FAPE3E5D77E952 CRC64;

Query Match 71.1%; Score 1095; DB 2; Length 357;
 Best Local Similarity 75.5%; Pred. No. 1.7e-77;
 Matches 209; Conservative 26; Mismatches 42; Indels 0; Gaps 0;

QY 6 YRCQNTTSVEKGNVAGVGVLFSTCLLCNLALGLIARSLGRCRRRLPLPSVYVYLV 65
 DB 5 YRCQTSTWVERGSSATMGAVLFGAGLLGNLALVLLARSLGRCRPGPLHPPSPVYVYLV 64
 QY 66 CGLTVTDLLGKCLSPVVLAAAYANRSLRVLPALDNLSCQAFAPFMFFGLSLSTLQLLA 125
 DB 65 CGLTVTDLLGNCLISPMVLAAYANQSLKELLPSGNQLCETFAFLMSFFGLASTLQLLA 124
 QY 126 MALECWLSLGHPPFYRRHITRLGALVAPVVSASFALCALPFMGFGKVFQVCPGTWCPI 185
 DB 125 MAVECWLSLGHPPFYRRHITRLGALVAPVVSAAFCLAFALCALPFMGFGKVFQVCPGTWCPI 184
 QY 186 QMWHEEGSLVGYSLVYSSLMALLVLTATVLCNIGAMRNLYAMHRLQHRPSCRTDCAE 245
 DB 185 QMIHKERSFVIGFVSVLSLALLVLTATVLCNIGAMRNLYAMHRLQHRPSCRTDCAE 244

QY 246 PRADGREASPOPLELDHLLALLMTVLTFTWCSLPVI 282
 DB 245 SGSDYRHGSLHPLLELDHFLVLLALMTVLTFTWCSLPVI 281

RESULT 6
 ID PE22 CANFA STANDARD; PRT; 361 AA.
 AC Q9XT82;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Prostaglandin E2 receptor, EP2 subtype (Prostanoid EP2 receptor) (PGE
 DE receptor, EP2 subtype).
 GN Name=PTGER2;
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99338573; PubMed=10410384; DOI=10.1016/S0090-6980(98)00081-1;
 RA Hibbs T.A., Lu B., Smock S.L., Vestergaard P., Pan L.C., Owen T.A.;
 RT "Molecular cloning and characterization of the canine prostaglandin E


```

DR PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS00262; G-PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Receptor; Transmembrane.
SQ SEQUENCE 308 AA; 34246 MW; F16274B0A6C1815C CRC64;

Query Match      38.5%; Score 593.5; DB 2; Length 308;
Best Local Similarity 44.7%; Pred. No. 2.1e-38;
Matches 132; Conservative 51; Mismatches . 93; Indels 19; Gaps 8;

QY 8 CONTTSVEKGNVAVGGVLFSTGLLGNLLALGLLARSGLG--WCSRRRLPLRPLPSVYMLV 65
DB 14 CKSRQWLLSGESPAISSVMFSAGVLGNLIALALLARRWRGDTGCSAGS-RTSISLFHLV 72
QY 66 CGLTVDLLGKLLSPVVLAAQVRSRLVAPALDNLSCQAFAPFMSFFGLSSTLQLLA 125
DB 73 TELVFTDLLGTCLISPVVLAASRNQTLVALAP--ESHACTYFAFTMTPTFSLATMLLFA 130
QY 126 MALECMWLSLGHFFRRHITLRLGALVAPVVSAPSLAFALCFMGFGVQVCPGTWCFI 185
DB 131 MALERYLSIGYFYFRRHLRSGGLAVLVITVYAGSLLPILNYGEYVQVCPGTWCFI 190
QY 186 QWVHEGSLVGLSVLYSSLMALLVLATVLCNLGAMRNLYAMHRRLQHRHPRSCTRDCAE 245
DB 191 R--HGR-----TAYQLQVATMELLIVAVLACNIVSLNLRHRSRR--SRCGLSGSS 241
QY 246 PRADG---REASQPLELDHLLALLMTVLFTMCSLP--VIAFVGVPAKTPGS 295
DB 242 LRPGSRRRGERTSMAEETHLLILLAIMTITPAICSLPFTVSHLCFHPSPASSPRS 296

RESULT 9
PE22 HUMAN STANDARD; PRT; 358 AA.
AC P43116;
ID 01-NOV-1995 (Rel. 32, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Prostaglandin E2 receptor, EP2 subtype (Prostanoid EP2 receptor) (PGE
DE receptor, EP2 subtype).
GN Name=PTGER2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=94359483; PubMed=8078484;
RA Regan J.W., Bailey T.J., Pepperi D.J., Pierce K.L., Bogardus A.M.,
RA Donello J.E., Fairbairn C.E., Kedzie K.M., Woodward D.F., Gil D.W.;
RT "Cloning of a novel human prostaglandin receptor with characteristics
RT of the pharmacologically defined EP2 subtype.";
RL Mol. Pharmacol. 46:213-220(1994).
RN [2]
RP SEQUENCE FROM N.A.
RA Oakley C.J.;
RN Submitted (JAN-1995) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=99453300; PubMed=10521663; DOI=10.1016/S0378-1119(99)00323-6;
RA Smock S.L., Pan L.C., Castleberry T.A., Lu B., Mather R.J., Owen T.A.;
RT "Cloning, structural characterization, and chromosomal localization of
RT the gene encoding the human prostaglandin E2 receptor EP2 subtype.";
RL Gene 237:393-402(1999).
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RA Warren C.N., Aronstam R.S., Sharma S.V.;
RT "cDNA clones of human proteins involved in signal transduction
RT sequenced by the Guthrie cDNA resource center (www.cdna.org).";
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Receptor for prostaglandin E2 (PGE2). The activity of
CC this receptor is mediated by G(s) proteins that stimulate

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adenylate cyclase. The subsequent raise in intracellular cAMP is
responsible for the relaxing effect of this receptor on smooth
muscle.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- TISSUE SPECIFICITY: Placenta and lung.
-!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.

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or send an email to license@isb-sib.ch).

EMBL; U19487; AAA61681.1; -.
EMBL; X83868; AAA58749.1; -.
EMBL; AF134202; AAD44177.1; -.
EMBL; AF134201; AAD44177.1; JOINED.
EMBL; AY275471; AAP32303.1; -.
PIR; I38920; I38920.
PIR; S51312; S51312.
Genew; HGNC:9594; PTGER2.
MIM; 176804; -.
GO; GO:0005887; C: integral to plasma membrane; TAS.
GO; GO:0004957; F: prostaglandin E receptor activity; TAS.
GO; GO:0007186; P: G-protein coupled receptor protein signalin. .; TAS.
InterPro; IPR001923; EP2 Receptor.
InterPro; IPR000276; GPCR_Rhodopsin.
InterPro; IPR008365; Prostanoidrecept.
InterPro; IPR001105; Tbox_receptor.
Pfam; PF00001; 7tm_1; 1.
PRINTS; PR00237; GPCR_RHODOPSIN.
PRINTS; PR01788; PROSTANOIDS.
PRINTS; PR00581; PRSTNOIDEP2R.
PRINTS; PR00429; THROMBOXANER.
PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; 1.
PROSITE; PS00262; G-PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; GPCP; Transmembrane.
DOMAIN 1 23
TRANSMEM 24 47
DOMAIN 48 65
CYTOPLASMIC (Potential).
TRANSMEM 66 91
DOMAIN 92 111
EXTRACELLULAR (Potential).
TRANSMEM 112 132
DOMAIN 133 151
CYTOPLASMIC (Potential).
TRANSMEM 152 176
DOMAIN 177 198
EXTRACELLULAR (Potential).
TRANSMEM 199 223
DOMAIN 224 262
CYTOPLASMIC (Potential).
TRANSMEM 263 286
DOMAIN 287 299
EXTRACELLULAR (Potential).
TRANSMEM 300 323
DOMAIN 324 358
CYTOPLASMIC (Potential).
FT DISULFID 109 187
FT CARBOHYD 3 3
FT CARBOHYD 6 6
FT CARBOHYD 96 96
FT CARBOHYD 287 287
FT CONFLICT 150 150
R -> A (in Ref. 1 and 3).
SQ SEQUENCE 358 AA; 39760 MW; B3B0E2AA3CF2E363 CRC64;

Query Match      38.0%; Score 585; DB 1; Length 358;
Best Local Similarity 45.2%; Pred. No. 1.1e-37;
Matches 128; Conservative 45; Mismatches 92; Indels 18; Gaps 7;

QY 8 CONTTSVEKGNVAVGGVLFSTGLLGNLLALGLLARSGLG--WCSRRRLPLRPLPSVYMLV 65
DB 13 CETRQWLLPGESPAISSVMFSAGVLGNLIALALLARRWRGDTGCSAGRSSI-SLFHLV 71
QY 66 CGLTVDLLGKLLSPVVLAAQVRSRLVAPALDNLSCQAFAPFMSFFGLSSTLQLLA 125
DB 72 TELVFTDLLGTCLISPVVLAASRNQTLVALAP--ESHACTYFAFTMTPTFSLATMLLFA 129

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QY 126 MALECWLSLGHFFYRRHITLRLGALVAPVWSAFSLAFALPFGMGFKFVQYCPGTWCFI 185
 DB 130 MALEWLSLGHFFYRRHITLRLGALVAPVWSAFSLAFALPFGMGFKFVQYCPGTWCFI 189
 QY 186 QMVHEGSLVGLSVYSSLMALLVATVLCNLGAMRNLYAMHRLQRPSCSTRDCAE 245
 DB 190 R--HGR-----TAYLQLYATALLLIVSVLACNFSVILNIRHRSRR--SRCGPSLGS 240
 QY 246 ----PRADGREASPOPLELDHLLALMTVLFVTCMSLPVIAF 284
 DB 241 CRGGPCARRRGERSVMAEETHLLIATMTITFAVCSLPFTIF 283

RESULT 10
 Q8HY57
 ID Q8HY57 PRELIMINARY; PRT; 361 AA.
 AC Q8HY57;
 DT 01-MAR-2003 (TREMBlrel. 23, Created)
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Prostaglandin E2 receptor EP2.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Guan Y., Stillman B.A., Zhang Y., Schneider A., Saito O., Davis L.S.,
 RA Breyer M.D.;
 RT "Cloning of rabbit prostaglandin E2 receptor EP2.";
 RL J. Am. Soc. Nephrol. 7:1646-1646 (1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX PubMed=12037143; DOI=10.1186/1471-2210-2-14;
 RA Guan Y., Stillman B.A., Zhang Y., Schneider A., Saito O., Davis L.S.,
 RA Redha R., Breyer R.M., Breyer M.D.;
 RT "Cloning and expression of the rabbit prostaglandin EP2 receptor.";
 RL BMC Pharmacol. 2:14-14 (2002).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
 CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 DR EMBL; AY166779; AA013013.1; -
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0004957; P:prostaglandin E2 receptor activity; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
 DR GO; GO:0004960; F:thromboxane receptor activity; IEA.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
 DR InterPro; IPR001923; EP2 receptor.
 DR InterPro; IPR000276; GPCR Rhodopsin.
 DR InterPro; IPR008365; Prostanoidrecept.
 DR InterPro; IPR001105; Thbox_receptor.
 DR Pfam; PF00001; 7tm1; 1.
 DR PRINTS; PR00237; GPCRHHODOPSN.
 DR PRINTS; PR01788; PROSTANOIDR.
 DR PRINTS; PR00581; PRSTNOIDEP2R.
 DR PRINTS; PR00429; THROMBOXANER.
 DR PROSITE; PS00237; G-PROTEIN RECEPTOR FL1; 1.
 DR PROSITE; PS0262; G-PROTEIN RECEPTOR FL2; 1.
 KW G-protein coupled receptor; Receptor; Transmembrane.
 SQ SEQUENCE 361 AA; 39945 MW; E735BC61F60B1D9D CRC64;

Query Match 36.9%; Score 569; DB 2; Length 361;
 Best Local Similarity 43.9%; Pred. No. 28-36;
 Matches 126; Conservative 41; Mismatches 94; Indels 26; Gaps 7;
 8 CQNTSVKGNAGVGGVLFSTGLGNLALGLLARSGLGWSRRPLRPLP-SVFVFLVC 66
 13 CTRQWLPSEGSFATSAVNFSGVGLNLIALLARRWRADGRAGRTSLSLFVLVT 72
 67 GLTVTDLLGKLLSPVLAAYANQSLRVLAPALDNSLCOAFPMSPFLGSLTQLLAM 126
 73 ELVFTDLGCTFISPVLAAYARNOTLVALEP--DGRACVAFAMTFFSLATMLMFAM 130

QY 127 ALECWLSLGHFFYRRHITLRLGALVAPVWSAFSLAFALPFGMGFKFVQYCPGTWCFI 186
 DB 131 ALERYLSLGHFFYRRHITLRLGALVAPVWSAFSLAFALPFGMGFKFVQYCPGTWCFI 190
 QY 187 MVHEGSLVGLSVYSSLMALLVATVLCNLGAMRNLYAMHRLQRPSCSTRDCAE 246
 DB 191 --HGR-----TAYLQLYATALLLIVSVLACNLSVICNLVHMYRRARR-----SRCGPS 237
 QY 247 RADGREASPOPLELDHLLALMTVLFVTCMSLPVIAF 284
 DB 238 SGSGR--GGPTRRRGERSVMAEETHLLIATMTITFAVCSLPFTIF 283

RESULT 11
 Q6NZ15
 ID Q6NZ15 PRELIMINARY; PRT; 371 AA.
 AC Q6NZ15;
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE MGC69060 protein.
 GN Name=MGC69060;
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Spleen;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Tothiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Butterfield Y.S.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Schrein J.E.,
 RA Krzywinski M.I., Skalska U., Smalish U., Schnerch A., Schrein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Spleen;
 RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
 RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
 RA Richardson P.;
 RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
 RT initiative.";
 RL Dev. Dyn. 225:384-391 (2002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Spleen;
 RA Klein S., Strausberg R.;
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC066120; AAH66120.1; -
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0004957; F:prostaglandin E2 receptor activity; IEA.
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
 DR GO; GO:0004960; F:thromboxane receptor activity; IEA.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
 DR InterPro; IPR001923; EP2_receptor.


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DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE EP2 receptor.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22694625; PubMed=12810564; DOI=10.1210/en.2002-0088;
RA Arsh J.A., Banu S.K., Chapdelaine P., Emond V., Kim J.J.,
RA MacLaren L.A., Fortier M.A.;
RT "Molecular Cloning and Characterization of Bovine Prostaglandin E(2)
RT Receptors EP2 and EP4: Expression and Regulation in Endometrium and
RT Myometrium during the Estrous Cycle and Early Pregnancy.";
RL Endocrinology 144:3076-3091(2003).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
DR EMBL: AF539402; AAN01234.1; -.
DR GO: GO:0016021; C:integral to membrane; IEA.
DR GO: GO:0004957; F:prostaglandin E receptor activity; IEA.
DR GO: GO:0004872; F:receptor activity; IEA.
DR GO: GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO: GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro: IPR001923; EP2 receptor.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR InterPro: IPR008365; Prostanoidrecept.
DR Pfam: PF00001; 7tm 1; 1.
DR PRINTS: PR00237; GPCRHOPOPSN.
DR PRINTS: PR01788; PROSTANOIDR.
DR PRINTS: PR00581; PRSTNOIDEP2R.
DR PROSITE: PS02237; G-PROTEIN_RECEP_F1_1; 1.
DR PROSITE: PS0262; G-PROTEIN_RECEP_F1_2; 1.
DR G-protein coupled receptor; Receptor; Transmembrane.
KW G-PROTEIN COUPLED RECEPTOR; RECEPTOR; TRANSMEMBRANE.
SQ SEQUENCE 352 AA; 39726 MW; 9BB8FBF445B37287 CRC64;

Query Match 36.1%; Score 556; DB 2; Length 352;
Best Local Similarity 45.0%; Pred. No. 2e-35;
Matches 121; Conservative 46; Mismatches 88; Indels 14; Gaps 5;

Qy 17 GNSAVMGVLFSTGLGNLLALGLARSLGWCRRRLPLP-SVFYMLVGLTDTLLG 75
Dy 17 GNSAVMGVLFSTGLGNLLALGLARSLGWCRRRLPLP-SVFYMLVGLTDTLLG 75
Qy 22 GSPAISSVMFTAGVLENLIALLVRRWRGDSRSEGRGNSLSLHVLTVELTDLG 81
Dy 22 GSPAISSVMFTAGVLENLIALLVRRWRGDSRSEGRGNSLSLHVLTVELTDLG 81
Qy 76 KLLSPVVLAAAYQNRSLRVAPALDNLSCQAFAPFFSFGSLSTLQLLAMALECWL 135
Dy 76 KLLSPVVLAAAYQNRSLRVAPALDNLSCQAFAPFFSFGSLSTLQLLAMALECWL 135
Dy 82 TCLISPVVLASYAQRNLVALGP--ERRVCTYFAFSMTFFSLATMLMLFAMALERYLAIG 139
Qy 136 HPFYRRHITLRLGALVAPVVSFAFLAFALPFGKFGVQYCGTWCFTQMVHEEGLS 195
Dy 140 HPFYRRHITLRLGALVAPVVSFAFLAFALPFGKFGVQYCGTWCFTQMVHEEGLS 195
Qy 196 VLGSYLVLYSSLMALLVATLVCNLGNLWNLVYHRRILQHRPSRTRCDEPRADGRASP 255
Dy 196 VLGSYLVLYSSLMALLVATLVCNLGNLWNLVYHRRILQHRPSRTRCDEPRADGRASP 255
Dy 196 ---YLRVATYLLILLIATVACNFSVIVNLVHRRGRRCGFSLSGSHRRRAERVSMA- 251
Qy 256 QPLEDHLHLLALLMTVLFTWCSLPVTAF 284
Dy 252 ---BETDHLILLATMTITFAVCSLPFTIF 277

RESULT 14
ID P12R BOVIN STANDARD; PRT; 385 AA.
AC P79393;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 25-JAN-2005 (Rel. 46, Last annotation update)
DE Prostacyclin receptor (prostanoid IP receptor) (PGI receptor)
DE (Prostaglandin 12 receptor).
GN Name=PTGIR;
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185	Qy	IOM-VHEGSLSVLCYSVLVYGSLLMALLVTLVLCNLGAMRNLIYAMHRLQRLHPRSTRDC	243
172	Db	IRMSAPGGCAFL---LAYASLVALLVAAIIVLCNGSVTLSLCRMVYQQRHQACPR--	226
244	Qy	ABPRADGREALPQPLEELDHLILLALLMTVLTFTMCSLPVIAFPVG	287
227	Db	--PRAGE-----DEVDHLIILALMTGIMAVCSLPITPQIRG	260

RESULT 15

P12R_MOUSE	ID	P12R_MOUSE	STANDARD;	PRT;	415 AA.
AC	P43252;				
DT	01-NOV-1995	(Rel. 32, Created)			
DT	01-NOV-1995	(Rel. 32, Last sequence update)			
DT	25-JAN-2005	(Rel. 46, Last annotation update)			
DE	Prostacyclin receptor (Prostanoid IP receptor) (PGI receptor) (Prostaglandin I2 receptor).				
DE	Names=Ptgir;				
GN	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
OC	NCBI_TaxID=10090;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RA	MEDLINE=94193694; PubMed=7511597;				
RA	Namba T., Oida H., Sugimoto Y., Negishi M., Kakizuka A., Ichikawa A.,				
RA	Narumiya S.;				
RT	"CDNA cloning of a mouse prostacyclin receptor. Multiple signaling				
RT	pathways and expression in thymic medulla.";				
RL	J Biol. Chem. 269:9986-9992(1994).				
CC	-I- FUNCTION: Receptor for prostacyclin (prostaglandin I2 or PGI2).				
CC	The activity of this receptor is mediated by G(s) proteins which				
CC	activate adenylate cyclase.				
CC	-I- SUBCELLULAR LOCATION: Integral membrane protein.				
CC	-I- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.				
CC	-----				
CC	This SWISS-PROT entry is copyright. It is produced through a collabor				
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CC	the European Bioinformatics Institute. There are no restrictions on				
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CC	entities requires a license agreement (See http://www.isb-sib.ch/anno				
CC	or send an email to license@isb-sib.ch).				
CC	-----				
EMBL	D26157; BAA05144.1; ALT_INIT.				
DR	MGD; MG1:99535; Ptgir.				
DR	InterPro; IPR000276; GPCR_Rhodpsn.				
DR	InterPro; IPR000370; IP_receptor.				
DR	InterPro; IPR008365; Prostanoidrecept.				
DR	InterPro; IPR001105; Tbxox_receptor.				
DR	Pfam; PF00001; 7tm1; 1.				
DR	PRINTS; PR00237; GPCR_RHODOPS.				
DR	PRINTS; PR01788; PROSTANOIDR.				
DR	PRINTS; PR00429; THROMBOXANER.				
DR	PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.				
DR	PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.				
KW	G-protein coupled receptor; Glycoprotein; Lipoprotein; Palmitate;				
KW	Transmembrane.				
KW	DOMAIN 1 44 Extracellular (Potential).				
FT	TRANSMEM 45 66 1 (Potential).				
FT	DOMAIN 67 79 Cytoplasmic (Potential).				
FT	TRANSMEM 80 104 2 (Potential).				
FT	DOMAIN 105 122 Extracellular (Potential).				
FT	TRANSMEM 123 143 3 (Potential).				
FT	DOMAIN 144 162 Cytoplasmic (Potential).				
FT	TRANSMEM 163 186 4 (Potential).				
FT	DOMAIN 187 215 Extracellular (Potential).				
FT	TRANSMEM 216 236 5 (Potential).				
FT	DOMAIN 237 263 Cytoplasmic (Potential).				
FT	TRANSMEM 264 288 6 (Potential).				
FT	DOMAIN 289 301 Extracellular (Potential).				

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OM nucleic - nucleic search, using sw model

Run on: April 22, 2005, 10:47:36 ; Search time 4915.42 Seconds

(without alignments)
10646.432 Million cell updates/sec

Title: US-10-689-861-3

Sequence: 1 atgaagtcgcgcgtctaccg.....acatggatccagctcgtga 1080

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

GenBank: 1: gb_ba: 2: gb_hgt: 3: gb_in: 4: gb_om: 5: gb_ov: 6: gb_pat: 7: gb_ph: 8: gb_pl: 9: gb_pr: 10: gb_ro: 11: gb_scs: 12: gb_sy: 13: gb_un: 14: gb_vl:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1080	100.0	1488	6 AR075987	AR075987 Sequence
2	1080	100.0	1488	6 AR371655	AR371655 Sequence
3	1080	100.0	2970	9 BC040968	BC040968 Homo sapi
4	846	78.3	1216	6 AR270911	AR270911 Sequence
5	846	78.3	1216	9 HSU31332	U31332 Human DP pr
6	846	78.3	156808	2 AC012407	AC012407 Homo sapi
7	846	78.3	187947	2 CNS05TR6	AL365475 Human chr
8	846	78.3	197817	9 CNS05TCS	AL358833 Human chr
9	657	60.8	1315	10 RNU92289	U92289 Rattus norv
10	655.4	60.7	1074	10 AF120101	AF120101 Rattus no
11	655.4	60.7	1240	6 E10040	E10040 Base sequen
12	653.8	60.5	1071	6 E10039	E10039 Mus musculu
13	543.8	50.4	895	10 D29764S1	D29764 Mus musculu
14	540.6	50.1	67632	2 AC095991_3	AC095991_3 Continuati
15	540.6	50.1	110000	2 AC112324_0	AC112324_0 Continuati
16	540.6	50.1	110000	2 AC112324_1	AC112324_1 Continuati
17	540.6	50.1	110000	2 AC115635_2	AC115635_2 Continuati
18	540.6	50.1	299134	2 AC128783	AC128783 Rattus no
19	540.6	50.1	349877	2 AC115218	AC115218 Rattus no

C	20	537.4	49.8	57027	2 AC112324_3	Continuation (4 of
C	21	537.4	49.8	110000	2 AC095991_0	AC095991 Rattus no
C	22	537.4	49.8	110000	2 AC099237_3	Continuation (4 of
C	23	537.4	49.8	110000	2 AC099237_4	Continuation (5 of
C	24	537.4	49.8	110000	2 AC115635_1	Continuation (2 of
C	25	537.4	49.8	254094	2 AC120220	AC120220 Rattus no
C	26	537.4	49.8	349877	2 AC115218	AC115218 Rattus no
C	27	436	40.4	495	6 AC1549001	AC1549001 Sequence
C	28	436	40.4	495	9 HSU31099	U31099 Human DP pr
C	29	359	33.2	205345	2 AC128247	AC128247 Rattus no
C	30	359	33.2	232703	2 AC098748	AC098748 Rattus no
C	31	234.4	21.7	2935	4 AY166779	AY166779 Oryctolag
C	32	220.6	20.4	1077	9 AY275471	AY275471 Homo sapi
C	33	220.6	20.4	1077	9 HSRP2PR	X83688 H.sapiens m
C	34	220.6	20.4	2296	6 AR372105	AR372105 Sequence
C	35	220.6	20.4	2296	6 CQ720365	CQ720365 Sequence
C	36	220.6	20.4	2373	6 AF075602	AF075602 Canis fam
C	37	220.6	20.4	2550	4 CQ867605	CQ867605 Sequence
C	38	219	20.3	2372	6 AR270878	AR270878 Sequence
C	39	219	20.3	2372	6 AX549005	AX549005 Sequence
C	40	219	20.3	2372	6 HSU19487	U19487 Human prost
C	41	219	20.3	2372	9 AR208580	AR208580 Sequence
C	42	219	20.3	6446	6 BT293039	B293039 B. taurus pr
C	43	217.8	20.2	1428	4 AX280935	AX280935 Sequence
C	44	214.2	19.8	1077	6 AR035825	AR035825 Sequence
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ALIGNMENTS

RESULT 1	AR075987	1488 bp	DNA	linear	PAT 30-AUG-2000
LOCUS	AR075987				
DEFINITION	Sequence 4 from patent US 5958723.				
ACCESSION	AR075987				
VERSION	AR075987.1	GI:10002733			
KEYWORDS	Unknown.				
SOURCE	Unknown.				
ORGANISM	Unclassified.				
REFERENCE	1 (bases 1 to 1488)				
AUTHORS	Abrahamovitz, M., Boie, Y., Metters, K., Sawyer, N. and Slipetz, D.M.				
TITLE	DNA encoding prostaglandin receptor DP				
JOURNAL	Patent: US 5958723-A 4 28-SEP-1999;				
FEATURES	Location/Qualifiers				
source	1..1488				
ORIGIN	/organism="unknown"				
	/mol_type="unassigned DNA"				
Query Match	100.0%;	Score 1080;	DB 6;	Length 1488;	
Best Local Similarity	100.0%;	Pred. No. 6.3e-196;			
Matches 1080;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
QY	1	ATGAAGTGGCGCTTACCGCTGCGGACGACACCACTGTGGAAAGCAACTGGCG	60		
DB	350	ATGAAGTGGCGCTTACCGCTGCGGACGACACCACTGTGGAAAGCAACTGGCG	409		
QY	61	GTGATGGCGGAGTGTCTTACGACACCGGCTCTGGGCAACTGCTGGCGGCTTG	120		
DB	410	GTGATGGCGGAGTGTCTTACGACACCGGCTCTGGGCAACTGCTGGCGGCTTG	469		
QY	121	CTGGCGCGCTGCGGCTGCGGAGTGTCTGCGGCTGCACTGCGCGGCTGCTGGCTC	180		
DB	470	CTGGCGCGCTGCGGCTGCGGAGTGTCTGCGGCTGCACTGCGCGGCTGCTGGCTC	529		
QY	181	TTCTACATGCTGATGTGTGCGGACGACGACGACGACGACGACGACGACGACGACG	240		
DB	530	TTCTACATGCTGATGTGTGCGGACGACGACGACGACGACGACGACGACGACGACG	589		
QY	241	CCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	300		

Db 590 CCGGTGTCGTGGCTGCTACGCTCAGAACCGGAGTCTGGGGTGGCTTGGCCCGCATTTG 649
QY 301 GACAACTCGTGTGGCCAAAGCCTTGGCCTTCTTCATGCTCTTTGGAGCTCTCTGACGA 360
Db 650 GACAACTCGTGTGGCCAAAGCCTTGGCCTTCTTCATGCTCTTTGGAGCTCTCTGACGA 709
QY 361 CTGCAACTCTGGCCATGAGCATGAGATGCTGGCTCTCCCTAGAGGCACTTTTCTTCTAC 420
Db 710 CTGCAACTCTGGCCATGAGCATGAGATGCTGGCTCTCCCTAGAGGCACTTTTCTTCTAC 769
QY 421 CGACGGCAATACACCTGGCCCTGGAGCGACATGATGGCCCGGATGGATGGAGCCCTCTCC 480
Db 770 CGACGGCAATACACCTGGCCCTGGAGCGACATGATGGCCCGGATGGATGGAGCCCTCTCC 829
QY 481 CTGGCTTTCTGCGCGCTACCTTTATGAGCTTGGGAAATTCGTGCAATGACTCCCGCG 540
Db 830 CTGGCTTTCTGCGCGCTACCTTTATGAGCTTGGGAAATTCGTGCAATGACTCCCGCG 889
QY 541 ACCTGTGCTTTATTCAGATGTCACAGAGAGGCTCGCTGTGCGGTGGGATCTT 600
Db 890 ACCTGTGCTTTATTCAGATGTCACAGAGAGGCTCGCTGTGCGGTGGGATCTT 949
QY 601 GTGCTTACTTCCAGCCTCATGAGGCTGTGCTGTCTGCGCACTGTGCTGTGCAACTCTGCG 660
Db 950 GTGCTTACTTCCAGCCTCATGAGGCTGTGCTGTCTGCGCACTGTGCTGTGCAACTCTGCG 1009
QY 661 GCCATCGCAACTCTCATGAGATGACACCGGCGCTGCAAGCGGCACTCGCTCTGCAAC 720
Db 1010 GCCATCGCAACTCTCATGAGATGACACCGGCGCTGCAAGCGGCACTCGCTCTGCAAC 1069
QY 721 AAGGACTGTGCGCGAGCGCGCGCGGAGCGGAGGAAAGCGTCCCTCAGCCCTGAGAGAG 780
Db 1070 AAGGACTGTGCGCGAGCGCGCGCGGAGCGGAGGAAAGCGTCCCTCAGCCCTGAGAGAG 1129
QY 781 CTGGAATCACTCTCTGCTGTGCTGGGCTGATACCTGTCTCTTCACTATGTTTCTTGCC 840
Db 1130 CTGGAATCACTCTCTGCTGTGCTGGGCTGATACCTGTCTCTTCACTATGTTTCTTGCC 1189
QY 841 GTAATTTATCGCCTTACTATGAGATTTAAGATGTCAAGAGAAAAACAGACCTCT 900
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Db 1370 AGACCTCTTATGATGACAGAGCCGATGACAGATTTCACTAATGAGATTCAGTCTGTGA 1429

RESULT 2
AR371655 1488 bp DNA linear PAT 12-SEP-2003
LOCUS AR371655 Sequence 4 from patent US 6395499.
DEFINITION AR371655
ACCESSION AR371655 GI:34608648
VERSION AR371655.1
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE
1 (bases 1 to 1488)
Abriemovitz, M., Metters, K., Boie, Y., Sawyer, N. and Slipetz, D.M.
Methods of identifying modulators of a DP prostaglandin receptor
Patent: US 6395499-A 4 28-MAY-2002;
Location/Qualifiers
1..1488
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 100.0%; Score 1080; Dn 6; Length 1488;
Best Local Similarity 100.0%; Pred. No. 6.3e-196;
Matches 1080; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGAACTGCGCCGTTCTTACCGCTGCGAGAACACCACTCTGTGAGAAAAAGCAACTCGGCG 60
Db 350 ATGAACTGCGCCGTTCTTACCGCTGCGAGAACACCACTCTGTGAGAAAAAGCAACTCGGCG 409
QY 61 GTGATGAGGAGGAGTGTCTTTCAGACACCGGCTCTCTGGGAAACCTGTGGCCCGGAGCTG 120
Db 410 GTGATGAGGAGGAGTGTCTTTCAGACACCGGCTCTCTGGGAAACCTGTGGCCCGGAGCTG 469
QY 121 CTGACGCGCTCGGAGGCTGAGGATGTGCTGCGAGCGCTCACTGCGCCGCTGCGCTGCTG 180
Db 470 CTGACGCGCTCGGAGGCTGAGGATGTGCTGCGAGCGCTCACTGCGCCGCTGCGCTGCTG 529
QY 181 TTCTATATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 240
Db 530 TTCTATATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 589
QY 241 CCGGTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
Db 590 CCGGTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 649
QY 301 GACAACTCGTGTGCAAGCCTTTCGCTTCTTATGCTGCTTGTGGGCTCTCTGACGA 360
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QY 361 CTGCAACTCTGTGCGCACTGAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 420
Db 710 CTGCAACTCTGTGCGCACTGAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 769
QY 421 CGACGGCAATACACCTGGCCCTGGAGCGACATGATGGCCCGGATGGATGGAGCCCTCTCC 480
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QY 481 CTGGCTTTCTGCGCGCTACCTTTATGAGCTTGGGAAATTCGTGCAATGACTCCCGCG 540
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QY 541 ACCTGTGCTTTATTCAGATGTCACAGAGAGGCTCGCTGTGCGGTGGGATCTT 600
Db 890 ACCTGTGCTTTATTCAGATGTCACAGAGAGGCTCGCTGTGCGGTGGGATCTT 949
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QY 781 CTGGAATCACTCTCTGCTGTGCTGGGCTGATACCTGTCTCTTCACTATGTTTCTTGCC 840
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Db 1310 TGGATTTTATCATTTTTCAGATCTCCAGATTTTCGATTTTTCAGAAATTTTCAAT 1369

QY 1021 AGACCTTACGATACAGAGCCGATGACGATTCACATTCAGATGAGATCAGTCTGTGA 1080
DB 1370 AGACCTTACGATACAGAGCCGATGACGATTCACATTCAGATGAGATCAGTCTGTGA 1429

RESULT 3
LOCUS BC040968
DEFINITION Homo sapiens prostaglandin D2 receptor (DP), mRNA (cDNA clone
MGC:49004 IMAGE:5769056), complete cds.
BC040968
VERSION BC040968.1 GI:26454885
KEYWORDS MGC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
1 (bases 1 to 2970)
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
Altauer, R.D., Collins, F.S., Wagner, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, V., Hsieh, F.,
Diachenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carinci, P., Prange, C., Raha, S.S., Loguercio, N.A., Peters, G.J.,
Abramson, R.D., Mullany, S.J., Bosak, S.A., McEwan, P.D.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hui, S.W.,
Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahy, J., Helton, E., Ketterman, M., Madan, A., Rodriguez, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakeley, R.W., Touchman, D.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmitt, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalins, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J., and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

JOURNAL
PUBMED 12477932
REFERENCE 2 (bases 1 to 2970)
AUTHORS Strausberg, R.
TITLE Direct Submission
JOURNAL Submitted (06-DEC-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA

REMARK
COMMENT NIH-MGC Project URL: <http://mgc.ncl.nih.gov>
Contact: MGC help desk
Email: cgabs-rt@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Institute for Systems Biology
<http://www.systemsbio.org>
contact: amadansystemsbio.org
Anup Madan, Jessica Fahey, Erin Helton, Mark Ketterman, Anuradha
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting

FEATURES
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Location/Qualifiers
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ORIGIN
Query Match 100.0%; Score 1080; DB 9; Length 2970;
Best Local Similarity 100.0%; Pred. No. 6; Le-196;
Matches 1080; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 ATGAAGTCGCGCTTCTACCGCTCCAGAACACCACTCTGTGGAAAAAGCACTGGCG 60
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QY 61 GTGATGGGGGGGGTCTCTTACGACACCGGCTCTGGGCAACTGCTGGCCCTGGGGCTG 120
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QY 121 CTGGGGCGGCTGGGGGGTGGGGGTGGTGTGCGGGCGTCACTGGGGCGGCTGGCTG 180
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DB 283 TTCTACATGCTGTGTGTGTGGCTGACCGGTACCGACTTGTGGGCAAGTCTCTTAAG 342
QY 241 CCGGTGTGCTGTGGCTGTACGCTCAGAACCGGAGTCTGGGTCTTGGCCCGCATTG 300
DB 343 CCGGTGTGCTGTGGCTGTACGCTCAGAACCGGAGTCTGGGTCTTGGCCCGCATTG 402
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DB 403 GACAAGCTGTGTGGCAAGCTTGGCTTCTTCAATGCTCTTGGGGCTCTCTGACA 462
QY 361 CTGCAACTCTGTGGCAATGCACTGAGTGTGCTCTTCTTGAAGGCACTTCTTCTAC 420
DB 463 CTGCAACTCTGTGGCAATGCACTGAGTGTGCTCTTCTTGAAGGCACTTCTTCTAC 522
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DB 643 ACCTGTGCTTATCAGATGTGCAAGAGAGGCTGCTGTGCTGTGAGGTA 702
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DB 703 GTGCTTACTCAGGCTTATGAGCGGCTGTGTCTTGTGCAAGGCTGTGCAAGCTGCGC 762

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RESULT 4
AR270911 1216 bp DNA linear PAT 10-APR-2003
LOCUS AR270911
DEFINITION Sequence 1474 from patent US 6500938.
ACCESSION AR270911
VERSION AR270911.1 GI:29702145
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1216)
AUTHORS Au-Young, J. and Seilhamer, J. J.
TITLE Composition for the detection of signaling pathway gene expression
JOURNAL Patent: US 6500938-A 1474 31-DEC-2002;
FEATURES
Location/Qualifiers
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source

ORIGIN

Query Match 78.3%; Score 846; DB 6; Length 1216;
Best Local Similarity 100.0%; Pred. No. 2.8e-151;
Matches 846; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1190 GTAATT 1195
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RESULT 5
HSU31332 1216 bp DNA linear PRI 11-AUG-1995
LOCUS HSU31332
DEFINITION Human DP prostanoid receptor (PTGDR) gene, 5' region and partial
cds..
ACCESSION U31332
VERSION U31332.1 GI:940378
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1216)
AUTHORS Boile, Y., Sawyer, N., Slipetz, D. M., Metters, K. M. and Abramovitz, M.
TITLE Molecular cloning and characterization of the human prostanoid DP
receptor
JOURNAL J. Biol. Chem. 270 (32), 18910-18916 (1995)
MEDLINE 95370201
PUBMED 7642548
REFERENCE 2 (bases 1 to 1216)
AUTHORS Abramovitz, M. and Boile, Y.
TITLE Direct Submission
JOURNAL Submitted (10-JUL-1995) Mark Abramovitz, Biochemistry and Molecular
Biology, Merck Frosst Center for Therapeutic Research, P.O. Box
1005, Pointe Claire-Dorval, Quebec H9R 4P8, Canada
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intron

78.3%; Score 846; DB 9; Length 1216;
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RESULT 6
AC012407/c
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VERSION
AC012407.4 GI:8569158
KEYWORDS
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SOURCE
Homo sapiens (human)
ORGANISM
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 156808)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens chromosome 14, clone RP11-221N7
Unpublished
2 (bases 1 to 156808)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.,
Baldwin,J., Barna,N., Beckerly,R., Boguslavsky,L., Boukhgalter,B.,
Brown,A., Casale,A., Colangelo,M., Collins,S., Collymore,A.,
Cooke,P., Dearellano,K., Dewar,K., Domingo,M., Donelan,L., Doyle,M.,
Ferreira,P., Fitzhugh,W., Forrest,C., Funke,R., Gage,D.,
Galagan,J., Gardyna,S., Grant,G., Hagos,B., Heatford,A., Horton,L.,
Howland,J.C., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J.,
Lehoczy,J., Lieu,C., Locke,K., MacDonald,P., Marquis,N.,
McEwan,P., McGuire,A., McKernan,K., McLaughlin,J., Meldrum,J.,
Morrow,J., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,
Peterson,K., Pollara,V., Riley,R., Roy,A., Santos,R., Severy,P.,
Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
Testaye,S., Tittel,A., Vassiliev,H., Vo,A., Wheeler,J., Wu,X.,
Wyman,D., Ye,W.J., Zimmer,A. and Zody,M.
Direct Submission
Submitted (27-OCT-1999) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 156808)
REFERENCE
AUTHORS
Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
Anderson,S., Baldwin,J., Barna,N., Baeten,V., Beda,F.,
Boguslavsky,L., Boukhgalter,B., Brown,A., Burkett,G.,
Campopiano,A., Casale,A., Choepel,Y., Colangelo,M., Collins,S.,
Collymore,A., Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S.,
Dodge,S., Domingo,M., Doyle,M., Ferreira,P., Fitzhugh,W., Gage,D.,
Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L.,
Grand-Pierre,N., Grant,G., Hagos,B., Heatford,A., Horton,L.,
Howland,J.C., Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A.,
Klein,J., Larocque,K., Lamazares,R., Landers,T., Lehoczy,J.,
Levine,R., Lieu,C., Liu,C., Liu,G., Locke,K., MacDonald,P., Marquis,N.,
McCarthy,M., McEwan,P., McGuire,A., McKernan,K., McSheeters,R.,
Meldrum,J., Menueu,L., Mihova,T., Miranda,C., Mienga,V., Morrow,J.,
Murphy,T., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,
O'Neill,D., Olivier,T., Oliver,J., Peterson,K., Platerre,N.,
Pisani,C., Pollara,V., Raymond,C., Riley,R., Rogov,P., Rothman,D.,
Roy,A., Santos,R., Schauer,S., Severy,P., Spencer,B.,
Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
Testaye,S., Theodore,J., Tittel,A., Travers,M., Triggillo,J.,
Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J.,
Young,G., Zainoun,J., Zimmer,A. and Zody,M.
Direct Submission
Submitted (24-AUG-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Jun 16, 2000 this sequence version replaced gi:8096911.
All repeats were identified using RepeatMasker:
Smit,A.F.A. & Green,P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html

Genome Center

TITLE
JOURNAL
COMMENT

Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: <http://www-seq.wi.mit.edu>
Contact: sequence.submissions@genome.wi.mit.edu
----- Project Information -----
Center project name: L2358
Center clone name: 221_N_7
----- Summary Statistics -----
Sequencing vector: M13; M7815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 142459 bases at least Q40
Consensus quality: 149548 bases at least Q30
Consensus quality: 152199 bases at least Q20
Insert size: 168000; agarose-fp
Insert size: 154308; sum-of-contigs
Quality coverage: 3.4 in Q20 bases; agarose-fp
Quality coverage: 3.7 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 26 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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* 5008 5107: gap of 100 bp
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* 7123 7222: gap of 100 bp
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* 11283 11382: gap of 100 bp
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FEATURES
source
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 LOCUS 187947
 DEFINITION Human chromosome 14 DNA sequence BAC R-452D12 of library RPI-11
 from chromosome 14 of Homo sapiens (Human), complete sequence.
 ACCESSION AL365475.1 GI:9187973
 VERSION AL365475.1
 KEYWORDS HTG.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 187947)
 Heilig, R., Petit, J.L., Vico, V., Dasilva, C., Robert, C., Mincker, P., Broetier, P., Catolico, L., Barde, V., Pelletier, E., Artiguenave, F.,

TITLE
 JOURNAL
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT
 Levy, M., Eckenberg, R., Bruls, T., deBerardinis, V., Cruaud, C., Gyapay, G., Saurin, W. and Weissbach, J. Sequencing of the human chromosome 14 Unpublished 2 (bases 1 to 187947)
 Genoscope.
 Direct Submission
 Submitted (04-MAY-2001) Genoscope - Centre National de Sequencage : BP 191 91006 Evry cedex - FRANCE (E-mail : segref@genoscope.cns.fr
 Web : www.genoscope.cns.fr)
 Genoscope Center
 Center: Genoscope / Centre National de Sequencage
 Center code: GS
 Web site: http://www.genoscope.cns.fr/
 Contact: Segref@genoscope.cns.fr

The following BAC sequence is oriented from the T7 to the SP6 end.
 Upstream BAC (overlapping the T7 end) : R-262M8 (AC=AL355833)
 Downstream BAC (overlapping the SP6 end) : R-1033H12
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 Assembly program: Phrap; version 2.0
 Quality coverage: 5.57x in Q20 bases; sum-of-contigs

 Overall quality chart :
 Range : bases
 0 :
 1 - 9 :
 10 - 19 : 3
 20 - 29 : 18
 30 - 39 : 234
 40 - 49 : 2840
 50 - 59 : 6632
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 70 - 79 : 35818
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Percentage of bases with a quality value >= 40 : 99 %.

FEATURES

source

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ORIGIN

Query Match 78.3%; Score 846; DB 9; Length 187947;
 Best Local Similarity 100.0%; Pred. No. 2.2e-151;
 Matches 846; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy	781	CTGGATCACCTCTCTGCTGGCGCTGATGACCGTGTCTTCACTATGTGTCTCTGCC	840
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RESULT 8

CNS05TCS/c

LOCUS CNS05TCS 197817 bp DNA linear PRI 02-MAY--2001

DEFINITION Human chromosome 14 DNA sequence BAC R-262M8 of library RPc1-11 from chromosome 14 of Homo sapiens (Human), complete sequence.

ACCESSION ALJ55833

VERSION ALJ55833.4 GI:13990340

KEYWORDS HTG.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 197817)

Hellig,R., Petit,J.L., Vico,V., Dasilva,C., Robert,C., Wincker,P., Broccoli,P., Catalicco,L., Barde,V., Pelletier,E., Attigneneve,F., Levy,M., Eckenberg,R., Bruls,T., deBerrardinis,V., Crnaud,C., Gypay,G., Saurin,W. and Weissendach,J.

AUTHORS

JOURNAL TITLE
Sequencing of the human chromosome 14
REFERENCE
Unpublished
2 (bases 1 to 197817)
AUTHORS
Genoscope,
Direct Submission
TITLE
Submitted (02-MAY-2001) Genoscope - Centre National de Sequençage :
JOURNAL
BP 101 91006 Evry cedex FRANCE (E-mail : serveur.genoscope.cns.fr)

COMMENT

Sequencing of the human chromosome 14
Unpublished
2 (bases 1 to 197817)
Genoscope.
Direct Submision
Submitted (02-MAY-2001) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr)
- Web : www.genoscope.cns.fr -
On May 7, 2001 this sequence version replaced gi:13897294.
----- Genome Center -----
Center: Genoscope / Centre National de Sequencage
Center code: GS
Web site: <http://www.genoscope.cns.fr/>
Contact: segref@genoscope.cns.fr

```

The following BAC sequence is oriented from the T7 to the SP6 end
Upstream BAC (overlapping the T7 end) : R-452D12
Downstream BAC (overlapping the SP6 end) : R-933I1 (AC=AL157971)
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Summary Statistics
Assembly program: Phrap, version 2.0
Quality coverage: 8.90x in Q20 bases, sum-of-contigs

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Overall quality chart :

0	Range	:	:	Bases	:	:	2
1	-	9	:	4	:	:	4
10	-	19	:	11	:	:	4
20	-	29	:	112	:	:	876
30	-	39	:	:	:	:	:
40	-	49	:	4041	:	:	:
50	-	59	:	8035	:	:	:
60	-	69	:	5755	:	:	:
70	-	79	:	10473	:	:	:
80	-	89	:	37260	:	:	:
90	-	99	:	13114	:	:	:

Percentage of bases with a quality value >= 40 : 99 % .

FEATURES

1. .197817

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Identified using the e-PCR software (G. Schuler)
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ST5

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STS

ORIGIN

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Best Local Similarity	100.0%	Pred. No. 2.2e-151		
Matches 846	Conservative 0	Mismatches 0	Gaps 0	

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[illegible]

JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source

J Neurochem. 71 (3), 937-945 (1998)
9838714
9721719
2 (bases 1 to 1315)
Gerashtchenko,D., Kanaoka,Y., Beuckmann,C. and Urade,Y.
Direct Submission
Submitted (07-MAR-1997) Molecular Behavioral Biology, Osaka
Bioscience Institute, 6-2-4 Furuedai, Suita, Osaka 565, Japan
Location/Qualifiers
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ORIGIN

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QY	72	GGTCTCTTCAGCAACCGGCTCTCTGGGCAACTGCTGGCTCTGGGGGCTGTGGCGGCTC	131
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QY	132	GGGGCTGGGGGTGTGCTTCGCGGCTCCACTGCGCCCGCTGCTCGGTCTTACATGCT	191
Db	189	CGGGCTGGGGGTCTCGCGGCGGCAAGTCACTCGCGCGCTCTTGTATGTGCT	248
QY	192	GGTGTGTGCGCTGACCGTCACCGACTTGTGGGGAATGGCTCCTAAGCCCGGTGTGCT	251
Db	249	AGTGTGTGCGCTTACCGTCACTTGTGGGGAAGTGTATGATACGCCGATGTGCT	308
QY	252	GGCTGCTTACGCTCAGAAACCGAAGTCTGCGGGTCTTTCGCCGCAATTGACCACTCGTT	311
Db	309	GGCTGCTTACCGCGAAATTCGAAACCTTAAGAACTGTGCTGCTCAGGCAATCACTT	368
QY	312	GTGCGAAGCTTGGCTCTTTCATGTCTTCTTGGGCTCTCTTGACACTGCAACTGCT	371
Db	369	ATGTGAAGCTTGGCTCTTCGTAATGTCTTCTTGGGTACCTTCGACTTACAGCTACT	428
QY	372	GGGCAATGCACTGGAATGCTGAGCTCTCCCTTAAGGCACTTCTTCTTACCGACGGCAAT	431
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QY	432	CACCTGCGGCTGGGGGCACTGTGTGGGCGCGGTGTGAGCGCTTCTCCGTGGCTTCTG	491
Db	489	CACCGCGCGCGGGGAATGCTGTGTGGGCGCAATGCAAGCGCTTCTTCTTGGCTTCTG	548
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QY	552	TATTCAAATAGTCCACAGAGAGGGCTGCTGTGCTGTGGGGTAACTGTGCTCTACTC	611
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QY	612	TAGCCTAATGGCGGCTGCTGCTGCTCGCCACCGTGTGTGGAACCTCGGCGCATATGGCA	671
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QY	672	CCTCTATGTCGATGCAACCGGCGGCTGTGCACGGCGCATCCGGCTCTTGTGCACACGAGGACTGTGC	731
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Db	789	CCAGTTCAGGCTTCAGACTACAGGCAATGGGCTCCCGGATCTTTGGAGAGCTGGAGACCACTT	848
QY	792	CCTGCTGTGCGCGCTGATGACCGTGGCTCTCACTATGTGTCTCTGCGCCGTAATATATATCG	851
Db	849	TGTTCTGTGTGCTCTCACGACAGTGTCTTTACCATGTGTTCCTGCTTTAATTTATATCG	908
QY	852	CGCTTACTATGAGACATTTAAGATGTGCAGAGAAAAACAGACCTTGTAAAGAACGAGA	911
Db	909	TGCTTACTATGAGAGCTTTAAACTTGT-----GGACAGAGCTGACGGAGACTCCGA	959
QY	912	AGACCTCCGAGCCTTGGCATTTTCTATCTGTGATTTCAATTGTGGACCTTGGATTTTAT	971
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QY	1032	GTAACAGAGCCGGTGCACAAATTC-----ACTAACATGGAATCAATCTGTGA	1080
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RESULT 10	AF120101	AF120101	AF120101	LOCUS	DEFINITION	ACCESSION	VERSION
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					Rattus norvegicus prostaglandin D2 receptor mRNA, complete cds.		
	AF120101						
	AF120101.1	GI:4567037					

SOURCE	Rattus norvegicus (Norway rat)
ORGANISM	Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

REFERENCE	AUTHORS	TITLE
1 (bases 1 to 1074)	Wright, D.H., Nantel, F., Metters, K.M. and Ford-Hutchinson, A.W	A novel biological role for prostaglandin D2 is suggested by

distribution studies of the rat DP prostanoïd receptor
Eur. J. Pharmacol. 377 (1), 101-115 (1999)
JOURNAL MEDLINE 99376163

PUBMED	10448933
REFERENCE	2 (bases 1 to 1074)
AUTHORS	Wright, D.H. and Abramovitz, M.

TITLE Direct Submission
JOURNAL Submitted (13-JAN-1999) Biochemistry and Molecular Biology, Merck
Frost Centre for Therapeutic Research, P.O. Box 1005, Pointe

FEATURES	
source	
Claire - Dorval, Quebec H9R 4P8, Canada	Location/Qualifiers
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Query Match	60.7%;	Score 655.4;	DB 10;	Length 1074;
Best Local Similarity	77.1%;	Pred. No. 6,6e-115;		
Matches 829;	Conservative 0;	Mismatches 231;	Indels 15;	Gaps 2;

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Qy 72 GGTGCTCTTTCAGCACCGGCGCTCTCTGGGCAACTGCTGCGCCCTTGAGGCTGCTGCGCGCTC 131

Db 69 TGTGGCTTTCAGTGCAGACTGCTGGGCAACCTCTGGGGCTGGTGTCTCTGCGCGATC 128

Qy 132 GGGGCTGGGGTGGCTCGCGGGCTCACCCTGGCGCCCGCTCGCTTCACATGT 191
 Db 129 CGGGCTGGGGTCTCTGCGGGCAGGGCCACTGATCGCGCGCCCTCGGCTTTTACGTCT 188

192 GGTCTGTGGCCTGACGGTACACCACTTGGTGGCAAGTCCCTCTAAGCCGGGTGCT 251

Db 189 AGTGTGCGGGCTGACAGTCAACCGACTTGCTGGGCGAAGTCTCTGATCAGCCCGAGTGCTCT 248

Qy 252 GGCTGCTTACGCTTCAGAACCGGAGTCTGCGGGTGCTTGCGCCCGCATTGGACAACTCGTT 311

Db
249 GGCTGCATACGGCGAAATCGAGCCTTAAGAACTGCTGCTCCTCAGGCAACCAATT 308

QY	312	GTGCGAAGCCTTGACCTTTCATGTCCTTTGGGGCTCTCCGACACTGCAACTCCT	371
Db	309	ATGGAAGCCTTGCGCTTCTCGATGTCCTTCTTGGGGTTAGCCTCGACTTACAGCTACT	368

372 GGCATGSCACTGAGTGTGCTCTCCCTAGGACACCTTTCTTCTACCGACGACAT 431

Db 365 GGGTATGGCACTAGAGTGGCTGTCTCTGGGACACCCCTTTCTTCTACCAAAAGGACAT 428

Ov 432 CACCCTGGCGCTGGGCGCACTGGTGGCCCGGTGGTGAAGCGCTTCTCCCTGGCTTTCTG 491

Db
429 CACCGCCGCGGGGAGTGTGTGGACACAGTCGCGGGCGCTTCTCTTTGGCTTTCTG 488

QY 492 CGGCTACTTTCATGGGCTTCGGGAATTCGTGCAGTCTGCCCGGACCTGGTGCTT 551

Db 489 TGGCTCCCTTTCGTGGCTTTCGGGAATTCGTGCAGTCTGCCCGGACCTGGTGCTT 548

552 TATCCAGATGTTCCACGAGAGGGGCTCGCTGTGGGTGCTGGGTACTGTGTCTTACTC 611

Db 549 CATTCAATGATCCACCAAGGCGCTATTCTCGATAATAGGCTTCTGTGTGCTTACTC 608

DB 609 CAGCCTCATGCGCTGTGCTGCTCCGCACTGTGCTGTCACCTGGGTCATGTCCTCA 668

672 CCTTATGCGATGACCCGGCGGCTGCGAGCGGACCCCGCGCTCTGCGACCGAGGACTGTGC 731
669 CCTTATGCGATGACCGGCGGCGAGGACCATCCCCCGCGCTGCTCCAGGAGACCGCGC 728

732 CGAGCCGCGCGGACGGAGGAGCGTCCCTCAGCCCTGTGAGAGCTGATCACT 791

Db 729 CCACTCAGGCTCAGACTACAGGCA TGGGTC CCCCAGATCCTTTGGAGAGACTGGACCACTT 788

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Qy	192	GATGTGTGGCTGACCGGTACCGGACTTGGTGGGGGAGTGGCTCCTTAAGCCCGGGTGC	251
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Qy	252	GGCTGTCCACGCTCAGAAACCGAGTCTGGCGGGTCTTGGCGCCCGCATTTGACACTGCT	311
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Qy	312	GTGCCAAGCCTTGGCCCTTCTCAATGTCTTCTTTGGGCTCTTCTTCGACACTGCACCTCT	371
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Qy	372	GGCATGAGCACTGAGTGTCTGGCTCTCCCTTGGGGCACCTTTCTTTCACGACGGACAT	431
Db	405	GGCTATGGCGGTGGAGTGTCTGGCTCTCTGGGACACCCCTTCTTTCACAAAGGACGT	464
Qy	432	CACCTTGCGCTGGGGCGCACTGTGGCCCGGGTGTAGCGGCTTCTGCTGGCTTCTG	491
Db	465	CACCTTGCAGCGGGGAGTGTGGGACCGGCTGTGGCGGCTTCTGTTGGCTTCTG	524
Qy	492	CGGCTACCTTTCATGGGCTTCGGGAGTTCGTGTGACATACGCGCCCGGACCTGGTGTCT	551
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Qy	552	TATCAGATGTTCACGAGAGGGCTCGCTGTGGTCTGGGGTACTCTGTGCTTACTC	611
Db	585	CATCAGATGATTCACAAGGAGCGTTTCAATTTTGGTAATAGGCTTCTCTGTGCTTACTC	644
Qy	612	CAGCTTATGGCGGTGTGTGTCTGTCCGACCGTGTCTGTGCAACTCGGCGCCATGGCGCA	671
Db	645	CAGCTTATGGCGGTGTGTGTCTGTCCGACCGTGTGTGCAACTGGGTGTCCATGTACAA	704
Qy	672	CCTTATGCGATGACCGGCGGCTGACAGGGGCAACCCCGCTCCGACACAGGGGACTGTGC	721
Db	705	CTTCTATGACATGACAGGCGCCAGAGGCACTATCTTCAACGCTGTCTCCAGGAGCGCGC	764
Qy	732	CGAGCGCGCGGACGGAGGGAGAGCGTCCCTCAGCGCCCTGTGAGGAGCTGTATCACT	791
Db	765	CGAGTCAAGGCTCAAGACTTACAGGCAAGGCTCCCTGCATCTTTGGAGGAGCTGAGCACTT	824
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Continuation (4 of 4) of AC095991 from base 300001 (AC095991 Rattus norvegicus clone CH2)

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QY	252	GGCTGCTTACGCTCAGAACCGAGTGTGGCGGGTGTCTTGGCCCGGATTTGAACATCTGTT	311
Db	63384	GGCTGGCTATGGGCAAAATGGAGGCTTAAAGAACTGTGCTGCTGCTTACGGCAACAGTT	63443
QY	312	GTGCGAAGCCTTGGCTTCTTCAATGTCTCTTTGGGCTCTCTCGACATCGAACCTCT	371
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QY	372	GGCGATGGCACTGGAGTGTGGCTGTCCCTAGGGGCAACCTTCTCTTACCGACGGCACT	431
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QY	432	CACCTTGGCGCTGGGGGCACTGGTGGCCCGGTGGTGAAGCGGCTTCTCCCTGGCTTTCG	491
Db	63564	CACCGCCCGCGGGAGAGTGTGTGGACACAGTCCGGGCGGCTTCTCTTTGGCTTTCG	63623
QY	492	CGCGCTACCTTTTCAATGAGGCTTCGGGAAGTTGTGTGAGTACTGCCCCCGGACCTGTGCTT	551
Db	63624	TGCGCTCCCTTGTCTGTGGCTTTTGGGAAGTTCTGTCCAGTACTCTCCGGGTACCTGTGGCTT	63683
QY	552	TATCCAGATGTGCCAGAGAGAGGCGTCCGTGTCCGTGGGGTACTGTGTCTTACTGC	611
Db	63684	CATCCAGATGATCCACAAAGGCGTCACTTCTCGTAATAGGCTTCTGTCTCTTACTGC	63743
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Db	63744	CAGCCTCATGGCGCTCTGTGTCCTCTCGCAACTGTGTGTGCAACTCTGGGTGCATGTCCAA	63803
QY	672	CCTCTATGGCATGACCGGCGGCTGACGGGAGCAACCGCGCTCTGTACACCGAGGACTGTGC	731
Db	63804	CTCTATATGCATGACAGGGCGCAAGAGGACCATCCCGCGCTGTCCAGGGACCGGCG	63863
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QY	792	CCAGCTGTGGCGCTGATGACCGTGTCTTTCACTAATGTGTTCTTCCCGCTAAT	846
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RESULT 15
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AC112324_3 300001 357027
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DEFINITION Rattus norvegicus clone CH230-75L12, *** SEQUENCING IN PROGRESS
*** 11 unordered pieces.

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KEYWORDS	HTG: HTGS_PHASE1: HTGS_DRAFT: HTGS_ENRICHED.
SOURCE	Rattus norvegicus
ORGANISM	Rattus norvegicus
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE	1 (bases 1 to 357027)
AUTHORS	Muzny, D., Marie, J., Metzker, M., Lee, A., Abramson, S., Adams, C., Alter, J.,

TITLE	REFERENCE AUTHORS	REFERENCE TITLE	REFERENCE JOURNAL
Submitted	Allen, C., Allen, H., Alebrooks, S., Amin, A., Anguiano, D., Alyalebechi, V., Aoyagi, A., Ayoccej, M., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benhamed, F., Biancato, K., Blair, J., Blankenbuck, K., Blyth, P., Brown, M., Bryant, N., Buhay, C., Burch, P., Butrell, K., Calderon, E., Cadenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., d'Souza, L., Dayila, M.L., Davis, C., Davy-Carroll, L., De Anda, C., Decker, D., Delgado, L., Denison, S., Dermoco, C., Ding, Y., Dinh, H., Dwyer, K., Diexper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K., Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G., Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P., Fraser, C.M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M., Georgopoulos, E., Geer, K., Gill, R., Grady, M., Guerra, W., Gervaza, M., Gharatne, P., Haaland, W., Hamil, C., Hamilton, C., Hamilton, K., Gunaratne, P., Hawes, A., Henderson, N., Hernandez, J., Hernandez, R., Hines, S., Hladun, S.L., Hodgson, A., Hogues, M., Hollins, B., Howells, S., Huliy, S., Hume, J., Idlebird, D., Jackson, A., Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolyet, A., Karpaty, S., Kelly, S., Kelly, S., Khan, Z., King, J., Kovar, C., Kovats, C., Kraft, C.L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J., Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J., Lounsbuher, L., Louiseged, H., Lozada, R.J., Lu, X., Ma, U., Maheshwari, M., Mahindaratne, M., Mahmood, M., Malloy, K., Mangum, A., Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E., Mawhinney, S., McLeod, M.P., McNeill, T.Z., Meenen, E., Miklosavljevic, A., Miner, G., Mirja, E., Montemayor, J., Moore, S., Morgan, M., Morris, K., Morris, S., Mundaas, M., Murphy, M., Naif, L., Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Nwokenemah, O., Okwunonu, G., Olarnunsegon, A., Pal, S., Parks, K., Pasernak, S., Paul, H., Perez, A., Perez, L., Phamkoc, C., Plopper, F., Poindexter, A., Popovic, D., Primus, E., Pu, L.-L., Puzo, M., Quiroz, J., Rachlin, E., Reeves, K., Regier, M.A., Reish, R., Rellly, B., Rellly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F., Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S.J., Sanders, W., Savery, G., Scherer, S., Scott, G., Shatsman, S., Shen, H., Sheth, J., Shvartsbeyn, A., Slisom, I., Sitter, C.D., Smajs, D., Snead, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, U., Steimle, M., Strong, R., Sutton, A., Svatek, A., Taber, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trelois, Z., Uman, K., Valas, R., Vera, V., Villaseana, D., Waldron, L., Walker, B., Wang, J., Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, F., Williams, G., Willson, R., Wleczek, R., Wooden, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von Weidenhausen, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Weinstock, G. and Gibbs, R.A.	Submitted	Submitted
Submitted	Unpublished	Unpublished	Unpublished
Submitted	2 (bases 1 to 357027)	2 (bases 1 to 357027)	2 (bases 1 to 357027)
Submitted	Worley, K.C.	Worley, K.C.	Worley, K.C.
Submitted	Submitted	Submitted	Submitted
Submitted	Submitted (21-FEB-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA	Submitted (21-FEB-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA	Submitted (21-FEB-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
Submitted	3 (bases 1 to 357027)	3 (bases 1 to 357027)	3 (bases 1 to 357027)
Submitted	Rat Genome Sequencing Consortium.	Rat Genome Sequencing Consortium.	Rat Genome Sequencing Consortium.
Submitted	Submitted (26-SEP-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA	Submitted (26-SEP-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA	Submitted (26-SEP-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
Submitted	On Sep 26, 2002 this sequence version replaced gi:21737250. The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). As a result, the sequence may extend beyond the ends of the clone and there may be contigs that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.	On Sep 26, 2002 this sequence version replaced gi:21737250. The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). As a result, the sequence may extend beyond the ends of the clone and there may be contigs that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.	On Sep 26, 2002 this sequence version replaced gi:21737250. The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). As a result, the sequence may extend beyond the ends of the clone and there may be contigs that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

Center: Baylor College of Medicine
Center code: BCM

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Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project Information -----
Center project name: G0UG
Center clone name: CH230-75L12
----- Summary Statistics -----
Assembly program: Phrap; version 0.990329
Consensus quality: 294995 bases at least Q40
Consensus quality: 299994 bases at least Q30
Consensus quality: 302651 bases at least Q20
Estimated insert size: 390689; sum-of-conf: contigs estimation
Quality coverage: 3x in Q20 bases; sum-of-conf: contigs estimation
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* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/genbank\_drift\_data.html)
* NOTE: This sequence may represent more than one clone.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 11 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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* 1 7987: contig of 7987 bp in length
* * 7988 8087: gap of unknown length
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* * 15584 15683: gap of unknown length
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* * 261675 261774: gap of unknown length
* * 261775 274519: contig of 12745 bp in length
* * 274520 274619: gap of unknown length
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* * 285174 327168: contig of 41995 bp in length
* * 327169 327268: gap of unknown length
* * 327269 331337: contig of 4069 bp in length
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/note="wgs contig"
misc_feature 342450..344641
/note="wgs contig"
ORIGIN

Query Match 50.1%; Score 540.6; DB 2; Length 110000;
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Matches 651; Conservative 0; Mismatches 184; Indels 0; Gaps 0;

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QY 72 GGTGCTCTTACAGACCGGCTCTGTGGGCAACTGTGAGCCGTGGGGGTGTGGGGGCTC 131
DB 108290 TGTGCTTTCAGTCAGAGACTGCTGGGCAACTCTGTGGCGCTGTGTGCTGGGCGGATC 108231
QY 132 GGGGCTGGGGTGGTGTGCGGGCTGCATGCGCGCGCTGCGCTCTTACATGCT 191
DB 108230 CGGGCTGGGGTCTGCGCGCAAGGCACTGCATCCGCGCGCTCTTACATGCT 108171
QY 192 GGTGTGTGCTGACCGCTCACCGACTTGTGGCAAGTGTCTCTTAAAGCCGGTGTCT 251
DB 108170 AGTGTGCGGCTTGACAGTCAACCACTGTGGCAAGTGTGTATCAGCCCGATGTGCT 108111
QY 252 GGCTGCTACGCTCAAGACCGAGTCTGGGGGTGTGGCGCGCAATTGGACAATCGTT 311
DB 108110 GGCTGCTACGCGCAAAATGGAGCTTAAAGAACTGTGCTGCTCTCAAGCAACAGTT 108051
QY 312 GTGCCAAGCTTTCGCTTTCATGTCTTCTTTGGGCTCTCTCGACACTGCACTCT 371
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QY 372 GGCCATGSCATGAGTGTGCTCTCTCCAGGCACTTCTTCTTACCGACGCAAT 431
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QY 432 CACCGTGGGCTGGGGGCACTGTGTGCGCGCGGTGGAGGGCTTCTCCGTGCTTCTG 491
DB 107930 CACCGCGCGCGGAGTGTGTGTGACCAAGTGGCGGCGCTTCTTGTGGCTTCTG 107871
QY 492 CGCGCTACCTTTCATGGGCTTTCGGAAGTTCGTGCACTACTGCCCGGCACTGTGCTT 551
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DB 107810 CATCCAGATGATCCAAAGAGGCTCATTTCTGATATAGGCTTCTGTGTCTACTC 107751
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DB 107690 CTTCTATGCAATGCAAGGCGCGCAAGGACATCCCGCGGTCTCAAGGAGCGGCG 107631
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DB 107630 CCAGTCAGGCTCAGACTACAGGATGGGTCCCGAATCTTTGAGAGAGTGGACACTT 107571
QY 792 CCTGTGTGCTGGGCTGTATACCGTGTCTTCACTATGTGTCTGTGCGCGTAAAT 846
DB 107570 TGTGTGTGCTGTCTTCACAGCAAGTGTCTTACCAATGTGTCTTAAAT 107516

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Job time : 4919.42 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 22, 2005, 09:24:18 ; Search time 652.51 Seconds
(without alignments)
9798.042 Million cell updates/sec

Title: US-10-689-861-3

Perfect score: 1080

Sequence: 1 atgaagtcgcccgtttaccg.....acatggaatccagtcgtgtga 1080

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 4: Geneseqn2001as:*
- 5: Geneseqn2001bs:*
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- 8: Geneseqn2003as:*
- 9: Geneseqn2003bs:*
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- 11: Geneseqn2003ds:*
- 12: Geneseqn2004as:*
- 13: Geneseqn2004bs:*

Préd. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1080	100.0	1253	4	ABA09244 Human pro
2	1080	100.0	1253	4	AAK53126 Human pol
3	1080	100.0	1253	10	AD08862 Novel DNA
4	1080	100.0	1303	4	AAK52142 Human pol
5	1080	100.0	1488	2	AAT37402 Prostagla
6	1077	99.7	1077	12	ADO30026 Human GPC
7	1051.6	97.4	1264	3	AA27056 Human cel
8	900.4	83.4	1505	10	AD07082 Novel cod
9	846	78.3	1216	3	AA35105 Human ade
10	846	78.3	1216	3	AAF21227 Human low
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12	846	78.3	1216	10	ACA56876 Human sig
13	846	78.3	1216	11	ABD20770 Human pul
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28	436	40.4	495	10	AB296920	Ab296920 Human nuc
29	436	40.4	495	11	ABD20769	Abd20769 Human pul
30	436	40.4	495	13	ADP55148	Adp55148 Human PRO
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36	220.6	20.4	2296	2	AAV12457	Aav12457 Human CDN
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40	220.6	20.4	9060	3	AAF21047	Aaf21047 Human low
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42	220.6	20.4	9060	11	ABD20590	Abd20590 Human pul
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ALIGNMENTS

RESULT 1
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ID ABA09244 standard; cDNA; 1253 BP.

XX ABA09244;

DT 11-JAN-2002 (first entry)

XX Human prostaglandin DP receptor homologue cDNA, SEQ ID NO:1020.

XX Human; cytokine; cell proliferation; cell differentiation; growth factor;
KW haematopoiesis regulation; tissue growth; immunomodulator; activin;
KW inhibin; chemotaxis; chemokinesis; cancer; thrombolysis; oncogenesis;
KW proliferation; metastasis; cancer; tumour; haematopoietic disorder;
KW myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;
KW chronic inflammatory condition; proliferative retinopathy;
KW atherosclerosis; coronary heart disease; arterial ischaemia;
KW bone disorder; osteoporosis; vascular growth disorder;
KW tissue regeneration; wound healing; infection; immune disorder;
KW cell culture; drug screening; gene therapy; antiinflammatory;
KW antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic;
KW cytotstatic; osteopathic; vasotropic; cardiant; virucide; antibacterial;
KW antifungal; vulnery; antiulcer; ss.

XX Homo sapiens.

XX WO200157188-A2.

XX 09-AUG-2001.

XX 05-FEB-2001; 2001WO-US003800.

XX 03-FEB-2000; 2000US-00496914.

XX 27-APR-2000; 2000US-00560875.

XX (HYSE-) HYSEQ INC.

XX Tang YT, Liu C, Drmanac RT;

XX WPI; 2001-457740/49.

XX P-PSDB; ABB12000.

XX Human proteins and DNA encoding sequences useful for preventing, treating

or ameliorating a medical condition in a mammalian subject e.g. arthritis and cancer.

Claim 1; Page 860-861; 1963pp; English.

Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and sequences ABA08225-ABA09574 represent nucleic acids encoding them. The invention also relates to vectors and recombinant host cells comprising a nucleotide of the invention, methods of producing the novel polypeptides, antibodies against the polypeptides, methods of detecting the nucleotides, or polypeptides in a sample, and methods of identifying compounds which bind to polypeptides of the invention. Although novel, many of the polypeptides of the invention have homology to known proteins, thereby giving an insight into their probable biological activities, and hence potential therapeutic applications. The polypeptides of the invention may have various activities, including cytokine, cell proliferation or cell differentiation activities; stem cell growth factor activity; haematopoiesis regulatory activity; tissue growth activity; immunomodulatory activity; activin- or inhibin-related activities; chemotactic or chemokinetic activities; haemostatic, thrombotic or thrombolytic activities; receptor or ligand activities; or may be involved in oncogenesis, cancer cell proliferation or metastasis. Depending on their biological activities, polypeptides and nucleotides of the invention are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Such conditions include cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell disorders), chronic inflammatory conditions (e.g., asthma or arthritis), proliferative retinopathy, atherosclerosis, coronary heart disease, arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal vascular growth. Polypeptides involved with tissue regeneration and repair (or nucleic acids encoding them) may be used to promote wound healing (e.g., of burns, incisions and ulcers), while those with immunomodulatory activities may be used in the treatment of viral, bacterial and fungal infections in addition to immune disorders. Polypeptides with growth factor activity may be used in cell cultures to promote cell growth. For example, such polypeptides may be used to manipulate stem cells in culture to give rise to neuroepithelial cells that can be used to augment or replace cells damaged by illness, autoimmune disease or accidental damage. The polypeptides and nucleotides may also be used in the diagnosis of the above conditions, and in drug screening techniques. The present sequence represents a cDNA encoding a novel human polypeptide of the invention

Sequence 1253 BP; 190 A; 405 C; 358 G; 300 T; 0 U; 0 Other;

Query Match 100.0%; Score 1080; DB 4; Length 1253;

Best Local Similarity 100.0%; Pred. No. 1.8e-243; Mismatches 0; Indels 0; Gaps 0;

Matches 1080; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 GTGATGGGCGGGTGTCTTTACGACCGCGCTCTCGGGCAACCTGTGGCCCTCGGGGTG 120
 DB 182 GTGATGGGCGGGTGTCTTTACGACCGCGCTCTCGGGCAACCTGTGGCCCTCGGGGTG 241

QY 121 CTGGCGCGCTCGGGGTGGGGTGGTGTCTCGCGCGTCCACTGGCCGCTCGCTCGGTC 180
 DB 242 CTGGCGCGCTCGGGGTGGGGTGGTGTCTCGCGCGTCCACTGGCCGCTCGCTCGGTC 301

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QY 301 GACAACTCGTGTGGCAAGCCTTGGCTTCTTCATGTCCTTTGGGCTCTCTCGACA 360
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QY 361 CTGCAACTCTCTGGCCATGGCACTGGAGTGTCTCTCCCTAGGACACCTTTCTTTCTAC 420
 DB 482 CTGCAACTCTCTGGCCATGGCACTGGAGTGTCTCTCCCTAGGACACCTTTCTTTCTAC 541

QY 421 CGACGGCAATCACCTCGGCTTGGGCGCACTGGTGGCCCGGCTGGTGGAGCCCTTCTCC 480
 DB 542 CGACGGCAATCACCTCGGCTTGGGCGCACTGGTGGCCCGGCTGGTGGAGCCCTTCTCC 601

QY 481 CTGGCTTTCTGGCGCTACCTTTTCAATGAGCTTCGCGGAAGTTGCTGAGTACTGCCCCG 540
 DB 602 CTGGCTTTCTGGCGCTACCTTTTCAATGAGCTTCGCGGAAGTTGCTGAGTACTGCCCCG 661

QY 541 ACCTGGTCTTTATCCAGATGGTCCACGAGGAGGCTCGCTGTCTGGTGTCTGGGTACTCT 600
 DB 662 ACCTGGTCTTTATCCAGATGGTCCACGAGGAGGCTCGCTGTCTGGGTACTCTCT 721

QY 601 GTGCTTACTCAGGCTCATGGCGTGTCTGTCTCTGGCACCCTGTGTGCAACCTCGGC 660
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QY 721 AGGACTGTGGCGAGCCGCGCGGACCGGAGGAGGCTCCCTCAGCCCCCTGGAGGAG 780
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QY 781 CTGATACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 840
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QY 841 GTAATTTATCGCGTCTTACTTGGAGCATTTAAGGATGTCAGAGGAGAAAAACAGGACCTCT 900
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QY 901 GAAGAAGCAGAGACCTCCGAGCCCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 960
 DB 1022 GAAGAAGCAGAGACCTCCGAGCCCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1081

QY 961 TGGATTTTATCATTTTCAGATCTCCAGTATTTTCGATATTTTTCACAGATTTTTCATT 1020
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QY 1021 AGACCTCTTAGTACAGGAGCGGTGAGCAATTCACATGAATCCAGTCTGTGA 1080
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RESULT 2
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 XX AAK53126;
 AC AAK53126;
 DT 06-NOV-2001 (first entry)
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 DE Human; cytokine; cell proliferation; cell differentiation; gene therapy;
 XX Human vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;
 KW nervous system disorder; arthritis; inflammation; ss.
 XX Homo sapiens.
 OS Homo sapiens.
 XX WO200157190-A2.
 PN 09-AUG-2001.
 XX 05-FEB-2001; 2001WO-US004098.
 PF 03-FEB-2000; 2000US-00496914.
 PR

PR 27-APR-2000; 2000US-00560875.
PR 20-JUN-2000; 2000US-00598075.
PR 19-JUL-2000; 2000US-00620325.
PR 01-SEP-2000; 2000US-00654936.
PR 15-SEP-2000; 2000US-00663561.
PR 20-OCT-2000; 2000US-00693325.
PR 30-NOV-2000; 2000US-00728422.
XX (HYSE-) HYSEQ INC.
XX
XX Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y;
PI Ma Y, Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;
XX
XX WPI; 2001-476283/51.
DR P-PSDB; AAM79993.
XX
XX Nucleic acids encoding polypeptides with cytokine-like activities, useful
PT in diagnosis and gene therapy.
XX
XX Claim 1; Page 4907; 6221pp; English.
XX
XX The invention relates to polynucleotides (AAK51456-AAK51435) and the
CC encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111
CC (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the
CC sequence listing were missing at the time of publication
XX
XX Sequence 1253 BP; 190 A; 405 C; 358 G; 300 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 1080; DB 4; Length 1253;
Best Local Similarity 100.0%; Pred. No. 1.8e-243;
Matches 1080; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGAAGTCGCGGTTTACCGCTGCGAGAACACCACTCTGTGGAAGGCAACTCGCGG 60
DB 122 ATGAAGTCGCGGTTTACCGCTGCGAGAACACCACTCTGTGGAAGGCAACTCGCGG 181
QY 61 GTGATGGCGGGGTGCTCTTACGACCGCGCTCCGGCAACTGCTGCGCGCTGGGGCTG 120
DB 182 GTGATGGCGGGGTGCTCTTACGACCGCGCTCCGGCAACTGCTGCGCGCTGGGGCTG 241
QY 121 CTGGCGCGCTCGGGGTGGGGGTGGTGTCTCGCGCGCTCCCACTGCGCGCGCTCGCGTC 180
DB 242 CTGGCGCGCTCGGGGTGGGGGTGGTGTCTCGCGCGCTCCCACTGCGCGCGCTCGCGTC 301
QY 181 TTCTACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
DB 302 TTCTACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 361
QY 241 CCGGTGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
DB 362 CCGGTGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 421
QY 301 GACAACTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
DB 422 GACAACTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 481
QY 361 CTGCAACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
DB 482 CTGCAACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 541
QY 421 CGACGGCACATCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
DB 542 CGACGGCACATCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 601

QY 481 CTGGCTTTCTGGCGCTACCTTTTCATGGGCTTTCGGGAAGTTTCGTGAGTACTGCCCCCGGC 540
DB 602 CTGGCTTTCTGGCGCTACCTTTTCATGGGCTTTCGGGAAGTTTCGTGAGTACTGCCCCCGGC 661
QY 541 ACCTGGTGTCTTATCCAGATGCTCCAGAGGAGGCTCGCTGCTGCGGTGCTGGGGTACTCT 600
DB 662 ACCTGGTGTCTTATCCAGATGCTCCAGAGGAGGCTCGCTGCTGCGGTGCTGGGGTACTCT 721
QY 601 GTGGCTTACTCCAGGCTCATGCGGCTGCTGGTCTCTCGCCACCGTGTGTCGAACCTCGGC 660
DB 722 GTGGCTTACTCCAGGCTCATGCGGCTGCTGGTCTCTCGCCACCGTGTGTCGAACCTCGGC 781
QY 661 GCCATGCGCAACTCTATGCGATGACACCGCGGCTGTCAGCGGCACCGCGCTCTCTGAC 720
DB 782 GCCATGCGCAACTCTATGCGATGACACCGCGGCTGTCAGCGGCACCGCGCTCTCTGAC 841
QY 721 AGGGACTGTGCGGAGCGCGCGCGGAGCGGAGCGTCCCTCAGCCCCCTGGAGGAG 780
DB 842 AGGGACTGTGCGGAGCGCGCGCGGAGCGGAGCGTCCCTCAGCCCCCTGGAGGAG 901
QY 781 CTGGATCACTCTCTGCTGCTGCGCTGATGACCGTCTCTTCACTATGTGTTCTCTGCCC 840
DB 902 CTGGATCACTCTCTGCTGCTGCGCTGATGACCGTCTCTTCACTATGTGTTCTCTGCCC 961
QY 841 GTAATTTATCGCGCTTACTATGAGCATTTAAGGATGTCAGAGAGAAAAACAGGACTCT 900
DB 962 GTAATTTATCGCGCTTACTATGAGCATTTAAGGATGTCAGAGAGAAAAACAGGACTCT 1021
QY 901 GAAGAGCAGAGACCTCCGAGCCTTGGATTTCTCTGATTTCAATTTGAGACCT 960
DB 1022 GAAGAGCAGAGACCTCCGAGCCTTGGATTTCTCTGATTTCAATTTGAGACCT 1081
QY 961 TGGATTTTATCATTTTTCAGATCTCCAGTATTTTCGATATTTTTCACAGATTTTCAAT 1020
DB 1082 TGGATTTTATCATTTTTCAGATCTCCAGTATTTTCGATATTTTTCACAGATTTTCAAT 1141
QY 1021 AGACCTTTTAGTACAGAGCGGTGCGCAATTTCACTAACATGGAATCCAGTCTGTGA 1080
DB 1142 AGACCTTTTAGTACAGAGCGGTGCGCAATTTCCACTAACATGGAATCCAGTCTGTGA 1201

RESULT 3
ADE08862
ID ADE08862 standard; DNA; 1253 BP.
XX
AC ADE08862;
XX
DT 29-JAN-2004 (first entry)
XX
DE Novel DNA-related contig nucleotide sequence #106.
XX
KW novel gene; novel protein; tissue marker; molecular weight marker;
XX chromosome marker; genetic disorder; contig; ds.
OS Unidentified.
XX
PN WO2003054152-A2.
XX
PD 03-JUL-2003.
XX
PF 10-DEC-2002; 2002WO-US039555.
XX
PR 10-DEC-2001; 2001US-0339739P.
PR 11-DEC-2001; 2001US-0339453P.
PR 14-MAR-2002; 2002US-0365091P.
PR 14-MAR-2002; 2002US-0365384P.
PR 12-APR-2002; 2002US-0372381P.
PR 22-APR-2002; 2002US-0372615P.
PR 24-APR-2002; 2002US-0376045P.
XX
PA (HYSE-) HYSEQ INC.

XX Tang YT, Asundi V, Goodrich RW, Ren F, Zhang J, Zhao QA, Wang J;
PI Ghosh M, Xue AJ, Wehrman T, Wang G, Zhou P, Drmanac RT, Wang Z;
PI Ma Y, Wang D, Chen R, Xu C, Boyle BJ;
XX WPI; 2003-569235/53.
XX
XX New polynucleotides, useful for expressing recombinant proteins for
PT analysis, characterization or therapeutic use, or as markers for tissues
PT in which the corresponding protein is preferentially expressed.
XX
XX Disclosure; SEQ ID NO 1928; 1177pp; English.
XX
XX The invention comprises the amino acid and coding sequences of novel
CC proteins. The DNA and protein sequences of the invention are useful as:
CC markers for tissues in which the corresponding protein is preferentially
CC expressed; as molecular weight markers on gels; as chromosome markers or
CC tags; to identify chromosomes or to map related gene positions; and to
CC compare with endogenous DNA sequences in patients to identify potential
CC genetic disorders. The present DNA sequence was used in the
CC exemplification of the invention.
XX
XX SQ Sequence 1253 BP; 190 A; 405 C; 358 G; 300 T; 0 U; 0 Other;
Query Match 100.0%; Score 1080; DB 10; Length 1253;
Best Local Similarity 100.0%; Pred. No. 1.8e-243;
Matches 1080; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGAAGTCGCCGTTTACCGCTGCCAGAACACCACTCTGTGGAAAGGCAACTCGGG 60
DB 122 ATGAAGTCGCCGTTTACCGCTGCCAGAACACCACTCTGTGGAAAGGCAACTCGGG 181
QY 61 GTGATGGGCGGGTGCTCTTACGACCGCCCTCTGGGCAACCTGCTGCCCTCGGGCTG 120
DB 182 GTGATGGGCGGGTGCTCTTACGACCGCCCTCTGGGCAACCTGCTGCCCTCGGGCTG 241
QY 121 CTGGCGCGCTCGGGCTGGGGTGCTCGCGCGTCCACTCGCGCGCTCGCCCTCGGTC 180
DB 242 CTGGCGCGCTCGGGCTGGGGTGCTCGCGCGTCCACTCGCGCGCTCGCCCTCGGTC 301
QY 181 TTCTACATGCTGGTGCTGCTGACCGTTCACCGTTCCTGGCAAGTGCCTCTTAAGC 240
DB 302 TTCTACATGCTGGTGCTGCTGACCGTTCACCGTTCCTGGCAAGTGCCTCTTAAGC 361
QY 241 CCGGTGGTCTGGTGCCTACGCTCAGAACCGAGTCTCGGGTGTGGCGCCCGCATG 300
DB 362 CCGGTGGTCTGGTGCCTACGCTCAGAACCGAGTCTCGGGTGTGGCGCCCGCATG 421
QY 301 GACAACTCGTGTGCCAAGCTTTCGCTTCTTCATGCTCTTCTTTGGGCTCTCCTCGACA 360
DB 422 GACAACTCGTGTGCCAAGCTTTCGCTTCTTCATGCTCTTCTTTGGGCTCTCCTCGACA 481
QY 361 CTGCAACTCTCGGCCATGACCTAGGAGTCTGGCTCTCCCTAGGGCACCTTTCTTAC 420
DB 482 CTGCAACTCTCGGCCATGACCTAGGAGTCTGGCTCTCCCTAGGGCACCTTTCTTAC 541
QY 421 CGACGGCACAATCACCTCGCCCTGGGCGACCTGCTGGGCGCCCGTGTGAGCCCTTCTCC 480
DB 542 CGACGGCACAATCACCTCGCCCTGGGCGACCTGCTGGGCGCCCGTGTGAGCCCTTCTCC 601
QY 481 CTGGCTTTCTGGCGCTACTCTTTCATGGGCTTCGGGAAGTCTGTCAGTACTGCCCGGC 540
DB 602 CTGGCTTTCTGGCGCTACTCTTTCATGGGCTTCGGGAAGTCTGTCAGTACTGCCCGGC 661
QY 541 ACTGGTGTATTCAGATGTCACAGAGAGGCTCGCTGCTGGTGTGGGGTACTCT 600
DB 662 ACTGGTGTATTCAGATGTCACAGAGAGGCTCGCTGCTGGTGTGGGGTACTCT 721
QY 601 CTGGCTTACTCAGCTCTAGGGCTGTGGTCTCGCCACCGTCTGTGCAACCTCGC 660
DB 722 GTGCTTACTCAGCTCTAGGGCTGTGGTCTCGCCACCGTCTGTGCAACCTCGC 781
QY 661 GCATGCGCAACTCTATGCGATGCAACCGCGGCTGCGAGCGCACCGCGCTCTGCGACC 720

DB 782 GCCATGCGCAACTCTATGCGATGACACCGCGGCTGCGAGCGGACCCCGCTCTCTGACC 841
QY 721 AGGAGCTGTGCGAGCGCGCGGAGGAGGAGCGTCCCTCAGCCCTGAGGAG 780
DB 842 AGGAGCTGTGCGAGCGCGCGGAGGAGGAGCGTCCCTCAGCCCTGAGGAG 901
QY 781 CTGATCACCTCTGCTGCTGCGGCTGATGACCGTCTTCACTATGTTCTCTGCC 840
DB 902 CTGATCACCTCTGCTGCTGCGGCTGATGACCGTCTTCACTATGTTCTCTGCC 961
QY 841 GTAAATTTATCGCGCTTACTATGAGGACATTTAAGGATGTCAAGGAGAAAAACAGGACCTCT 900
DB 962 GTAAATTTATCGCGCTTACTATGAGGACATTTAAGGATGTCAAGGAGAAAAACAGGACCTCT 1021
QY 901 GAAGAGCAGAGACCTCCGAGCCTTGCGATTTCTATCTGTGATTTCAATTTGTGACCT 960
DB 1022 GAAGAGCAGAGACCTCCGAGCCTTGCGATTTCTATCTGTGATTTCAATTTGTGACCT 1081
QY 961 TGGATTTTATCAATTTTCAGATCTCCAGTATTTTGGATATTTTTCACAAGATTTTCATT 1020
DB 1082 TGGATTTTATCAATTTTCAGATCTCCAGTATTTTGGATATTTTTCACAAGATTTTCATT 1141
QY 1021 AGACCTTTAGGTACAGGAGCGGTGCGAGCAATTTCCACTAATGGAATCCAGTCTGTGA 1080
DB 1142 AGACCTTTAGGTACAGGAGCGGTGCGAGCAATTTCCACTAATGGAATCCAGTCTGTGA 1201
RESULT 4
AAKS2142
ID AAK52142 standard; cDNA; 1303 BP.
XX AAK52142;
AC AAK52142;
XX 06-NOV-2001 (first entry)
XX Human polynucleotide SEQ ID NO 687.
DE Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorder; arthritis; inflammation; ss.
XX Homo sapiens.
XX WO200157190-A2.
XX 09-AUG-2001.
XX 05-FEB-2001; 2001WO-US004098.
XX 03-FEB-2000; 2000US-00496914.
PR 27-APR-2000; 2000US-00560875.
PR 20-JUN-2000; 2000US-00598075.
PR 19-JUL-2000; 2000US-00620325.
PR 01-SEP-2000; 2000US-00654936.
PR 15-SEP-2000; 2000US-00663561.
PR 20-OCT-2000; 2000US-00693325.
PR 30-NOV-2000; 2000US-00728422.
XX (HYSE-) HYSEQ INC.
XX Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y;
PI Ma Y, Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
PI Xue AJ, Yang Y, Wehrman T, Goodrich R;
XX WPI; 2001-476283/51.
DR P-PSDB; AAM79009.
XX Nucleic acids encoding polypeptides with cytokine-like activities, useful
PT in diagnosis and gene therapy.
XX
XX Claim 1; Page 2387-2388; 6221pp; English.

XX The invention relates to polynucleotides (AAK51456-AAK53435) and the
 CC encoded polypeptides (AAK78323-AAK80302) that exhibit activity relating to
 CC cytokine, cell proliferation or cell differentiation or which may induce
 CC production of other cytokines in other cell populations. The
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,
 CC e.g. stem cell growth factor activity, haematopoiesis regulating
 CC activity, tissue growth factor activity, immunomodulatory activity and
 CC activin/inhibin activity and may be useful in the diagnosis and/or
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
 CC inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111
 CC (AAK52582) and 3666 (AAK80020) are omitted as the relevant pages from the
 CC sequence listing were missing at the time of publication
 XX

Seq Sequence 1303 BP; 198 A; 426 C; 372 G; 307 T; 0 U; 0 Other;
 Query Match 100.0%; Score 1080; DB 4; Length 1303;
 Best Local Similarity 100.0%; Pred. No. 1.8e-243;
 Matches 1080; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGAAGTCGCGGCTTCTACCGCTGCGGAGCAACACCACTCTGTGGAAGGCAACCTCGGCG 60
 Db 166 ATGAAGTCGCGGCTTCTACCGCTGCGGAGCAACACCACTCTGTGGAAGGCAACCTCGGCG 225
 Qy 61 GTGATGGCGGGGCTCTTTCAGCAACCGGCTCTTGGGCAACCTGCTGCGCCCTGGGGCTG 120
 Db 226 GTGATGGCGGGGCTCTTTCAGCAACCGGCTCTTGGGCAACCTGCTGCGCCCTGGGGCTG 285
 Qy 121 CTGGCGCGCTGGGGCTGGGGTGGTCTCGGGGCTCCACTGCGCCCGCTGCGCTCGGTC 180
 Db 286 CTGGCGCGCTGGGGCTGGGGTGGTCTCGGGGCTCCACTGCGCCCGCTGCGCTCGGTC 345
 Qy 181 TTCTACATGCTGGTGTGGCTGACGCTCACCAGCTTGTGGGCAAGTGTCTCTAAGC 240
 Db 346 TTCTACATGCTGGTGTGGCTGACGCTCACCAGCTTGTGGGCAAGTGTCTCTAAGC 405
 Qy 241 CCGGTGGTGGTGGCTGCTACGCTCAGAACCGGAGTCTGCGGGTCTTGCGCCCGCATTTG 300
 Db 406 CCGGTGGTGGTGGCTGCTACGCTCAGAACCGGAGTCTGCGGGTCTTGCGCCCGCATTTG 465
 Qy 301 GACAACTGTTGTGCGAAGCCTTGCCTTCTCATGCTCTTGTGGCTCTCTCTGACA 360
 Db 466 GACAACTGTTGTGCGAAGCCTTGCCTTCTCATGCTCTTGTGGCTCTCTCTGACA 525
 Qy 361 CTGCAACTCTCGGCAATGGCACTGGAGTCTGGCTCTCCCTAGGCAACCTTCTTCTAC 420
 Db 526 CTGCAACTCTCGGCAATGGCACTGGAGTCTGGCTCTCCCTAGGCAACCTTCTTCTAC 585
 Qy 421 CGACGGCAATCACCTCGGCTGGGCGCACTGTGTGGCCCGCGGTGGTGGAGCGCTTCTCC 480
 Db 586 CGACGGCAATCACCTCGGCTGGGCGCACTGTGTGGCCCGCGGTGGTGGAGCGCTTCTCC 645
 Qy 481 CTGGCTTCTGGGCTACCTTTTCATGGGCTCGGGAAGTGTGTCAGTACTGCGCCCGC 540
 Db 646 CTGGCTTCTGGGCTACCTTTTCATGGGCTCGGGAAGTGTGTCAGTACTGCGCCCGC 705
 Qy 541 ACCTGGTCTTTATCCAGATGTCACGAGGAGGCTCGCTGTGGTCTGGGTCTGGGTACTCT 600
 Db 706 ACCTGGTCTTTATCCAGATGTCACGAGGAGGCTCGCTGTGGTCTGGGTCTGGGTACTCT 765
 Qy 601 GTGCTCTACTCAGCCTCATGGCTGTGTGCTCTGCGCAACCGTGTGTGCAACCTCGGC 660
 Db 766 GTGCTCTACTCAGCCTCATGGCTGTGTGCTCTGCGCAACCGTGTGTGCAACCTCGGC 825
 Qy 661 GCCATGCGCAACTTATGCGATGACCGCGGCTGTGAGCGGCAACCGGCTCTCTGCAAC 720
 Db 826 GCCATGCGCAACTTATGCGATGACCGCGGCTGTGAGCGGCAACCGGCTCTCTGCAAC 885
 Qy 721 AGGGAAGTGTGCGGAGCGCGGAGCGGAGGAGCGTCCCTCAGCCCTCGAGGAG 780
 Db 886 AGGGAAGTGTGCGGAGCGCGGAGCGGAGGAGCGTCCCTCAGCCCTCGAGGAG 945

Qy 781 CTGGATCACCTCTGCTGCTGCTGATGACCGTCTTCTCACTATGTTCTCTGCCC 840
 Db 946 CTGGATCACCTCTGCTGCTGCTGATGACCGTCTTCTCACTATGTTCTCTGCCC 1005
 Qy 841 GTAATTTATCGCGCTTACTATGGAGCATTTAAGGATGTCAAGGAGAAAAACAGGACCTCT 900
 Db 1006 GTAATTTATCGCGCTTACTATGGAGCATTTAAGGATGTCAAGGAGAAAAACAGGACCTCT 1065
 Qy 901 GAAGAAGCAGAGACCTCCGAGCCTTTCGATTTCTATCTGTGATTTCAATTTGTGACCCCT 960
 Db 1066 GAAGAAGCAGAGACCTCCGAGCCTTTCGATTTCTATCTGTGATTTCAATTTGTGACCCCT 1125
 Qy 961 TGGATTTTATCATTTTCAGATCTCCAGTATTTGGATATTTTTCACAAGATTTTCATT 1020
 Db 1126 TGGATTTTATCATTTTCAGATCTCCAGTATTTTCGGATATTTTTCACAAGATTTTCATT 1185
 Qy 1021 AGACTCTTAGGTACAGAGCCGTCGACAAATTCCTAATCAATGGAATCCAGTCTGTGA 1080
 Db 1186 AGACTCTTAGGTACAGAGCCGTCGACAAATTTCCACTAATGGAATCCAGTCTGTGA 1245

RESULT 5
 AAT37402
 ID AAT37402 standard; DNA; 1488 BP.
 XX
 AC AAT37402;
 XX
 DT 11-MAR-1997 (first entry)
 XX
 DE Prostaglandin DP receptor coding sequence.
 XX
 KW Prostaglandin DP receptor; human; prostanoid receptor; blood platelet;
 KW smooth muscle; nervous tissue; G protein-coupled receptor; modulator;
 KW mouse; prostaglandin-related disease; therapy; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 349..1429
 FT /*tag= a
 FT /product= "prostaglandin DP receptor"
 XX
 PN WO9623066-A2.
 XX
 PD 01-AUG-1996.
 XX
 PF 23-JAN-1996; 96WO-CA000047.
 XX
 PR 26-JAN-1995; 95US-00378682.
 XX
 PA (MERI) MERCK FROSST CANADA INC.
 XX
 PI Abramovitz M, Boie Y, Metters K, Sawyer N, Slipetz DM;
 XX
 DR WPI; 1996-362690/36.
 DR P-PSDB; AAW03516.
 XX
 PT Human prostaglandin DP receptor and related DNA - used to identify
 PT receptor modulators to treat prostaglandin-related diseases.
 XX
 PS Claim 4; Page 41-42; 49pp; English.
 XX
 CC This sequence represents the coding sequence for the human prostaglandin
 CC DP receptor. The DP receptor is the least ubiquitous and least abundant
 CC of the prostanoid receptors. The DP receptors are thought to be
 CC distributed mainly in blood platelets, smooth muscle of various tissues,
 CC and nervous tissue (including the central nervous system). However, many
 CC of the actions and distribution of the DP receptor is species dependent.
 CC The encoded DP receptor is a G protein-coupled receptor which can
 CC specifically bind prostaglandin molecules. This sequence was isolated
 CC using primers (see AAT37403 and AAT37404) based on the N-terminal
 CC sequence, and an internal sequence from purified mouse DP. The human
 CC prostaglandin DP receptor can be used to identify modulators of the

CC receptor. The identified modulators can then be used to treat
CC prostaglandin-related diseases, and for modulating the effects of
CC prostaglandins on the DP receptor

XX SQ Sequence 1488 BP; 232 A; 482 C; 423 G; 351 T; 0 U; 0 Other;

Query Match 100.0%; Score 1080; DB 2; Length 1488;

Best Local Similarity 100.0%; Pred. No. 1.9e-243;

Matches 1080; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy 1 ATGAAGTCGCGTCTTACCGTCGCCAGAACACCACTCTGTGGAAAAAGGCAACTCGGCG 60
Db 350 ATGAAGTCGCGGTTCTACCGTCGCCAGAACCACTCTGTGGAAAAAGGCAACTCGGCG 409
Qy 61 GTGATGGCGGGGTCTCTTCTAGACACCGGCTCTCTGGGCAACCTGCTGGCCCTGGGGCTG 120
Db 410 GTGATGGCGGGGTCTCTTCTAGACACCGGCTCTCTGGGCAACCTGCTGGCCCTGGGGCTG 469
Qy 121 CTGGCGCGCTCGGGGCTGGGGTGTGCTCGGGGGTCTCCACTGCGCGCGCTCGCTCGGTC 180
Db 470 CTGGCGCGCTCGGGGCTGGGGTGTGCTCGGGGGTCTCCACTGCGCGCGCTCGCTCGGTC 529
Qy 181 TTCTACATCTGTGTGTGGCTGTACCGGTACCGACTTGTGGGCAAGTGTCTCTTAAGC 240
Db 530 TTCTACATCTGTGTGTGGCTGTACCGGTACCGACTTGTGGGCAAGTGTCTCTTAAGC 589
Qy 241 CCGGTGGTGTGGTGTCTACGCTCAGAACCGGAGTCTGCGGGTCTTGGCGCGCGCATTCG 300
Db 590 CCGGTGGTGTGGTGTCTACGCTCAGAACCGGAGTCTGCGGGTCTTGGCGCGCGCATTCG 649
Qy 301 GACAACTGTTGTGCAAGCCTTCGCTCTTCTATGTCTTCTTTGGGCTCTCTTCGACA 360
Db 650 GACAACTGTTGTGCAAGCCTTCGCTCTTCTATGTCTTCTTTGGGCTCTCTTCGACA 709
Qy 361 CTGCAACTCTCTGGCATGGAATGTGAGTGTGGCTCTCCCTAGGGCACCTTTCTTCTAC 420
Db 710 CTGCAACTCTCTGGCATGGAATGTGAGTGTGGCTCTCCCTAGGGCACCTTTCTTCTAC 769
Qy 421 CGAGGACATACCTTCGCTGGCGCACTGTGTGGCGCGCGGTGTGAGCGCTTCTCC 480
Db 770 CGAGGACATACCTTCGCTGGCGCACTGTGTGGCGCGCGGTGTGAGCGCTTCTCC 829
Qy 481 CTGGCTTTCTCGCGCTACCTTTTCATGGGCTTCGGGAAGTTCTGTCAGTACTGCCCGCG 540
Db 830 CTGGCTTTCTCGCGCTACCTTTTCATGGGCTTCGGGAAGTTCTGTCAGTACTGCCCGCG 889
Qy 541 ACCTGGTCTTTATCCAGATGTGTCAAGAGAGGCTGTGTGCGGTGTGGGTACTCT 600
Db 890 ACCTGGTCTTTATCCAGATGTGTCAAGAGAGGCTGTGTGCGGTGTGGGTACTCT 949
Qy 601 GTGCTCTACTCAGCTCATGGCGTGTGTCTCGCCACCGTGTGTGCAACTCGGC 660
Db 950 GTGCTCTACTCAGCTCATGGCGTGTGTCTCGCCACCGTGTGTGCAACTCGGC 1009
Qy 661 GCCATGCGCAACCTCTATGCGATGACCGCGGCTGTGAGCGGCAACCGCGCTCTCGAC 720
Db 1010 GCCATGCGCAACCTCTATGCGATGACCGCGGCTGTGAGCGGCAACCGCGCTCTCGAC 1069
Qy 721 AGGACTGTGCGAGCGCGCGGACGAGGAGGAGGCTGTGTGCGCTGTGAGGAG 780
Db 1070 AGGACTGTGCGAGCGCGCGGACGAGGAGGAGGCTGTGTGCGCTGTGAGGAG 1129
Qy 781 CTGATACCTCTGCTGCTGCTGATGACCGTGTCTTCACTATGTGTCTCTGCC 840
Db 1130 CTGATACCTCTGCTGCTGCTGATGACCGTGTCTTCACTATGTGTCTCTGCC 1189
Qy 841 GTAATTTATCGCGCTTACTATGAGCAATTTAAGGATGTCAAGGAGAAAAACAGGACCTCT 900
Db 1190 GTAATTTATCGCGCTTACTATGAGCAATTTAAGGATGTCAAGGAGAAAAACAGGACCTCT 1249
Qy 901 GAAGAGCAGAGACCTCCGAGCCTTGGGATTTCTATCTGTGATTTCAATGTGACCT 960
Db 1250 GAAGAGCAGAGACCTCCGAGCCTTGGGATTTCTATCTGTGATTTCAATGTGACCT 1309
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Qy 961 TGGATTTTATCATTTTCAGATCTCCAGTATTTTCGGATATTTTTCACAGATTTTCATT 1020
Db 1310 TGGATTTTATCATTTTCAGATCTCCAGTATTTTCGGATATTTTTCACAGATTTTCATT 1369
Qy 1021 AGACCTCTTAGGTACAGGAGCGGTGCAGCAATTCCTAACTGGAATCCAGTCTGTGA 1080
Db 1370 AGACCTCTTAGGTACAGGAGCGGTGCAGCAATTCCTAACTGGAATCCAGTCTGTGA 1429

RESULT 6
ADO30026
ID ADO30026 standard; cDNA; 1077 BP.
XX AC ADO30026;
XX AC ADO30026;
XX DT 29-JUL-2004 (first entry)
XX Human GPCR PTGDR polynucleotide, SEQ ID NO:1128.
XX G protein-coupled receptor; GPCR; drug screening; diagnosis;
XX transgenic mouse; neurological disorder; adrenal gland disorder;
XX colon disorder; intestinal disorder; cardiovascular disorder;
XX muscular disorder; blood disorder; immune disorder; bone disorder;
XX joint disorder; metabolic disorder; nutritive disorder; cancer;
XX kidney disorder; liver disorder; lung disorder; breast disorder;
XX ovary disorder; uterus disorder; prostate disorder; testis disorder;
XX skin disorder; stomach disorder; pancreas disorder; spleen disorder;
XX thymus disorder; thyroid disorder; antiparkinsonian; antimanic;
XX cystostatic; antiinflammatory; vasotropic; antianginal; antiarrhythmic;
XX CNS; central nervous system; respiratory; antiarrhythmic; antidiabetic;
XX viricide; hepatotropic; antibacterial; antianaemic; antiseborrhoeic;
XX dermatological; antiulcer; antithyroid; antiallergic; anorectic;
XX immunosuppressive; nephrotropic; gene therapy; GPCR modulator; human;
XX gene; ss.
XX OS Homo sapiens.
XX WO2004040000-A2.
XX 13-MAY-2004.
XX 09-SEP-2003; 2003WO-US028226.
XX 09-SEP-2002; 2002US-0409303P.
XX 09-APR-2003; 2003US-0461329P.
XX (PRIM-) PRIMAL INC.
XX Gaitanaris GA, Bergmann JE, Gragerov A, Hohmann J, Li F;
XX Madisen L, McIlwain KL, Pavlova MN, Vassilatis D, Zeng H;
XX WPI; 2004-390329/36.
XX P-PSDB; ADO29614.
XX Novel mammalian G protein coupled receptors, useful for identifying
XX compounds that modulates diagnosing and treating disease condition
XX associated with GPCR dysfunction e.g. autoimmune diseases, angina
XX pectoris, Parkinson's disease.
XX Claim 151; SEQ ID NO 1128; 542pp; English.
XX The invention relates to human and mouse G protein-coupled receptors
XX (GPCRs) and nucleic acids encoding them. The invention also relates to
XX sequences at least 90% identical to the GPCR proteins and nucleic acids
XX of the invention; methods of treating, preventing or diagnosing diseases
XX associated with GPCRs of the invention; methods of screening for
XX compounds useful in the treatment of GPCR-related diseases; a transgenic
XX mouse comprising a GPCR gene of the invention; a mouse comprising a
XX mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived
XX from the transgenic mice; kits comprising several mice, each of which has
XX a mutation in a different GPCR gene of the invention; and kits comprising
XX probes which hybridise to GPCR polynucleotides of the invention. The
```

CC invention further discloses variants of the GPCR polypeptides and vectors
CC comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may
CC be used in the diagnosis, treatment or prevention of a wide variety of
CC diseases including neurological disorders (e.g., Alzheimer's disease,
CC depression, diabetic neuropathy, Parkinson's disease or schizophrenia);
CC disorders of the adrenal gland; disorders of the colon or intestine
CC (e.g., Crohn's disease, diarrhoea, food poisoning or irritable bowel
CC syndrome); cardiovascular disorders (e.g., angina, cardiac arrhythmia or
CC myocardial infarction); muscular disorders; blood disorders (e.g.,
CC anaemia or leukaemia); immune disorders (e.g., autoimmune disorders or
CC AIDS); bone and joint disorders (e.g., osteoarthritis, rheumatoid
CC arthritis, gout or osteoporosis); metabolic or nutritive disorders (e.g.,
CC obesity, enzyme deficiency-related diseases or vitamin deficiency-related
CC diseases); and disorders of the kidney, liver, lung, breast, ovary,
CC uterus, prostate, testis, skin, stomach, pancreas, spleen, thymus and
CC thyroid (e.g., cancers). The present sequence represents a GPCR-encoding
CC nucleic acid of the invention. Note: The full sequence data for this
CC patent did not form part of the printed specification; those sequences
CC not shown were obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 1077 BP; 169 A; 336 C; 310 G; 262 T; 0 U; 0 Other;

Query Match 99.7%; Score 1077; DB 12; Length 1077;
Best Local Similarity 100.0%; Pred. No. 8.6e-243;
Matches 1077; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAAGTCGCGGTCTTACCGCTCCAGAACACCACTCTGTGAAAGGCACTCGGG 60
DB 1 ATGAAGTCGCGGTCTTACCGCTCCAGAACACCACTCTGTGAAAGGCACTCGGG 60
QY 61 GTGATGGGCGGGTGTCTTTACGACACCGGCTCTCTGGGCAACCTGTGGCGCTGGGGCTG 120
DB 61 GTGATGGGCGGGTGTCTTTACGACACCGGCTCTCTGGGCAACCTGTGGCGCTGGGGCTG 120
QY 121 CTGGCGCGCTCGGGGTGGGGTGGTCTCGCGCGTCCACTGGCGCGCTGCCCTCGGTC 180
DB 121 CTGGCGCGCTCGGGGTGGGGTGGTCTCGCGCGTCCACTGGCGCGCTGCCCTCGGTC 180
QY 181 TTCTACATGCTGTGTGTGCGCTGACGCTCAGCGCTTGTGGGCAAGTGCCTCTCAAGC 240
DB 181 TTCTACATGCTGTGTGTGCGCTGACGCTCAGCGCTTGTGGGCAAGTGCCTCTCAAGC 240
QY 241 CCGGTGGTGTGGCTGCCTACGCTCAGAACCGGAGTCTGGGGTGTCTGGCGCGCATTTG 300
DB 241 CCGGTGGTGTGGCTGCCTACGCTCAGAACCGGAGTCTGGGGTGTCTGGCGCGCATTTG 300
QY 301 GACAACTCGTTGTGCCAAGCCTTTCATGCTCTTCTTTGGGCTCTCTCGACA 360
DB 301 GACAACTCGTTGTGCCAAGCCTTTCATGCTCTTCTTTGGGCTCTCTCGACA 360
QY 361 CTGCAACTCTGGCCATGGCACTGGAGTGTGGCTCTCCCTAGGGGACCCCTTCTCTAC 420
DB 361 CTGCAACTCTGGCCATGGCACTGGAGTGTGGCTCTCCCTAGGGGACCCCTTCTCTAC 420
QY 421 CGACGGCACATCAACCTTGGCGCTGGGCGCACTGGTGGCGCCCGGTGTGAGCGCTTCTCC 480
DB 421 CGACGGCACATCAACCTTGGCGCTGGGCGCACTGGTGGCGCCCGGTGTGAGCGCTTCTCC 480
QY 481 CTGGCTTTCTGGCGCTACCTTTTCATGGGGTTCGGGAAGTTCGTGAGTACTGCCCCGGC 540
DB 481 CTGGCTTTCTGGCGCTACCTTTTCATGGGGTTCGGGAAGTTCGTGAGTACTGCCCCGGC 540
QY 541 ACTGTGTCTTTATCCAGATGTTCACGAGGAGGCTCGCTGCGGTGTGGGTACTCT 600
DB 541 ACTGTGTCTTTATCCAGATGTTCACGAGGAGGAGGCTCGCTGCGGTGTGGGTACTCT 600
QY 601 GTGCTCTACTCCAGCTCTATGGCGCTGTGGTCTCTGCCACCGCTGTGCAACCTCGGC 660
DB 601 GTGCTCTACTCCAGCTCTATGGCGCTGTGGTCTCTGCCACCGCTGTGCAACCTCGGC 660
QY 661 GCCATCGCAACTCTTATCGATGTCACCGCGGCTGACGGGACCCGCGCTCTCGACC 720
DB 661 GCCATCGCAACTCTTATCGATGTCACCGCGGCTGACGGGACCCGCGCTCTCGACC 720

DB 661 GCCATCGCAACTCTTATCGATGTCACCGCGGCTGACGGGACCCGCGCTCTCGACC 720
QY 721 AGGGACTGTGCGGAGCGCGCGGAGCGGAGCGTCCCTCAGCCCCCTGGAGGAG 780
DB 721 AGGGACTGTGCGGAGCGCGCGGAGCGGAGCGTCCCTCAGCCCCCTGGAGGAG 780
QY 781 CTGGATCACCTCTGCTGCTGGGGCTGATGACCGTCTCTTCACTATGTGTTCTCTGCC 840
DB 781 CTGGATCACCTCTGCTGCTGGGGCTGATGACCGTCTCTTCACTATGTGTTCTCTGCC 840
QY 841 GTAATTTATCGCGCTTACTATGAGCATTTAAGGATGTCAAGGAGAAAAACAGACCTCT 900
DB 841 GTAATTTATCGCGCTTACTATGAGCATTTAAGGATGTCAAGGAGAAAAACAGACCTCT 900
QY 901 GAAGAAGCAGAAAGACCTCCGAGCCTTTCGATTTCTATCTGTGATTTCAATTTGGACCT 960
DB 901 GAAGAAGCAGAAAGACCTCCGAGCCTTTCGATTTCTATCTGTGATTTCAATTTGGACCT 960
QY 961 TGGATTTTATCATTTTTCAGATCTCCAGTATTTTCGGATATTTTTCACAAGATTTTCAT 1020
DB 961 TGGATTTTATCATTTTTCAGATCTCCAGTATTTTTCGGATATTTTTCACAAGATTTTCAT 1020
QY 1021 AGACCTCTTTAGGTACAGGAGCGGTGACCAATTTCCACTAATCCAGTCTG 1077
DB 1021 AGACCTCTTTAGGTACAGGAGCGGTGACCAATTTCCACTAATCCAGTCTG 1077
RESULT 7
AAZ27056
ID AAA27056 standard; cDNA; 1264 BP.
XX
AC AAA27056;
XX AC
DT 22-AUG-2000 (first entry)
XX
DE Human cell surface receptor protein cDNA sequence #13.
XX
KW Human; HCSR; cytostatic; antiarthritic; antirheumatic; antiasthmatic;
KW immunosuppressive; antiarteriosclerotic; antibacterial; antiparasitic;
KW neuroprotective; nootropic; anticonvulsant; cancer; leukaemia; melanoma;
KW rheumatoid arthritis; asthma; atherosclerosis; akathesia;
KW Alzheimer's diseases; multiple sclerosis; epilepsy; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 130..1239
FT /*tag= a
FT /product= "HCSR-13"
XX
PN WO200028032-A2.
XX
PD 18-MAY-2000.
XX
PF 12-NOV-1999; 99WO-US026742.
XX
PR 12-NOV-1998; 98US-00191280.
PR 07-DEC-1998; 98US-00206647.
PR 08-MAR-1999; 99US-0123404P.
XX
PA (INCY-) INCYTE PHARM INC.
XX
PI Tang YT, Corley NC, Guegler KJ, Yue H, Baughn MR, Lal P;
PI Hillman JL, Bandman O, Azimzai Y, Au-Young J;
XX
DR WPI; 2000-376546/32.
DR P-PSDB; AAY94346.
XX
PT New human cell surface receptor protein and polynucleotide useful for
PT diagnosis, prevention and treatment of cancer, immune disorders,
PT infection and neuronal disorders.
XX
PS Claim 9; Page 97; 97pp; English.

XX The present sequence encodes a novel human cell surface receptor protein
 CC (HCSR) designated HCSR-13. The nucleotide sequence was identified in
 CC Incyte Clone 3576503 from the cDNA library BRONOT01, which was made from
 CC RNA isolated from bronchial tissue. A number of Incyte Clones were used
 CC to assemble the consensus sequence. BLAST analysis showed that the
 CC sequence is homologous to DR prostanoil receptor g940379. HCSR and its
 CC antagonist are useful for preventing or treating disorders associated
 CC with decreased or increased expression or activity of HCSR. Such
 CC disorders include cancers such as leukaemia and melanoma, immune
 CC disorders such as rheumatoid arthritis, asthma and atherosclerosis,
 CC bacterial and parasitic infections and neuronal disorders such as
 CC akathisia, Alzheimer's disease, multiple sclerosis and epilepsy.
 CC Polynucleotides encoding HSCRs may be used as hybridisation probes to
 CC diagnose these conditions. Anti-HCSR antibodies may be used as
 CC antagonists, as a targeting or delivery mechanism for bringing
 CC pharmaceutical agents into contact with cells or tissues expressing HCSR
 CC and for diagnosis of HCSR-related disorders. HCSR and its catalytic or
 CC immunogenic fragments are useful for drug screening using libraries of
 CC compounds
 XX
 SQ Sequence 1264 BP; 189 A; 404 C; 368 G; 303 T; 0 U; 0 Other;

Query Match 97.4%; Score 1051.6; DB 3; Length 1264;
 Best Local Similarity 99.4%; Pred. No. 8.4e-237;
 Matches 1076; Conservative 0; Mismatches 4; Indels 2; Gaps 2;

1 ATGAAGTCGCGGTTTACCGCTCCGAGACACACACCTCTGTGGAAAGGCAACTCGGCG 60
 130 ATGAAGTCGCGGTTTACCGCTCCGAGACACACACCTCTGTGGAAAGGCAACTCGGCG 189

61 GTGATGGGGGGGTGCTCTTACGACCGGCTCCGAGCACTGCTGGCCCTGGGGCTG 120
 190 GTGATGGGGGGGTGCTCTTACGACCGGCTCCGAGCACTGCTGGCCCTGGGGCTG 249

121 CTGGCGCGCTCGGGGCTGGGGTGGTCTCGCGCGCTCCACTGCGCCGCTCGGCTC 180
 250 CTGGCGCGCTCGGGGCTGGGGTGGTCTCGCGCGCTCCACTGCGCCGCTCGGCTC 309

181 TTCTACATCTGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 240
 310 TTCTACATCTGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 369

241 CGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 300
 370 CGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 429

301 GACAACTCGTTGTGCAAGCCTTTCCTTTCATGTCCTTTCCTTTCCTTTCCTTTCCT 360
 430 GACAACTCGTTGTGCAAGCCTTTCCTTTCATGTCCTTTCCTTTCCTTTCCTTTCCT 489

361 CTGCAACTCTGCGCATGAGCTGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 420
 490 CTGCAACTCTGCGCATGAGCTGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 549

421 CGACGSCACATCACCTCGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGG 480
 550 CGACGSCACATCACCTCGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGG 609

481 CTGGCTTTCTGGGCGCTACCTTTTCATGGGCTTTCGGGAAGTTCGTGAGTACTGCCCGCG 540
 610 CTGGCTTTCTGGGCGCTACCTTTTCATGGGCTTTCGGGAAGTTCGTGAGTACTGCCCGCG 669

541 ACTGTGTCTTATTCAGATGTCACAGAGAGGCTCGCTGCTGGTGGTGGTGGTGGTGGTGG 600
 670 ACTGTGTCTTATTCAGATGTCACAGAGAGGCTCGCTGCTGGTGGTGGTGGTGGTGGTGG 729

601 GTGCTCTACTCAGGCTCATGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCT 660
 730 GTGCTCTACTCAGGCTCATGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCT 789

661 GCCATCGCAACCTCTATGCGATGACCGCGGCTGTCAGCGGACCGCGGCTCTCTGCACC 720

Db 790 GCCATCGCAACCTCTATGCGATGACCGGGGCTGACGGGACCCGGCTCTCTGCACC 849
 Qy 721 AGGACTGTGCGAGCGCGCGCGGAGGAGCGTCCCTCAGCCCTGGAGGAG 780
 Db 850 AGGACTGTGCGAGCGCGCGGAGGAGCGTCCCTCAGCCCTGGAGGAG 909
 Qy 781 CTGGATCACTCTGCTGCTGCGCTGATGACCGCTCTTTCACATGATGTTCTCTGCC 840
 Db 910 CTGGATCACTCTGCTGCTGCGCTGATGACCGCTCTTTCACATGATGTTCTCTGCC 969
 Qy 841 GTAATTATCGGCTTACTATGAGCATTTAAGGATGTCAAGGAGAAAAACAGGACCTCT 900
 Db 970 GTAATTATCGGCTTACTATGAGCATTTAAGGATGTCAAGGAGAAAAACAGGACCTCT 1029
 Qy 901 GAAGAGCAGA-AGACCTCCGAGCGCTTCGATTTCTATCTGATTTCAATTTGTGACCC 959
 Db 1030 GAAGAACAGAGAGACCTCCGAGCGCTTCGATTTCTATCTGATGTCAATTTGTGACCC 1089
 Qy 960 TTGGATTTTATCATTTTTCAGATCTCCAGTATTTTCGGATATTTTTCACAAGA-TTTTCA 1018
 Db 1090 TTGGATTTTATCATTTTTCAGATCTCCAGTATTTTCGGATATTTTTCACAAGA-TTTTCA 1149
 Qy 1019 TTAGACCTTTTAGGTACAGGAGCGGTGACGAATTCACATGAATCCAGTCTGT 1078
 Db 1150 TTAGACCTTTTAGGTACAGGAGCGGTGACGAATTCACATGAATCCAGTCTGT 1209
 Qy 1079 GA 1080
 Db 1210 GA 1211

RESULT 8
 ADE07082
 ID ADE07082 standard; DNA; 1505 BP.
 XX
 AC ADE07082;
 XX
 DT 29-JAN-2004 (first entry)
 XX
 DE Novel coding sequence (useful for identifying genetic disorders) #148.
 XX
 KW novel gene; novel protein; tissue marker; molecular weight marker;
 KW chromosome marker; genetic disorder; gene; ds.
 OS Unidentified.
 XX
 PN WO2003054152-A2.
 XX
 PD 03-JUL-2003.
 XX
 PF 10-DEC-2002; 2002WO-US039555.
 XX
 PR 10-DEC-2001; 2001US-0339739P.
 PR 11-DEC-2001; 2001US-0339453P.
 PR 14-MAR-2002; 2002US-0365091P.
 PR 14-MAR-2002; 2002US-0365384P.
 PR 12-APR-2002; 2002US-0372381P.
 PR 12-APR-2002; 2002US-0372615P.
 PR 22-APR-2002; 2002US-00128558.
 PR 24-APR-2002; 2002US-0376045P.
 XX
 XX (HYSE-) HYSEQ INC.
 XX
 PI Tang YT, Asundi V, Goodrich RW, Ren F, Zhang J, Zhao QA, Wang J;
 PI Ghosh M, Xue AJ, Wehrman T, Weng G, Zhou P, Drmanac R, Wang Z;
 PI Ma Y, Wang D, Chen R, Xu C, Boyle BJ;
 XX
 DR WPI: 2003-569235/53.
 DR P-PSDB; ADE07993.
 XX
 PT New polynucleotides, useful for expressing recombinant proteins for
 PT analysis, characterization or therapeutic use, or as markers for tissues
 PT in which the corresponding protein is preferentially expressed.

XX
PS
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CC
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SQ

Claim 1; SEQ ID NO 148; 1177pp; English.

The invention comprises the amino acid and coding sequences of novel proteins. The DNA and protein sequences of the invention are useful as: markers for tissues in which the corresponding protein is preferentially expressed; as molecular weight markers on gels; as chromosome markers or tags; to identify chromosomes or to map related gene positions; and to compare with endogenous DNA sequences in patients to identify potential genetic disorders. The present DNA sequence represents a gene of the invention.

Sequence 1505 BP; 265 A; 434 C; 441 G; 365 T; 0 U; 0 Other;

Query Match 83.4%; Score 900.4; DB 10; Length 1505;
Best Local Similarity 89.3%; Pred. No. 2.8e-201;
Matches 1034; Conservative 0; Mismatches 1; Indels 123; Gaps 1;

QY 1 ATGAAGTCCGCGTCTACCGCTGCCAGAACACCACTCTGTGAAAGGCAACTCGGCG 60
DB |||||
QY 61 GTGATGGGGGGTGTCTTTCAGCACCGGCTCTCTGGGCAACCTGTGGCCCTTGGGGCTG 120
DB |||||
QY 291 GTGATGGGGGGTGTCTTTCAGCACCGGCTCTCTGGGCAACCTGTGGCCCTTGGGGCTG 350
DB |||||
QY 121 CTGGCGCGTCTGGGGTGGGGTGGTCTCGCGCGTCCACTGCGCGCGCTGCCCTCGGTC 180
DB |||||
QY 351 CTGGCGCGTCTGGGGTGGGGTGGTCTCGCGCGTCCACTGCGCGCGCTGCCCTCGGTC 410
DB |||||
QY 181 TTCTACATGCTGTGTGGCTGTGAGGTCACCGACTTGTGGGCAAGTGCCTCTTAAGC 240
DB |||||
QY 411 TTCTACATGCTGTGTGGCTGTGAGGTCACCGACTTGTGGGCAAGTGCCTCTTAAGC 470
DB |||||
QY 241 CGGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 300
DB |||||
QY 471 CGGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 530
DB |||||
QY 301 GACAACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 360
DB |||||
QY 531 GACAACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 590
DB |||||
QY 361 CTGCAACTCTGGCCATGACATGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 420
DB |||||
QY 591 CTGCAACTCTGGCCATGACATGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 650
DB |||||
QY 421 CGAGGCAATACATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 480
DB |||||
QY 651 CGAGGCAATACATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 710
DB |||||
QY 481 CTGGCTTTCTGGCGCTACTCTTTTCATGGGCTTCGGGAAGTTCGTGAGTACTGCCCCGGC 540
DB |||||
QY 711 CTGGCTTTCTGGCGCTACTCTTTTCATGGGCTTCGGGAAGTTCGTGAGTACTGCCCCGGC 770
DB |||||
QY 541 ACCTGTGTCTTTATCCAGATGTTCACGAGAGGGCTCGTGTGTGTGTGTGTGTGTGTGTGTGT 600
DB |||||
QY 771 ACCTGTGTCTTTATCCAGATGTTCACGAGAGGGCTCGTGTGTGTGTGTGTGTGTGTGTGTGT 830
DB |||||
QY 601 GTGCTTACTCCAGCTCATGGCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 660
DB |||||
QY 831 GTGCTTACTCCAGCTCATGGCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 890
DB |||||
QY 661 GCATGCGCAACCTCTATGCGATGACACCGCGGCTCGAGCGGCAACCGGGCTCTCTGACCC 720
DB |||||
QY 891 GCATGCGCAACCTCTATGCGATGACACCGCGGCTCGAGCGGCAACCGGGCTCTCTGACCC 950
DB |||||
QY 721 AGGACTGTGCCAGCGCGCGCGGAGAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 780
DB |||||
QY 951 AGGACTGTGCCAGCGCGCGCGGAGAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1010
DB |||||
QY 781 CTGGATCACTCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 840
DB |||||
QY 1011 CTGGATCACTCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1070
DB |||||

QY 841 GTAATT----- 846
DB |||||
QY 1071 GTAATTGTGAGTCCCGGGCCCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1130
DB |||||
QY 847 ----- 846
DB |||||
QY 1131 CGGGGGGGAAGGTTGGAGCGGATCGGGATGAGCGGGCGCCAGGAGGAGGAGGAGGAGGAGGAGG 1190
DB |||||
QY 847 -----TATCGGCTTTACTATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 897
DB |||||
QY 1191 GCCAGGAAGTATCGGCTTACTATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1250
DB |||||
QY 898 TCTGAAGAGCAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 957
DB |||||
QY 1251 TCTGAAGAGCAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1310
DB |||||
QY 958 CTTTGGATTTTATCATTTTTCAGATCTCCAGTATTTTCGATATTTTCGATATTTTTCACAGATTTTC 1017
DB |||||
QY 1311 CTTTGGATTTTATCATTTTTCAGATCTCCAGTATTTTCGATATTTTTCGATATTTTTCACAGATTTTC 1370
DB |||||
QY 1018 ATTAGACCTCTTTAGGTAC 1035
DB |||||
QY 1371 ATTAGACCTCTTTAGGTAC 1388
DB |||||

RESULT 9
AAA35105
ID AAA35105 standard; DNA; 1216 BP.
XX
AC AAA35105;
XX
DT 28-JUL-2000. (first entry)
XX
DE Human adenosine receptor related polynucleotide SEQ ID NO:2794.
DE
KW Human; adenosine receptor; low adenosine antisense oligonucleotide;
KW phosphorothioate; impaired respiration; inflammation; inhibitor; allergy;
KW allergic disease; bronchoconstriction; analgesic; antinflammatory;
KW antiallergic; antiasthmatic; cytosolic; analgesic; impaired airway;
KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
OS Homo sapiens.
XX
PN WO200009525-A2.
XX
PD 24-FEB-2000.
XX
PF 03-AUG-1999; 99WO-US017712.
XX
PR 03-AUG-1998; 98US-0095212P.
XX
PA (UYBC-) UNIV EAST CAROLINA.
XX
PI Nyce JW;
XX
DR WPI; 2000-205971/18.
XX
PT New antisense oligonucleotides useful for treating e.g. pulmonary
PT vasoconstriction, inflammation, allergies, asthma, hypertension,
PT bronchitis; emphysema, respiratory distress syndrome, ischemia or
PT cancers.
XX
PS Disclosure; Page 1060; 1343pp; English.
XX
CC The present invention describes a new composition comprising an antisense
CC oligonucleotide (ON) with low adenosine (up to 15%), which targets
CC nucleic acids involved in bronchoconstriction, allergies, and/or
CC inflammation. The ON can have antinflammatory, antiallergic,
CC antiasthmatic, cytosolic and analgesic activities. The compositions are

receptors, CNS and peripheral nervous and non-nervous system peptide transmitters, defensins, growth factors, vasoactive peptides and receptors, binding proteins and malignancy associated proteins. The antisense oligonucleotides may be used in this way to treat disorders including respiratory obstruction (especially pulmonary obstruction and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or surfactant hypoproduction which are associated with a disease or condition selected from pulmonary vasoconstriction, inflammation, allergies, asthma, impeded respiration, respiratory distress syndrome (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary hypertension, emphysema, chronic obstructive pulmonary disease (COPD), pulmonary transplantation rejection, pulmonary infections, bronchitis, and/or cancer. AAF18434 to AAF21543 represent human polynucleotide fragments and antisense oligonucleotides used in the exemplification of the present invention

XX
SQ Sequence 1216 BP; 153 A; 431 C; 371 G; 261 T; 0 U; 0 Other;

Query Match 78.3%; Score 846; DB 3; Length 1216;
Best Local Similarity 100.0%; Pred. No. 1.6e-186;
Matches 846; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAAGTCGCGGTTCTTACCGCTGCCAGAACACACACCTCTGTGAAAAAGCAACTCGCGG 60
DB 350 ATGAAGTCGCGGTTCTTACCGCTGCCAGAACACACCTCTGTGAAAAAGCAACTCGCGG 409
QY 61 GTGATGGCGGGGTGCTTCTTACGACACCGCCCTCTCTGGGCAACCTGTGCGCCCTCGGGGTG 120
DB 410 GTGATGGCGGGGTGCTTCTTACGACACCGCCCTCTCTGGGCAACCTGTGCGCCCTCGGGGTG 469
QY 121 CTGGCGCGCTCGGGGTGCGGTGGTCTCGCGCGTCCACTGCGCCCGCTGCGCTCGGTTC 180
DB 470 CTGGCGCGCTCGGGGTGCGGTGGTCTCGCGCGTCCACTGCGCCCGCTGCGCTCGGTTC 529
QY 181 TTCTACATCTGCTGTGTGCGCTGAGGTCACCGAGTCTGCGGCAAGTCCCTCTTAAGC 240
DB 530 TTCTACATCTGCTGTGTGCGCTGAGGTCACCGAGTCTGCGGCAAGTCCCTCTTAAGC 589
QY 241 CCGGTGGTGTGCTGCTGCTACGCTCAGAACCGGAGTCTGCGGGTGTCTGCGCCCGCATTTG 300
DB 590 CCGGTGGTGTGCTGCTGCTACGCTCAGAACCGGAGTCTGCGGGTGTCTGCGCCCGCATTTG 649
QY 301 GACAACTGCTGTGCCAAGCCTTTCATGTCTCTTTTGGGTCTCTCTCGAC 360
DB 650 GACAACTGCTGTGCCAAGCCTTTCATGTCTCTTTTGGGTCTCTCTCGAC 709
QY 361 CTGGCACTCTCGGCATGCACTGGAGTCTGCTCTCCCTAGGCAACCTTCTTCTAC 420
DB 710 CTGGCACTCTCGGCATGCACTGGAGTCTGCTCTCCCTAGGCAACCTTCTTCTAC 769
QY 421 CGACGGCACAATCACCTCGCGCTGCGCGCACTGCTGGCCCGGTGTGAGCGCTTCTCC 480
DB 770 CGACGGCACAATCACCTCGCGCTGCGCGCACTGCTGGCCCGGTGTGAGCGCTTCTCC 829
QY 481 CTGGCTTTCTGGCGCTACTTTTCATGGGCTTCGGGAAGTTCGTGAGTACTGCCCCCGG 540
DB 830 CTGGCTTTCTGGCGCTACTTTTCATGGGCTTCGGGAAGTTCGTGAGTACTGCCCCCGG 889
QY 541 ACCTGTGCTTTTATCCAGATGTCCACGAGGAGGCTCGCTGCTGCTGGGTGCTGCTACT 600
DB 890 ACCTGTGCTTTTATCCAGATGTCCACGAGGAGGCTCGCTGCTGCTGGGTGCTGCTACT 949
QY 601 GTGCTTCTACTCCAGCTCATGCGGTGTGCTGCTGCTGCCACCGTGTGTGCAACTCTCGG 660
DB 950 GTGCTTCTACTCCAGCTCATGCGGTGTGCTGCTGCTGCCACCGTGTGTGCAACTCTCGG 1009
QY 661 GCATGCGCAACTCTATCGATGACACCGCGGCTGACGCGGACCCCGCTCTCTGACAC 720
DB 1010 GCATGCGCAACTCTATCGATGACACCGCGGCTGACGCGGACCCCGCTCTCTGACAC 1069
QY 721 AGGGAAGTGTGCGAGCGCGCGGACGAGGAGGCTGCTCCCTCAGCCCTGAGGAG 780
DB 1070 AGGGAAGTGTGCGAGCGCGCGGACGAGGAGGAGGCTGCTCCCTCAGCCCTGAGGAG 1129

QY 781 CTGGATCACCTCTCTGCTGCTGCGGTGATGACCGTGTCTTCACTATGTTCTCTGCC 840
DB 1130 CTGGATCACCTCTCTGCTGCTGCGGTGATGACCGTGTCTTCACTATGTTCTCTGCC 1189
QY 841 GTAATT 846
DB 1190 GTAATT 1195
RESULT 11
ABZ96921
ID ABZ96921 standard; DNA; 1216 BP.
XX AC ABZ96921;
XX DT 17-OCT-2003 (first entry)
XX Human nucleic acid sequence.
DE Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX Homo sapiens.
OS WO200295308-A2.
XX 31-OCT-2002.
PD 23-APR-2002; 2002WO-US013135.
PF 24-APR-2001; 2001US-0286137P.
PR (EPIG-) EPIGENESIS PHARM INC.
XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX WPI; 2003-229219/22.
DR Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX Disclosure; SEQ ID NO 12163; 872pp; English.
XX The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX Sequence 1216 BP; 153 A; 431 C; 371 G; 261 T; 0 U; 0 Other;
SQ

Query Match		78.3%;	Score 846;	DB 10;	Length 1216;		
Best Local Similarity		100.0%;	Pred. No. 1.6e-188;				
Matches 846;		Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;		
QY	1	ATGAAGTCGCGCTTTACCGCTGCCAGAACACCACTCTGTGTGAAAAAGGCAACTCGGCG	60				
Db	350	ATGAAGTCGCGCTTTACCGCTGCCAGAACACCACTCTGTGTGAAAAAGGCAACTCGGCG	409				
QY	61	GTGATGGGGGGGTGTCTTTACGACACCGGCTCTCTGGGCAACCTGCTGGGCCCTGGGGCTG	120				
Db	410	GTGATGGGGGGGTGTCTTTACGACACCGGCTCTCTGGGCAACCTGCTGGGCCCTGGGGCTG	469				
QY	121	CTGGCGCGCTCGGGGCTGGGGTGGTGTCTCGCGCGTCCACTGCGCCCGCTGCCTCGGTC	180				
Db	470	CTGGCGCGCTCGGGGCTGGGGTGGTGTCTCGCGCGTCCACTGCGCCCGCTGCCTCGGTC	529				
QY	181	TTCTACATGCTGGTGTGTGGCTGTGACCGGTCAACCGACTTGTGTGGCAAGTGCCTCTAAGC	240				
Db	530	TTCTACATGCTGGTGTGTGGCTGTGACCGGTCAACCGACTTGTGTGGCAAGTGCCTCTAAGC	589				
QY	241	CCGTTGTGTGGCTGCTACGCTCAGAACCGGAGTCTGCGGGTGTCTTGCGCCGCAATTG	300				
Db	590	CCGTTGTGTGGCTGCTACGCTCAGAACCGGAGTCTGCGGGTGTCTTGCGCCGCAATTG	649				
QY	301	GACAACTCGTTGTGCCAAGCCTTCGCCCTTCTTCATGTCTTCTTTGGGCTCTCTCTGACA	360				
Db	650	GACAACTCGTTGTGCCAAGCCTTCGCCCTTCTTCATGTCTTCTTTGGGCTCTCTCTGACA	709				
QY	361	CTGCAACTCTGGCCATGGCACTGGAGTGTGGCTCTCCCTAGGCAACCTTTCTTCTAC	420				
Db	710	CTGCAACTCTGGCCATGGCACTGGAGTGTGGCTCTCCCTAGGCAACCTTTCTTCTAC	769				
QY	421	CGACGGCACAATCACCCTGGGCGCACTGTTGGCCCGGTTGGTGGCTCTCTCC	480				
Db	770	CGACGGCACAATCACCCTGGGCGCACTGTTGGCCCGGTTGGTGGCTCTCTCC	829				
QY	481	CTGGCTTTCTGGCGCTACCTTTTCATGGGCTTCGGGAAGTTCGTGCAGTACTGCCCGGC	540				
Db	830	CTGGCTTTCTGGCGCTACCTTTTCATGGGCTTCGGGAAGTTCGTGCAGTACTGCCCGGC	889				
QY	541	ACCTGGTCTTTATCCAGATGTGCCAGAGAGGCTCGCTGTCGTGCTGGGGTACTCT	600				
Db	890	ACCTGGTCTTTATCCAGATGTGCCAGAGAGGCTCGCTGTCGTGCTGGGGTACTCT	949				
QY	601	GTGCTCTACTCCAGCTCATGGCGCTGCTGCTCTCGCCACCGTGTGTGCAACCTCGGC	660				
Db	950	GTGCTCTACTCCAGCTCATGGCGCTGCTGCTCTCGCCACCGTGTGTGCAACCTCGGC	1009				
QY	661	GCCATGCGCAACTCTATGCGATGCACCGCGGCTGCAGCGGCACCCGCGCTCTCTGACC	720				
Db	1010	GCCATGCGCAACTCTATGCGATGCACCGCGGCTGCAGCGGCACCCGCGCTCTCTGACC	1069				
QY	721	AGGGACTGTGCCGAGCGCGCGGAGCGGAGGAGCGTCCCTCAGCCCCCTGGAGGAG	780				
Db	1070	AGGGACTGTGCCGAGCGCGCGGAGCGGAGGAGCGTCCCTCAGCCCCCTGGAGGAG	1129				
QY	781	CTGGATCACTCTGCTGGGCTGTGATGACCGTGTCTTCACTATGTGTCTCTGCC	840				
Db	1130	CTGGATCACTCTGCTGGGCTGTGATGACCGTGTCTTCACTATGTGTCTCTGCC	1189				
QY	841	GTAAAT 846					
Db	1190	GTAAAT 1195					
RESULT 12							
ACA56876							
ID	ACA56876 standard; cDNA; 1216 BP.						
XX							
AC	ACA56876;						
XX							
DT	06-JUN-2003 (first entry)						

RESULT 12

ACAS6876
ID ACAS6876 standard; cDNA; 1216 BP.

XX ACAS6876;

AC ACAS6876;

XX DT 06-JUN-2003 (first entry)

XX	Human signalling pathway polynucleotide probe SEQ ID NO 1474.	
DE	Human; probe; ss; array element; Parkinson's disease;	
XX	signalling pathway population; cancer; adenocarcinoma; leukaemia;	
KW	immunopathy; AIDS; asthma; neuropathy; Alzheimer's disease; microarray.	
XX	Homo sapiens.	
XX	US6500938-B1.	
XX	31-DEC-2002.	
XX	30-JAN-1998; 98US-00016434.	
XX	30-JAN-1998; 98US-00016434.	
XX	(INCY-) INCYTE GENOMICS INC.	
PA	Au-Young J, Seilhamer JJ;	
PI	WPI; 2003-352189/33.	
XX	Combination of polynucleotide probes, useful as array elements in a	
PT	microarray for monitoring the expression of a number of target	
PT	polynucleotides.	
XX	Claim 1; SEQ ID NO 1474; 65pp; English.	
XX	The invention relates to a combination which, comprises a number of	
CC	polynucleotide probes comprising a sequence selected from one of the 1490	
CC	sequences mentioned in the specification. The combination is useful as an	
CC	array element in a microarray for monitoring the expression of a number	
CC	of target polynucleotides. The microarray is particularly useful in the	
CC	diagnosis and treatment of cancer and immunopathology and neuropathology.	
CC	The microarray is useful in diagnostics and treatment regimens, drug	
CC	discovery and development, toxicological and carcinogenicity studies,	
CC	forensics and pharmacogenomics. The microarray is also useful for	
CC	monitoring progression of diseases and for developing sophisticated	
CC	profiles for the effects of currently available therapeutic drugs. The	
CC	combination is also useful for purifying a subpopulation of mRNAs, cDNAs	
CC	and genomic fragments and in research and diagnostic applications. The	
CC	array can detect changes in expression in a large number of genes coding	
CC	for different signaling pathway populations which can be used to diagnose	
CC	various diseases including cancer e.g. adenocarcinoma and leukaemia,	
CC	immunopathies e.g. AIDS and asthma, neuropathies e.g. Alzheimer's disease	
CC	and Parkinson's disease. The present sequence represents a polynucleotide	
CC	probe of the invention. Note: The sequence data for this patent did not	
CC	form part of the printed specification but was obtained in electronic	
CC	format directly from USPTO at	
CC	seqdata.uspto.gov/sequence.html?DocID=06500938B1	
XX	Sequence 1216 BP; 153 A; 431 C; 371 G; 261 T; 0 U; 0 Other;	
Query Match		78.3%; Score 846; DB 10; Length 1216;
Best Local Similarity		100.0%; Pred. No. 1.6e-188;
Matches 846;		Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1	ATGAAGTCGCGCTTTACCGCTGCCAGAACACCACTCTGTGAAAAAGGCAACTCGCGG 60
Db	350	ATGAAGTCGCGCTTTACCGCTGCCAGAACACCACTCTGTGAAAAAGGCAACTCGCGG 409
QY	61	GTGATGGGGGGGGTCTCTTACGACACCGGCTCTCTGGGCAACCTGCTGGCCCTGGGGCTG 120
Db	410	GTGATGGGGGGGGTCTCTTACGACACCGGCTCTCTGGGCAACCTGCTGGCCCTGGGGCTG 469
QY	121	CTGGCGCGCTCGGGGCTGGGGTGGTGTCTCGCGCGCTCCACTGCGCGCGCTCGGTC 180
Db	470	CTGGCGCGCTCGGGGCTGGGGTGGTGTCTCGCGCGCTCCACTGCGCGCGCTCGGTC 529
QY	181	TTCTACATGCTGGTGTGTGGCTGTGACCGGTCACTGCTGGGCAAGTGCCTCTCTAAGC 240
Db	530	TTCTACATGCTGGTGTGTGGCTGTGACCGGTCACTGCTGGGCAAGTGCCTCTCTAAGC 589

QY	241	CCGGTGTGTGGCTGGCTACGCTCAGAACCGGAGTCTGGGGTGTCTTGGCCCGCGATTG	300
DB	590	CCGGTGTGTGGCTGGCTACGCTCAGAACCGGAGTCTGGGGTGTCTTGGCCCGCGATTG	649
QY	301	GACAACTCGTTGTGCCAAGCCTTCGCTTCTTCAATGTCCTTCTTTTGGCTCTCTCTCGACA	360
DB	650	GACAACTCGTTGTGCCAAGCCTTCGCTTCTTCAATGTCCTTCTTTTGGCTCTCTCTCGACA	709
QY	361	CTGCAACTCTCTGGCCATCGCACTGGAGTGTGGTCTCTCCCTAGGGCACCCCTTTCTTCTAC	420
DB	710	CTGCAACTCTCTGGCCATGSCACTGAGTGTGGTCTCTCCCTAGGGCACCCCTTTCTTCTAC	769
QY	421	CGACGGCACATACCCCTGCGCTTGGCGCACATGCTGTGCGCCCGTGTGAGCGCCTTCTTCC	480
DB	770	CGACGGCACATACCCCTGCGCTTGGCGCACATGCTGTGCGCCCGTGTGAGCGCCTTCTTCC	829
QY	481	CTGGCTTTCTGGCGCTACCTTTTCATGGGCTTCGGAAGTTCGTGCAGTACTGCCCCGGC	540
DB	830	CTGGCTTTCTGGCGCTACCTTTTCATGGGCTTCGGAAGTTCGTGCAGTACTGCCCCGGC	889
QY	541	ACCTGGTGTCTTTATCCAGATGGTCCACGAGGAGGGCTCGCTGTCTGGTGTCTGGGGTACTCT	600
DB	890	ACCTGGTGTCTTTATCCAGATGGTCCACGAGGAGGGCTCGCTGTCTGGTGTCTGGGGTACTCT	949
QY	601	GTGCTCTACTCCAGCCTCATGGCGCTGCTGTCTCTCGCCACCGTGTGTGCAACTTCGGC	660
DB	950	GTGCTCTACTCCAGCCTCATGGCGCTGCTGTCTCTCGCCACCGTGTGTGCAACTTCGGC	1009
QY	661	GCCATGGCGAACCTTATGATGATGACCGCGCGCTGCAGCGGCACCCGGCTCTCTGACC	720
DB	1010	GCCATGGCGAACCTTATGATGATGACCGCGCGCTGCAGCGGCACCCGGCTCTCTGACC	1069
QY	721	AGGACTGTGCCAGCCGCGCGCGAGCGGAGGAGGAGCGTCCCTCAGCCCTGGAGGAG	780
DB	1070	AGGACTGTGCCAGCCGCGCGCGAGCGGAGGAGGAGCGTCCCTCAGCCCTGGAGGAG	1129
QY	781	CTGGATCACCTCTGTCTGTGGCGCTGATGACCGTGTCTTCTCAATGTGTCTTCTGCC	840
DB	1130	CTGGATCACCTCTGTCTGTGGCGCTGATGACCGTGTCTTCTCAATGTGTCTTCTGCC	1189
QY	841	GTAATT 846	
DB	1190	GTAATT 1195	
RESULT 13			
ABD20770			
ID	ABD20770 standard; DNA; 1216 BP.		
XX			
AC	ABD20770;		
XX			
DT	29-JUL-2004 (first entry)		
XX			
DE	Human pulmonary and inflammatory target DNA #381.		
XX			
KW	Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;		
KW	respiratory tract inflammation; adenosine sensitivity; lung; cancer;		
KW	surfactant depletion; antiallergic; antiinflammatory; antiasthmatic;		
KW	analgesic; hypotensive; immunosuppressive; cycostatic; cystic fibrosis;		
KW	beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;		
KW	respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;		
KW	emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;		
KW	pulmonary transplantation rejection; ds.		
XX			
OS	Homo sapiens.		
XX			
PN	WO200285309-A2.		
XX			
XX	31-OCT-2002.		
PD			
XX			
XX	23-APR-2002; 2002WO-US013143.		
PF			
XX			

PR	24-APR-2001; 2001US-0286036P.
XX	(EPIG-) EPIGENESIS PHARM INC.
PA	
PI	Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI	Miller S, Tang L, Shahabuddin S;
XX	
DR	WPT: 2003-093058/08.
XX	
PT	Pharmaceutical composition for treating asthma, has antisense
PT	oligonucleotide containing less percentage of adenosine, targeted to
PT	nucleic acids associated with lung airway or lung dysfunction, and
PT	bronchodilating agent.
XX	
PS	Claim 15; SEQ ID NO 12163; 763pp; English.
XX	
CC	This invention describes a novel composition (a) a first active agent,
CC	comprising oligonucleotides, effective for alleviating
CC	bronchoconstriction, respiratory tract inflammation, allergies and
CC	reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors;
CC	surfactant depletion or hyposecretion, when administered to a mammal. The
CC	oligonucleotides are derived from a gene encoding or regulating
CC	expression of a target polypeptide associated with lung airway or lung
CC	dysfunction or cancer and can be anti-sense to the corresponding mRNA.
CC	The invention also describes a kit, that comprises: (a) a delivery
CC	device, in separate containers, (b) the oligonucleotides, (c)
CC	instructions for adding a carrier and for use of the kit. The composition
CC	of the invention has antiallergic, antiinflammatory, antiasthmatic,
CC	analgesic, hypotensive, immunosuppressive and cytostatic activity, is a
CC	beta-adrenergic agonist. The composition is useful for preventing or
CC	treating a respiratory, lung or malignant disease. The administered
CC	composition comprises oligo and is administered to reduce the production
CC	or availability, or to increase the degradation of the target mRNA or to
CC	reduce the amount of target polypeptide present in the lungs. The
CC	pulmonary obstruction, and/or bronchoconstriction and/or lung
CC	inflammation, allergies and/or surfactant hypo-production are associated
CC	with a disease or condition such as pulmonary vasoconstriction,
CC	inflammation, allergies, asthma, impeded respiration, respiratory
CC	distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
CC	hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary
CC	transplantation rejection, pulmonary infections, bronchitis or cancer.
CC	The reduced adenosine content of the anti-sense oligos corresponding to
CC	thymidines present in the target RNA serves to prevent the breakdown of
CC	the oligonucleotides into products that free adenosine into the system
CC	e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to
CC	prevent any unwanted effects due to it
XX	
SQ	Sequence 1216 BP; 153 A; 431 C; 371 G; 261 T; 0 U; 0 Other;
	Query Match 78.3%; Score 846; DB 11; Length 1216;
	Best Local Similarity 100.0%; Pred. No. 1.6e-188;
	Matches 846; Conservative 0; Mismatches 0; Indels 0; Gaps 0
Qy	1 ATGAAGTCGCGGTCTACCGTGCACAGACCACCACTCTGTGGAAAAGGCAACTCGCGC 60
Dd	350 ATGAGTCGCGGTCTACCGTGCCAGAACACCACTCTGTGGAAAAGGCAACTCGCGC 409
Qy	61 GTGATGGCGGGGTGCTCTTTACGACACCGGCCCTCTCGGGCAACCTGTGTGGCGCTG 120
Dd	410 GTGATGGCGGGGTGCTCTTTACGACACCGGCCCTCTCGGGCAACCTGTGTGGCGCTG 469
Qy	121 CTGGCGCGCTCGGGGCTGGGGTGGTCTCGGGGCTCCACTGCCGCCGCTCGCCCTCGGTC 180
Dd	470 CTGGCGCGCTCGGGGCTGGGGTGGTCTCGGGGCTCCACTGCCGCCGCTCGCCCTCGGTC 529
Qy	181 TTCTCATGCTGTGTGTGGCGCTGACCGGTCAACCGACTTGTGTGGCAAGTGCTCTTAAGC 240
Dd	530 TTCTCATGCTGTGTGTGGCGCTGACCGGTCAACCGACTTGTGTGGCAAGTGCTCTTAAGC 589
Qy	241 CGGTGTGTGTGTGTGCTGCCTACGCTCAGAACCGGAGTCTGGGGTGTCTTGCGCCGCATTG 300
Dd	590 CCGGTGTGTGTGTGTGCTGCCTACGCTCAGAACCGGAGTCTGGGGTGTCTTGCGCCGCATTG 649

Qy	661	GCCATGCGCAACTCTATGCGATGCACCGCGGCTGCGAGCGGCACCCGGCTCCTGCACC	720
Db	1505		1564
Qy	721	AGGGACTGTGCGAGCGCGCGGACGGGAGGGAAGCGTCCCTCAGCCCCCTGGAGGAG	780
Db	1565		1624
Qy	781	CTGGATCACCTCCTGCTGCTGGGCTGATGACCGTCTCTTCACTATGTGTTCTCTGCC	840
Db	1625		1684
Qy	841	GTAATT	846
Db	1685		1690

Search completed: April 22, 2005, 12:41:21
 Job time : 655.51 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 22, 2005, 10:55:17 ; Search time 4050.36 Seconds
(without alignments)
10149.570 Million cell updates/sec

Title: US-10-689-861-3
Perfect score: 1080
Sequence: 1 atgaagtcgcttaccg.....acatgaatccagtcgtgtga 1080

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 1: gb_est1:*
- 2: gb_est2:*
- 3: gb_hic:*
- 4: gb_est3:*
- 5: gb_est4:*
- 6: gb_est5:*
- 7: gb_est6:*
- 8: gb_gse1:*
- 9: gb_gse2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	950.6	88.0	1229	6	CD013871	CD013871 90116594
2	655.4	60.7	3190	3	AK032488	AK032488 Mus muscu
3	654	60.6	1053	5	BQ068035	BQ068035 AGENCOURT
C 4	434	40.2	486	1	AI460323	AI460323 AC95A01.X
5	393	36.4	495	7	CR747669	CR747669 CR747669
C 6	375.4	34.8	1996	3	AK016503	AK016503 Mus muscu
C 7	361.8	33.5	948	6	BY716183	BY716183 BY716183
8	333	30.8	520	1	AA105532	AA105532 mo57a09.r
9	313	29.0	632	2	BB622854	BB622854 BB622854
C 10	311	28.8	589	8	AZ291373	AZ291373 RPI-23-1
11	220.6	20.4	1077	9	AY410679	AY410679 Homo sapi
12	203.4	18.8	1038	3	BC017857	BC017857 Homo sapi
C 13	203.4	18.7	2020	3	CR601077	CR601077 full-length
C 14	202.4	18.7	565	8	BZ120059	BZ120059 CH230-523
15	194.8	18.0	2509	3	AK086904	AK086904 Mus muscu
16	192.6	17.8	1032	5	BM925026	BM925026 AGENCOURT
17	192.6	17.8	1077	9	AY410681	AY410681 Mus muscu
18	192.6	17.3	2619	3	AK054132	AK054132 Mus muscu
C 19	186.4	17.3	652	5	BX498371	BX498371 DKFZP779E
C 20	186.2	17.2	658	6	BY724253	BY724253 BY724253
21	185.6	17.2	765	1	AU132613	AU132613 AU132613
22	181.2	16.8	615	5	BP381970	BP381970 BP381970
23	180.6	16.7	3079	3	AK036531	AK036531 Mus muscu
24	180.4	16.7	2653	3	AK036474	AK036474 Mus muscu

25	176.4	16.3	571	8	AZ357037	AZ357037 1M0098D23
26	170.6	15.8	1062	5	BM925058	BM925058 AGENCOURT
27	166.2	15.4	635	7	CF131282	CF131282 UI-HF-FQ0
28	162.6	15.1	603	7	CK820125	CK820125 IF31906.Y
29	161.8	15.0	1019	1	AL552370	AL552370 AL552370
30	157.4	14.6	646	2	BM629330	BM629330 BM629330
31	154.2	14.3	577	4	BM354213	BM354213 IF31906.Y
32	150.2	13.9	562	6	CB609359	CB609359 AMGNNUC:N
33	150.2	13.9	573	4	BM273260	BM273260 IF28C08.Y
34	144.2	13.4	655	2	BB625385	BB625385 BB625385
35	139	12.9	771	4	BG919027	BG919027 602816763
36	132	12.2	479	2	AW240093	AW240093 PLR1C.PK0
37	130.4	12.1	364	4	BM338608	BM338608 ha97906.9
38	126.4	11.7	520	1	AA818108	AA818108 UI-R-A0-a
39	123.2	11.4	470	8	AZ278470	AZ278470 RPI-23-1
40	121.6	11.3	653	7	CN484094	CN484094 hW42a07.Y
41	121.2	11.2	584	8	BH341188	BH341188 CH230-51K
42	121.2	11.2	639	8	BH315818	BH315818 CH230-50L
43	121	11.2	733	9	AG414036	AG414036 Mus muscu
44	119.6	11.1	482	5	BM986638	BM986638 EST594232
C 45	118.2	10.9	848	7	CO959749	CO959749 AGENCOURT

ALIGNMENTS

RESULT 1
LOCUS CD013871 1229 bp mRNA linear EST 21-OCT-2003
DEFINITION Single gene library Homo sapiens cDNA, mRNA sequence.
ACCESSION CD013871
VERSION CD013871.1 GI:37777401
KEYWORDS EST:
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1229)
AUTHORS Jin, P., Fu, G.K., Wilson, A.D., Yang, J., Chien, D., Hawkins, P.R.,
Au-Yang, J. and Stuve, L.L.
TITLE PCR isolation and cloning of novel splice variant mRNAs from known
drug target genes
JOURNAL Genomics 83 (4), 566-571 (2004)
COMMENT Contact: Jin, P.
Incyte Corporation
3160 Porter Drive,
Palo Alto, CA 94304, USA
Tel: 650 621 8639
Fax: 650 621 8965
Email: pjin@incyte.com.

FEATURES
source Location/Qualifiers
1..1229
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="Single gene library"
/note="Vector: pDrive Cloning Vector; RT-PCR was performed
using gene-specific primers flanking the open-reading
frame. PCR products were subcloned into pDrive Cloning
Vector and sequenced completely using M13 forward and
reverse primers. Sequencing gaps were closed by
re-sequencing using primers flanking the gapped areas."

ORIGIN

Query Match 88.0%; Score 950.6; DB 6; Length 1229;
Best Local Similarity 91.7%; Pred. No. 2.5e-220;
Matches 1076; Conservative 0; Mismatches 4; Indels 93; Gaps 3;
QY 1 ATGAAGTCGCGCTTCTACCGTCCAGAACACCACTCTGTGGAAGCAACTCGCG 60
|||||
Db 4 ATGAAGTCGCGCTTCTACCGTCCAGAACACCACTCTGTGGAAGCAACTCGCG 63
|||||
QY 61 GTGATGGCGGGGTGCTCTTACAGACCGGCTCTCTGGGCAACCTGTCGCCCTGGGCTG 120
|||||

Db	64	GTGATGGCGGGGTGCTCTTACAGCACCGGCGCTCTCTGGGGCAACCTGCTGGGCCCTCGGGCGTGC	123
Qy	121	CTGGCGCGCTCGGGGCTGGGGTGTGCTCGCGGGTCCACTGCGCCCGCTGCCCCCTCGGTC	180
Db	124	CTGGCGGCTCGGGGCTGGGGTGTGCTCGCGGGTCCACTGCGCCCGCTGCCCCCTCGGTC	183
Qy	181	TTCTACATGCTGTGTGTGGGCTGACGGTCAACCGACTGTGTGGGCAAGTGCCTCTTAAGC	240
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Db	244	CCGGTGTGTGGTGTGCTACGCTCAGAAACCGGAGTCTGGGGGTGCTTGGCCCGGCAATG	303
Qy	301	GACAACTCGTTGTGCCAAGCCTTCGCTTCTTCAATGCTCTTTTGGGCTCTCTCTGACA	360
Db	304	GACAACTCGTTGTGCCAAGCCTTCGCTTCTTCAATGCTCTTTTGGGCTCTCTCTGACA	363
Qy	361	CTGCAACTCTCTGGCCATGGCACTGGAGTGTGGCTCTCCCTAGGGCAACCTTTCTTCTAC	420
Db	364	CTGCAACTCTCTGGCCATGGCACTGGAGTGTGGCTCTCCCTAGGGCAACCTTTCTTCTAC	423
Qy	421	CGACGGACATCACCCTGGCGCTGGGGCGCACTGGTGGCCCGGGTGTGGAGGCGCTTCTCC	480
Db	424	CGACGGACATCACCCTGGCGCTGGGGCGCACTGGTGGCCCGGGTGTGGAGGCGCTTCTCC	483
Qy	481	CTGGCTTTCTGGCGGCTACCTTTTCATGGGCTTCGGGAAAGTTCGTGCACTACTGCCCGGC	540
Db	484	CTGGCTTTCTGGCGGCTACCTTTTCATGGGCTTCGGGAAAGTTCGTGCACTACTGCCCGGC	543
Qy	541	ACCTGGTGTCTTATCCAGATGGTCCACGAGGAGGGCTCGTGTGGTGTGGGGTACTCT	600
Db	544	ACCTGGTGTCTTATCCAGATGGTCCACGAGGAGGGCTCGTGTGGTGTGGGGTACTCT	603
Qy	601	GTGCTCTACTCCAGCCTCATGGCGCTGCTGGTCTCTCGGCAACCGTGTGTGTGAACCTCGC	660
Db	604	GTGCTCTACTCCAGCCTCATGGCGCTGCTGGTCTCTCGGCAACCGTGTGTGTGAACCTCGC	663
Qy	661	GCCATGGCAACCTTATGGATGACCGGGCGGTGACGGGCAACCGCGCTCTGTGAC	720
Db	664	GCCATGGCAACCTTATGGATGACCGGGCGGTGACGGGCAACCGCGCTCTGTGAC	723
Qy	721	AGGACTGTGCGAGCGCGCGCGGAGGGAAGCGTCCCTCAGCCCCCTGGAGGAG	780
Db	724	AGGACTGTGCGAGCGCGCGCGGAGGGAAGCGTCCCTCAGCCCCCTGGAGGAG	783
Qy	781	CTGATCACCCTCTGCTGTGGCGCTGATGACCGGTCTTCTTCACTATGTGTCTCTGCC	840
Db	784	CTGATCACCCTCTGCTGTGGCGCTGATGACCGGTCTTCTTCACTATGTGTCTCTGCC	843
Qy	841	GTAATT-----	846
Db	844	GTAATTGATTTGTTCCTGGAGTCCCGGCCAAGACACTCGGGAGTAGGTGAGGCTTGAGG	903
Qy	847	-----TATCGCGCTTACTATGGAGCAT	869
Db	904	AAACATTTTCAGTGTCTCTCTCTCTTCTTCCCAAGTATCGCGCTTACTATGGAGCAT	963
Qy	870	TAAGGATGTCGAAGAGAAAAACAGGACCTCTGAAGAAGCAGA-AGACCTCCGAGCCTTGC	928
Db	964	TAAGGATGTCGAAGAGAAAAACAGGACCTCTGAAGAACACAGAGAGACCTCCGAGCCTTGC	1023
Qy	929	GATTTCTATCTGTGATTTCAATTTGTGACCTTGGATTTTATCATTTTTCAGATCTCCAG	988
Db	1024	GATTTCTATCTGTGATTTCAATTTGTGACCTTGGATTTCTTATCATTTTCAGATCTCCAG	1083
Qy	989	TATTTCCGATATTTTTTTCACAAGA-TTTTTCATTAGACCTCTTAGGTACAGGAGCCGCTGC	1047
Db	1084	TATTTCCGATATTTTTTTCACAAGATTTTTCATTAGACCTCTTAGGTACAGGAGCCGATGC	1143
Qy	1048	AGCAATTCCTAATCATGGAAATCCAGTCTGTGA	1080
Db	1144	AGCAATTCCTAATCATGGAAATCCAGTCTGTGA	1176

[illegible]

AK032488 3190 bp mRNA linear HTC 03-APR-2004
Mus musculus adult male olfactory brain cDNA, RIKEN full-length
enriched library, clone:6430566C09 product:prostaglandin D
receptor, full insert sequence.

AK032488
AK032488.1 GI:26328308
HTC; CAP trapper.
Mus musculus (house mouse)
Mus musculus
Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1
Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
10349636

2
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
20499374
11042159

3
Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
Konno, H., Akiyama, J., Nishi, K., Kitsuina, T., Tashiro, H., Itoh, M.,
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watabiki, M.,
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)
20530913
11076861

4
The RIKEN Genome Exploration Research Group Phase II Team and the
FANTOM Consortium.
Functional annotation of a full-length mouse cDNA collection
Nature 409, 695-690 (2001)

5
The FANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 3190)

6
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,
Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,
Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,
Horii, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,
Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,
Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohashi, N.,
Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,
Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,
Sugabe, Y., Tagami, M., Tagawa, K., Takahashi, F., Takaku-Akahira, S.,
Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
Muramatsu, M. and Hayashizaki, Y.
Direct Submission
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.jp).
URL: <http://genome.gsc.riken.jp/> Tel: 81-45-503-9222,

Fax: 81-45-503-9216)
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN, Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site for further details.
URL: <http://genome.gsc.riken.jp/>
URL: <http://fantom.gsc.riken.jp/>
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/dev_stage="adult"
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3170. 3175
polyA_signal
/notes="putative"
3190
polyA_site
/note="putative"
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Best Local Similarity 77.1%; Pred. No. 2.2e-148;
Matches 829; Conservative 0; Mismatches 231; Indels 15; Gaps 2;
QY 12 GTTCTACCGCTGCAGAACACCACTCTGTGGAAGGCAACTCGCGGCTGATGGCGG 71
DB 132 GTCTATCGCTGTGACACATCCACCTGGTGGAAAGGGCTCTCGCGACAGATGGCGC 191
QY 72 GGTGCTCTTTCAGCACCGGCTCTCGGCAACCTGTGGCCCTGGGCTGTGGCGGCTC 131
DB 192 TGTGCTCTTCGGTGGGGCTTCTGGGCAATCTTCTGGCGTGGTCTGCTGGCGGCTC 251
QY 132 GGGGCTGGGGTGTGTCGGGGGTCCACTGCGCGCTGCGCTCGGCTCTTCTACATGCT 191
DB 252 GGGACTGGGGTCTTGGCGGCGAGGGCACTACACCGCGCGCTCGTCTTATGCT 311
QY 192 GGTGTGTGCGCTGACGGTCCAGGCTGTGTTGGCAAGTGCCTCCTAAGCCCGTGTGCT 251
DB 312 GTGTGTGCTGTACGGTCCAGGCTGTGTTGGCAATGCTGTGATCAGCCCGATGCTCT 371
QY 252 GGTGCTACGCTCAGAACCGGAGTGTGGGGTGTGTCGCGCGCAATTGGACAACCTCGT 311
DB 372 GGTGCTACGCGCAAAACAGAGCTAAGGAACCTGCTGCTGCTCAGGCAATCAGTT 431
QY 312 GTGCCAAGCTTGGCTCTTCTATGTCCTTCTTGGGCTCTCTGCACTGCAACTCTCT 371
DB 432 ATGCGAAAGCTTGGCTCTTCTATGTCCTTCTTGGGCTAGGCTCAGCTTACAGTGT 491
QY 372 GGCATGGCACTGGAGTGTGCTCTCCCTAGGGACACCTTCTTCTACCGAGCGCAT 431
DB 492 GGTATGGCGGTGGAGTGTGCTGCTCTGGGACACCCCTTCTTCTACAAAGGCACT 551

QY 432 CACCTGCGGCTGGGGCGCACTGGTGGCCCGGCTGGTGGAGGCGCTTCTCCTCGCTTCTG 491
DB 552 CACCTTGGCGCGGGAGTGTGGTGGACACCGGCTGGTGGCGGCTTCTGCTTGGCTTCTG 611
QY 492 CGCGCTTACCTTTTCATGGGCTTGGGAAGTTTCGTGCAAGTACTGCGCGGACACTGGTCT 551
DB 612 TGGCTTCCCTTGTGCTGGTGGGAAGTTTCGTGCAAGTACTGCGCGGACACTGGTCT 671
QY 552 TATCCAGATGGTCCACAGAGAGGCTCGTGTGGTGTGCTGGGCTACTCTGTGCTTACTC 611
DB 672 CATCCAGATGATCCACAAGAGGCTTCATTTTCGGTAATAGGCTTCTCTGCTTACTC 731
QY 612 CAGCTCATGGGCTGTGCTGCTGCTGCCACCGTGTGTGCAACTCGGCGCCATGCGCAA 671
DB 732 CAGCTCATGGGCTGTGCTGCTGCCAACCCTGGTGTGTGCAACTCGGCTGCTGATCAA 791
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DB 792 CTTCTATGATGATGACCGGCTGCGAGCGGACCTATCTCTACCGCTGTCTCAGGACCGCGC 851
QY 732 CGAGCGCGCGGCGGAGGAGGAGCGTCCCTCAGCCCTCGAGGAGCTGGATCACCT 791
DB 852 CCAGTCAGCTCAGACTACAGGACCGGCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTG 911
QY 792 CTTCTGCTGGGCTGTGATGACCGTGTCTTCTACTATGTGTCTCTGCTGCTGCTGCTGCT 851
DB 912 TGTGCTGCTGGCTCTCATGACAGTGTCTTCTCAGCTGTGCTGCTGCTGCTGCTGCTGCT 971
QY 852 CCGTCTACTGATGAGCAATTTAAGGATGTCAAGGAGAAACAGGACCTCTGAAGAAGCAGA 911
DB 972 TCGTACTATGAGGCTTTAAACTTG-----AGAAAGCTGGAAGGAGCTCAGA 1022
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DB 1023 AGACCTCCAGCTTGGTTCCTGCTGATTTCCATAGTAGGACCTCGATTTCTCAT 1082
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DB 1083 CATCTTCAGGACTTCAGTATTCGGATGTTATTTTCAAGAGTTTTCACAAGAGCTCTGAT 1142
QY 1032 GTACAGGAGCGGTGCGAGCAATTC-----ACTACATGGAATCCAGTCTGTGA 1080
DB 1143 CTACAGAACTGGAGAGGCAATTCAGCAAGTAACGTGGAATCCATTTTGTGA 1197
BQ068035 1053 bp mRNA linear EST 02-APR-2002
AGENCOURT_6792268 NIH_MGC_121 Homo sapiens cDNA clone IMAGE:5769056
5', mRNA sequence.
BQ068035
BQ068035.1 GI:19897081
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1053)
NIH-MGC <http://mgc.nci.nih.gov/>
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM12829 row: o column: 09
High quality sequence stop: 645.

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FEATURES
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Location/Qualifiers
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/clone="IMAGE:5769056"
/lab_host="DH10B"
/clone_lib="NIH_MGC_121"
/note="Organ: Brain; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 3 fetal brains, female age 20 weeks, female age 24 weeks, and male age 26 weeks. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.7 kb, insert size range 0.7-3.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 017. Note: this is a NIH_MGC Library."

ORIGIN
Query Match 60.6%; Score 654; DB 5; Length 1053;
Best Local Similarity 96.0%; Pred. No. 3.8e-148;
Matches 714; Conservative 0; Mismatches 25; Indels 5; Gaps 4;

QY 1 ATGAAGTCCGCTTCTACCGCTGCCAGAACACACCTCTGTGAAAGGCAACTCGGCG 60
DB 122 ATGAAGTCCGCTTCTACCGCTGCCAGAACACACCTCTGTGAAAGGCAACTCGGCG 181
QY 61 GTGATGGCGGGGTGCTTCTACAGCACCGGCTCTCTGGGCAACCTGTGCGCCCTGGGGGTG 120
DB 182 GTGATGGCGGGGTGCTTCTACAGCACCGGCTCTCTGGGCAACCTGTGCGCCCTGGGGGTG 241
QY 121 CTGGCGCGCTCGGGGTGGGGTGGTCTCGGGCGTCACTGCGGCGGCTGCGGCTCGGTC 180
DB 242 CTGGCGCGCTCGGGGTGGGGTGGTCTCGGGCGTCACTGCGGCGGCTGCGGCTCGGTC 301
QY 181 TTCTACATCTGTGTGTCGCTGACGCTCAGGTCACGACTTGTGCGGCAAGTCTCTTAAGC 240
DB 302 TTCTACATCTGTGTGTCGCTGACGCTCAGGTCACGACTTGTGCGGCAAGTCTCTTAAGC 361
QY 241 CCGGTGGTGTGCTGCTGCTACGCTCAGAACCGGAGTCTCGGGGTGCTTGGCCCGGATG 300
DB 362 CCGGTGGTGTGCTGCTGCTACGCTCAGAACCGGAGTCTCGGGGTGCTTGGCCCGGATG 421
QY 301 GACAACTCTGTGCGCAAGCTTGGCTTCTTCATGCTCTTCTTGGGCTCTCTCGACA 360
DB 422 GACAACTCTGTGCGCAAGCTTGGCTTCTTCATGCTCTTCTTGGGCTCTCTCGACA 481
QY 361 CTGCAACTCTGCGCATGCACTGAGTGTGCTGCTCTGCTAGGGCAACCTTCTTCTAC 420
DB 482 CTGCAACTCTGCGCATGCACTGAGTGTGCTGCTCTGCTAGGGCAACCTTCTTCTAC 541
QY 421 CGACGSCACATCACCTGCGCCTGCGGCACTGTGTCGCGCCCGGTGTGAGCGCTTCTCC 480
DB 542 CGACGSCACATCACCTGCGCCTGCGGCACTGTGTCGCGCCCGGTGTGAGCGCTTCTCC 601
QY 481 CTGGCTTTCTGCGCGTACTCTTTCATGCGCTTGGGAAGTT-CTGTCAGTACTGCCCGG 539
DB 602 CTGGCTTTCTGCGCGTACTCTTTCATGCGCTTGGGAAGTTCTGTCAGTACTGCCCGG 661
QY 540 CACCTGGTCTTTATCCAGATGTTCCACGAGGAGGCTCGTGTGCTGCTGCGGTACTC 599
DB 662 CACCTGGTCTTTATCCAGATGTTCCACGAGGAGGCTCGTGTGCTGCTGCGGTACTC 721
QY 600 TGTGCTTCTACTCCAGCCTCATGCGCTGTGTCCTGCGCACCGTGTGCTGTGCAACCTCGG 659
DB 722 TGTGCTTCTACTCCAGCCTCATGCGCTGTGTCCTGCGCACCGTGTGCTGTGCAACCTCGG 781
QY 660 CG-CCATGGCAACCTTCTATGAGTACAC--CGGCGGCTGACAGCGCA-CCGCGCTCTCT 715
DB 782 CGCCCTTGGGCACTTCTATGCGAGCAACCGGCTTGACTGAACCGGCAACCCGCGCTCT 841
QY 716 GCACCGGAGTGTGCGGAGCCGC 739
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Db 842 GCACCGGAGTGTGCGGAGCC 865

RESULT 4
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LOCUS
DEFINITION
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IMAGE:1953576 3' similar to SM:PD2R_HUMAN Q13258 PROSTAGLANDIN D2
RECEPTOR 1, mRNA sequence.
AI460323.1 GI:4313204
EST.
Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 486)
Hillier, L., Allen, M., Bowles, L., Dubuque, T., Gaisel, G., Jost, S.,
Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M.,
Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, P.,
Theising, B., White, Y., Wyllie, J., Waterston, R. and Wilson, R.
WashU-NCI human EST Project
Unpublished (1997)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LBNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Possible reversed clone: polyT not found
Seq primer: -400P from Gibco
High quality sequence stop: 423.
Location/Qualifiers
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/clone="IMAGE:1953576"
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/dev_stage="72 years"
/lab_host="SOLR"
/clone_lib="Schiller meningioma"
/note="Organ: brain; Vector: pBluescript SK- (Stratagene); Site_1: EcoRI; Site_2: XhoI; Double-stranded cDNA was prepared from human meningioma using primer 5'-GAGAGAGAGAGAGAGAGAACTAGTCTGAGT(18)-3'. An EcoRI adaptor was used on the 5' end of the cDNA as follows: 5'-AATTCGACGAG-3'. The library was size-selected and went through one round of amplification. Average insert size is 1.7 kb, with a range from 0.4-12 kb. Tumor identification by consensus pathology. This library was constructed by Dr. Martin Schiller (Johns Hopkins University)."
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ORIGIN
Query Match 40.2%; Score 434; DB 1; Length 486;
Best Local Similarity 100.0%; Pred. No. 1.2e-94;
Matches 434; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 647 TGTGCAACTCTGCGCGCATGCGCAACCTCTATGCATGACCGCGGCTGCGAGCGCAC 706
DB 486 TGTGCAACTCTGCGCGCATGCGCAACCTCTATGCATGACCGCGGCTGCGAGCGCAC 427
QY 707 CGCGCTCTCTGACACGAGGACTGTGCGAGCGCGGAGCGGAGGAGCGTCTCCCTC 766
DB 426 CGCGCTCTCTGACACGAGGACTGTGCGAGCGCGGAGCGGAGGAGGAGCGTCTCCCTC 367
QY 767 AGCCCTCTGAGGAGTGTGATCACTCTGCTGCTGCTGATGACCGTGTCTTCACTA 826
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Db      366 AGCCCTGAGGAGCTGGATCACCTCTGCTGCTGCGGCTGATGACCGTCTCTTCACTA 307
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Db      306 TGTGTTCTCTGCCCGTAATTTATTCGCGCTTACTATGAGCAATTAAGGATGTCAAGGAGA 247
QY      887 AAAACAGGACCTCTGAAGAGCAGAGACCTCCGAGCCTTGCATTTCTATCTGTGATTT 946
Db      246 AAAACAGGACCTCTGAAGAGCAGAGACCTCCGAGCCTTGCATTTCTATCTGTGATTT 187
QY      947 CAATTGTGACCTCTGGATTTTATCATTTTTCAGATCTCCAGTATTTTCGATATTTTTC 1006
Db      186 CAATTGTGACCTCTGGATTTTATCATTTTTCAGATCTCCAGTATTTTCGATATTTTTC 127
QY      1007 ACAAGATTTTCAATTAGACCTCTTAGTACAGGAGCGGTGCAGCAATTCACCTAACATGG 1066
Db      126 ACAAGATTTTCAATTAGACCTCTTAGTACAGGAGCGGTGCAGCAATTCACCTAACATGG 67
QY      1067 AATCCAGTCTGTGA 1080
Db      66 AATCCAGTCTGTGA 53

RESULT 5
CR747669
LOCUS
DEFINITION
CR747669 NIH_MGC_121 Homo sapiens cDNA clone IMAGE99800912829 ;
IMAGE:5769056 5', mRNA sequence.
ACCESSION
CR747669
VERSION
CR747669
KEYWORDS
CR747669.1 GI:51661368
SOURCE
EST.
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 495)
Ebert, L., Heil, O., Hennig, S., Korn, B., Neubert, P., Partsch, E.,
Peters, M., Radelof, U. and Schneider, D.
I.M.A.G.E. cDNA Clone Collection
Unpublished (2004)
Contact: Inge Ariart
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Email: www.rzpd.de
RZPD; IMAGE99800912829.
RZPDLIB; I.M.A.G.E. cDNA Clone Collection;
Contact: Inge Ariart
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 100
Fax: +49 30 32639 111
www.rzpd.de
This clone is available royalty-free from RZPD;
contact RZPD (clone@rzpd.de) for further information. Seq primer:
M13r, Primer sequence: TTTCACAGGAACAGCTATGAC.
FEATURES
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Location/Qualifiers
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/clone="IMAGE99800912829 ; IMAGE:5769056"
/lab_host="DH10B"
/clone_lib="NIH_MGC_121"
/note="Organ: brain; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: EcoRV (destroyed); RNA source anonymous pool of 3
fetal brains, female age 20 weeks, female age 24 weeks,
and male age 26 weeks. Library is oligo-dT primed and
directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.7 kb, insert size range
0.7-3.5 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(invitrogen). Research Genetics tracking code 017. Note:
this is a NIH_MGC Library."

```

```

ORIGIN
Query Match      36.4%; Score 393; DB 7; Length 495;
Best Local Similarity 100.0%; Pred. No. 1.1e-84;
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QY      1 ATGAAGTCCCGTTTACCGCTGCCAGAACACCACTCTGTGAAAAAGGCAACTCGGCG 60
Db      103 ATGAAGTCCCGTTTACCGCTGCCAGAACACCACTCTGTGAAAAAGGCAACTCGGCG 162
QY      61 GTGATGGGCGGGTGTCTTTACAGCACCGGCTCTTGGGCAACCTGTGCGCCCTGGGGCTG 120
Db      163 GTGATGGGCGGGTGTCTTTACAGCACCGGCTCTTGGGCAACCTGTGCGCCCTGGGGCTG 222
QY      121 CTGGGCGCTCGGGGGTGGGGTGGTCTCGCGCGCTGCACCTGCGCCCGCTGCCCTCGGTC 180
Db      223 CTGGGCGCTCGGGGGTGGGGTGGTCTCGCGCGCTGCACCTGCGCCCGCTGCCCTCGGTC 282
QY      181 TTCTACATGCTGTGTGTGGCTTACCGGTACCGGTACCGGTACCGGTACCGGTACCGGTACCG 240
Db      283 TTCTACATGCTGTGTGTGGCTTACCGGTACCGGTACCGGTACCGGTACCGGTACCGGTACCG 342
QY      241 CGGTTGTGCTGGCTGCGCTTACCGTACCGTACCGTACCGTACCGTACCGTACCGTACCGTACCG 300
Db      343 CGGTTGTGCTGGCTGCGCTTACCGTACCGTACCGTACCGTACCGTACCGTACCGTACCGTACCG 402
QY      301 GACAACTCTGTTGTGCAAGCCCTTCGCTTCTTCATGTCCTTCTTTGGGCTCTCTCTCGACA 360
Db      403 GACAACTCTGTTGTGCAAGCCCTTCGCTTCTTCATGTCCTTCTTTGGGCTCTCTCTCGACA 462
QY      361 CTGCAACTCTGCGCATGCGTACCGTACCGTACCGTACCGTACCGTACCGTACCGTACCGTACCG 393
Db      463 CTGCAACTCTGCGCATGCGTACCGTACCGTACCGTACCGTACCGTACCGTACCGTACCGTACCG 495

RESULT 6
AKO16503/c
LOCUS
DEFINITION
AKO16503
Mus musculus adult male testis cDNA, RIKEN full-length enriched
library, clone:4931433C03 product:unknown EST, full insert
sequence.
ACCESSION
AKO16503
VERSION
AKO16503.1 GI:12855271
KEYWORDS
HTC; CAP trapper.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1
Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
PUBMED 10349636
AUTHORS
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
20499374
PUBMED 11042159
AUTHORS
Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
Konno, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M.,
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M.,
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)
JOURNAL
TITLE
AUTHORS

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[illegible]

ORIGIN

Query Match 29.0%; Score 313; DB 2; Length 632;
Best Local Similarity 76.2%; Pred. No. 3.5e-65;
Matches 385; Conservative 0; Mismatches 120; Indels 0; Gaps 0;

QY 12 GTTCTACCGCTCCAGAACACACACCTCTCTGGAAAGGCAACTCGGCGGTGATGGCGG 71
DB 128 GTTCTATCTGTCAGACATTCACCTGGGTGGAAAGGGCTCTCTGGCGACCATGGGCGC 187
QY 72 GGTGTCTTTTTCAGCACCGGCTCTCTGGGCAACCTGCTGGGCGGCTCTGGGCGGCTC 131
DB 188 TGTGTCTTTTGGTGGGGCTTCTGGGCAATCTTCTGGGCGGCTCTGGGCGGCTC 247
QY 132 GGGGTGGGGTGGTGTCTCGCGGCTCCATCTGGCGCGCTGCGGCTCGGCTCTTACATGCT 191
DB 248 GGGACTGGGGTCTTGGCGGCCAGGGCACTACACCGCGCGCTCGGCTCTTATATGCT 307
QY 192 GGTGTGGGCTGAGGCTACCGACTTGTGGCAAGTCCCTTAAGCGCGGCTGGTGTCT 251
DB 308 CGTGTGGGCTTGGGCTTACCGACTTGTGGCAATTTGTGATCAGCCCGATGGTCTCT 367
QY 252 GGTGTGCTACGCTCAGAACCGGAGTCTGGGGTGTCTGGCGCGCAATTCGACAACTCGTT 311
DB 368 GGTGTGCTACGCGCAACAGAGCTTAAGAGACTGCTGCTCTAGGCAATCAGTT 427
QY 312 GTGCCAAGCTTTGCGCTCTTTCATGTCCTTTTGGGCTCTCTCGACACTGCAACTCTCT 371
DB 428 ATGCGAAAGTTTGGCTTCTCTGATGCTCTTTTGGGCTAGCTCGACCTTACAGCTGT 487
QY 372 GGCATAGGACTGGAGTGTGCTCTCTAGGCAACCTTTCTTACCGAGCGGCAAT 431
DB 488 GGTATGGCGGTGGAGTGTGCTCTCTGGGCAACCTTTCTTACCAAAAGCACT 547
QY 432 CACCTGTGCGGCGGCACTGTCGCGCGGCTGGTGGGCTCTCTCGGCTTCTCTGCTTCTG 491
DB 548 CACCTTGGCGCGGAGTGTGTCGACCGGTGGGCGGCGGCTCTCTGCTTGGCTTCTG 607
QY 492 CCGCTACCTTTTCATGGGCTTCGGG 516
DB 608 TCGCGCTCCCTTGTGGTTTGGG 632

RESULT 10

AZ291373/c
LOCUS 589 bp DNA linear GSS 27-JUL-2000
DEFINITION RPCI-23-131N24, TV RPCI-23 Mus musculus genomic clone
RPIC-23-131N24, genomic survey sequence.

ACCESSION

AZ291373

VERSION

AZ291373.1 GI:9533213

KEYWORDS

GSS.

SOURCE

Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 589)

Akinret, B., Levens, M., McGann, S., Tsegaye, G., Geer, K., Krol, M., de

Jong, P., and Fraser, C.M.

Mouse BAC End Sequences from Library RPCI-23

Unpublished (1999)

Other GSSs: RPCI-23-131N24.TJ

Contact: Shaying Zhao

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0200

Fax: 301 838 0208

Email: szhao@tigr.org

Clones are derived from the mouse BAC library RPCI-23. For BAC

library availability, please contact Pieter de Jong

(pieter@dejong.med.buffalo.edu). Clones may be purchased from

BACPAC Resources (<http://bacpac.med.buffalo.edu/orderingframe.htm>)

FEATURES
source

Location/Qualifiers
1..589

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="RPCI-23-131N24"

/sex="Female"

/lab_host="DH10B"

/clone_lib="RPCI-23"

/note="Organ: Kidney/Brain; Vector: pBACE3.6; Site 1:

EcoRI; Site 2: EcoRI; Female C57BL/6J mouse kidney and/or

brain genomic DNA was isolated and partially digested

with a combination of EcoRI and EcoRI Methylase. Size

selected DNA was cloned into the pBACE3.6 vector at the

EcoRI sites. The ligation products were transformed into

DH10B electrocompetent cells (BRL Life Technologies)."

ORIGIN

Query Match 28.8%; Score 311; DB 8; Length 589;

Best Local Similarity 78.8%; Pred. No. 1e-64;

Matches 371; Conservative 0; Mismatches 100; Indels 0; Gaps 0;

QY 376 ATGGCACTGGAGTGTGCTCTCCCTAGGGACACCTTTCTTACCGCGGACATCACC 435
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QY 496 CTACCTTTTCATGGGCTTCGGGAAGTTCTGTGAGTACTGCGCCCGGCACTGTGTGCTTTATC 555
DB 468 CTCCCTTTTGTGCTTTTGGGAAGTTCTGTGAGTACTGTCCAGGACCTGTGTGTTTCTC 409
QY 556 CAGATGTTCCAGAGGAGGCTCGCTGCGGTGGGGTACTGTGCTTACTTCCAGC 615
DB 408 CAGATGATCCAGAGGAGGCTTCTTTCGGTAATAGGCTTCTGTGCTTACTTCCAGC 349
QY 616 CTATGGCGCTGCTGCTCTCGCCACCGTGTGTGCAACCTCGGGCCATGCGCAACCTC 675
DB 348 CTATGGCGCTGCTGCTCTCGCAACCGTGTGTGCAACCTGGGTGCCATGTACAACTC 289
QY 676 TATGGGATGACCGGCGCTGTGAGGGCACCGCGCTCTGTGACAGGAGTGTGCGGAG 735
DB 288 TATGACATGCACAGGCGCCAGAGGCACTATCTCACCCTGTCTCCAGGAGACCGGCGCCAG 229
QY 736 CCGCGCGGAGGAGGAGGAGGAGCGTCCCTCAGCCCTGGAGGAGTGTGATCACCCTCTG 795
DB 228 TCAGGCTCAGACTACAGGACCGGCTTCTGTCATCTTTGGAGGAGTGTGACCATATTG 169
QY 796 CTGCTGGCGCTGATGACCGTGTCTTCTACATATGTCTTCTGCTCCCGCTTAAT 846
DB 168 CTGCTGGCTCTCATGACAGTGTCTTTCACCATGTGTTCCTGCTTAAAT 118

RESULT 11

AY410679

LOCUS

AY410679

DEFINITION

Homo sapiens PTGER2 gene, VIRTUAL TRANSCRIPT, partial sequence,

genomic survey sequence.

ACCESSION

AY410679

VERSION

AY410679.1

GI:39766647

KEYWORDS

GSS.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

AY410679 1077 bp DNA linear GSS 16-DEC-2003

Homo sapiens PTGER2 gene, VIRTUAL TRANSCRIPT, partial sequence,

genomic survey sequence.

AY410679

AY410679.1 GI:39766647

GSS.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Email: cgabbs-r@mail.nih.gov
 Tissue Procurement: CLONTECH
 cDNA Library Preparation: CLONTECH Laboratories, Inc.
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)
 DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305
 Web site: <http://www.shgc.stanford.edu>
 Contact: (Dickson, Mark) mcd@paxil.stanford.edu
 Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LIML at: <http://image.llnl.gov>
 Series: IRAL Plate: 36 Row: 1 Column: 5
 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 4506262
 This clone has the following problem: retained intron.

FEATURES

source
 1..1038
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
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 /note="Vector: pDNR-LIB"

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 Best Local Similarity 61.6%; Pred. No. 1.8e-38;
 Matches 381; Conservative 0; Mismatches 226; Indels 12; Gaps 3;
 QY 98 GCAACCTGCTGGGCTGCTGGCGGCTGGGGCTGGGGTGGTCTGGCGCGTC 157
 DB 112 GCACCTGATGTTCTGGCGGCTGGTGGGCAACGGGCTGGCCCTGGGCATCCTGAGCG 171
 QY 158 CACTGGCC---CGTGGCCCTGGTCTTCTACATGCTGGTGGTGGCTGACGGTCAACGG 214
 DB 172 CACGGCGACCGGGCGGCGCCCTGGCGCTTGGCGTGTGGTACCGGACTGGGGCGCACCG 231
 QY 215 ACTTGTGGGCAAGTGCCTCTAAGCCCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 274
 DB 232 ACCTGTGGGCAACGACTTCTGAGCGCGCGCGTGTGGTGGCCATGCGCGCAACAGCT 291
 QY 275 GTCTGGGCTGTGGCGCGCATTTGGCAACTCTGTTGGCAAGCTTGGCTTCTTCTCA 334
 DB 292 CCTGTGGGCT---GGCCGAGGGCGGCGCCCTGTGGATGGCTTGGCTTGGCCATCGCCA 348
 QY 335 TGTCTCTTTTGGGCTCTCTCGACACATGCAACTCTGGCCCATGGCACTGGAGTGTGGC 394
 DB 349 TGACCTTCTTGGGCTGGCGTCCATGCTCATCTCTTTGGCCATGGCGGTGGAGCGTGGC 408
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 DB 469 CGCTGGCAGCAATACAGGCTTCTGGGTCTCTTCTGGCGGCTTGGCCCTGTGGGCTGG 528
 QY 515 GGAAGTTCTGTCAGTACTGCCCCCGACCTGGTGTCTTTATCCAGATGTTCCACGAGGAG 574
 DB 529 GCCAACACAGCAGTACTGCCCCCGGCGAGCTGGTGTCTTCTCCGATGCGC-----TGGG 582
 QY 575 GCTCGCTGCGTGGGCTACTCTGTGCTCTACTCCAGCCTCATGGGCGCTGTGGTCC 634
 DB 583 CCAGCGGGCGGCGCGCTTCTCGCTGGCCCTACGCGGCGTGGTGGGCGCTGCTGGTGG 642
 QY 635 TCGCCACCGTGTGTGCAACCTCGGCGCATGCGCAACCTCTATGCGATGACCGCGCGCG 694
 DB 643 CTGCCATCTTCTCTGCAACGGCTGGTTCACCTCTAGCCTCTGCGGCATGTACCGCCAGC 702

QY 695 TGCAGGGGACCCGCGCTC 713
 DB 703 AGAAGCGCCACCGGCTC 721
 RESULT 13
 LOCUS CR601077 2020 bp mRNA linear HTC 21-JUL-2004
 DEFINITION full-length cDNA clone CS0D1069YD07 of Placenta Cot 25-normalized
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 ACCESSION CR601077
 VERSION CR601077.1 GI:50481884
 KEYWORDS HTC; CNSLT_cDNA.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 2020)
 AUTHORS Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished
 REMARK Contact : Feng Liang Email : fliang@lifetech.com URL :
<http://fulllength.invitrogen.com/> Invitrogen Corporation 1600
 Faraday Avenue
 REFERENCE 2 (bases 1 to 2020)
 AUTHORS Genoscope.
 TITLE Direct Submission
 JOURNAL Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
 BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
 - Web : www.genoscope.cns.fr
 COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
 end enriched, double-strand cDNA was digested with Not I and cloned
 into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
 was normalized. Library was constructed by Life Technologies, a
 division of Invitrogen.
 FEATURES
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 Query Match 18.8%; Score 203.4; DB 3; Length 2020;
 Best Local Similarity 61.6%; Pred. No. 2.1e-38;
 Matches 381; Conservative 0; Mismatches 226; Indels 12; Gaps 3;
 QY 98 GCAACCTGCTGGGCTGTGGCGCGCTCGGGGCTGGGGTGGTGGTGGTGGTGGTGGTGG 157
 DB 135 GCACCTGATGTTCTGGCGCGGTGTGGTGGGCAACGGGCTGGCCCTGGGCACTCTGAGCG 194
 QY 158 CACTGGCC---CGTGGCCCTGGTCTTCTACATGCTGGTGGTGGTGGTGGTGGTGGTGG 214
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 QY 275 GTCTGGGCTGTGGCGCGCGCATTTGGACAACCTGTTGTGGCAAGCTTGGCTTCTTCTCA 334
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 QY 395 TCTCCCTAGGCGACCCCTTTCTTCTACCGACGCGACATCACCTGCGGCTGGGGCGCACTGG 454
 DB 432 TGGCGCTGAGCACCCCTACCTCTACGCGCAGCTGGACGGGCGCGGCTGGCGCCGCTGG 491

Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-Format
sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)
20530913
11076861

4
The RIKEN Genome Exploration Research Group Phase II Team and the
FANTOM Consortium.
Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)

5
The FANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)

6 (bases 1 to 2509)
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,
Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,
Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,
Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,
Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,
Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
Nakamura, M., Mishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N.,
Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,
Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,
Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,
Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
Muramatsu, M. and Hayashizaki, Y.
Direct Submission

TITLE
JOURNAL
Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail: genome-res@gsr.riken.jp,
URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222,
Fax: 81-45-503-9216)

COMMENT
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.

Please visit our web site for further details.

URL: http://genome.gsc.riken.jp/

URL: http://fantom.gsc.riken.jp/

FEATURES
Location/Qualifiers

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/mol_type="mRNA"
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(MGDI|MG:197794, GB|NM_008964, evidence: BLASTN, 100%,
match=988)
putative"

ORIGIN

Query Match 18.0%; Score 194.8; DB 3; Length 2509;
Best Local Similarity 55.1%; Pred. No. 2.7e-36;
Matches 523; Conservative 0; Mismatches 372; Indels 55; Gaps 5;
Qy 59 CGGTGATGGCGGGGTCTCTTCAGCACCGGCTCTCTGGGCAACCTGTGGCCCTGGGGC 118
Db 845 CAGCCATCAGTCGGGTGATGTTCTCGGCCGGGGTCTGGGGGAATCTCATCGCACTGGCAC 904

Qy 119 TCGTGGCGCGCTCGGGGCTGGGTGCTCGGGGCTCACTGCGCCGCTGCC---CT 175
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Qy 176 CGGTCTTCTACATGCTGGTGTGGGCTGACCGTCAACCGACTTGTGGGCAAGTGCTCTCC 235
Db 965 CTTTGTTCACGCTGCTGGTAACGGAATTGGTCTCACTGACCTGTGGGAACTGGCTCA 1024
Qy 236 TAAGCCGGTGTGTGGTGTGGCTAGCTCAAGAACCGGAGTGTGGGGTGTGGCCCG 295
Db 1025 TCAGCCGGTGTGTGGTGTGGCTTCAATTCAGAAACACAGACCTGTGGGCTGGCTCCCG 1084
Qy 296 CATTGGACAACCTGTTGTGCAAGCTTTCGCTTCTTCACTGCTCTTCTTCTTGGGCTCTCT 355
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Qy 356 CGACACTGCAACTCTCGGCTGCGCACTGGAGTGTGGCTCTCCCTAGGCAACCTTTCT 415
Db 1139 CGATGCTCATGCTCTTGGCTATGGCCCTGGAACGCTACCTCTCCATCGGGTACCTTACT 1198
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Db 1199 TCTACAGGCGCACCTTATCGCGCGCGGGGTCTGGCGGTGCTGCTGCTCATCTATGGGG 1258
Qy 476 TCTCCTCGCTTCTGCGGCTACCTTTTCATGGGCTTCGGGAAGTTCGTCAGTACTGCC 535
Db 1259 CTTCTTGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1318
Qy 536 CCGGACCTGTTGCTTTTATCAGATGTTCCACGAGGAGGCTCGCTGTCGGTGTGGGGT 595
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Qy 596 ACTCTGTGCTTACTTCCAGCTTCATGGCGCTGCTGGTCTCTCGCCACCGTGTGTGCAACC 655
Db 1358 ACTTTCAGCTGTACGCCACGATGCTCTGCTTATCTGCTGTGCTGCTGCTGCTGCTGCTG 1417
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Db 1697 ATTGACCTTGGTCTTTGGCCATCTTAGGCCACCGGCTCTCGAGGTTAAT 1746

Search completed: April 22, 2005, 17:53:00
Job time : 4053.36 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 22, 2005, 12:36:32 ; Search time 203.43 Seconds
(without alignments)

8686.931 Million cell updates/sec

Title: US-10-689-861-3

Perfect score: 1080

Sequence: 1 atgaagtcgcgtttaccg.....acatggaatccagttgtga 1080

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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6: /cgn2_6/prodata/1/ina/backfile1.seq.*

Pred. No: is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1080	100.0	1488	2	US-08-812-203-4
2	1080	100.0	1488	3	US-09-300-864-4
3	1080	100.0	1488	3	US-09-598-418-4
4	846	78.3	1216	4	US-09-016-434-1474
5	220.6	20.4	2296	1	US-08-239-431A-3
6	220.6	20.4	2296	3	US-09-267-423-3
7	219	20.3	2372	4	US-09-016-434-1441
8	219	20.3	6446	3	US-09-293-170-2
9	214.2	19.8	1077	4	US-09-826-509-558
10	211	19.5	1074	2	US-08-463-081B-29
11	211	19.5	1074	2	US-08-461-379A-29
12	211	19.5	1074	2	US-08-462-390B-29
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14	211	19.5	1074	3	US-08-465-585C-29
15	211	19.5	1074	3	US-08-652-446-29
16	211	19.5	2450	2	US-08-463-081B-5
17	211	19.5	2450	2	US-08-461-379A-5
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21	211	19.5	2450	3	US-08-652-446-5
22	201.8	18.7	1356	1	US-08-134-012-5
23	201.8	18.7	1356	1	US-08-520-519-5
24	201.8	18.7	1356	3	US-09-039-798-5
25	201.8	18.7	1417	1	US-08-134-012-4
26	201.8	18.7	1417	1	US-08-520-519-4
27	201.8	18.7	1417	3	US-09-039-798-4

28 201.8 18.7 1417 4 US-09-016-434-1403 Sequence 1403, Ap
29 201.8 18.7 1498 1 US-08-134-012-6 Sequence 6, Appli
30 201.8 18.7 1498 1 US-08-520-519-6 Sequence 6, Appli
31 201.8 18.7 1498 3 US-09-039-798-6 Sequence 6, Appli
32 107.2 9.9 1209 4 US-09-826-509-556 Sequence 556, App
33 107.2 9.9 1376 4 US-09-016-434-1361 Sequence 1361, Ap
34 107.2 9.9 1394 2 US-08-068-729-3 Sequence 3, Appli
35 107.2 9.9 1394 3 US-09-255-671-3 Sequence 3, Appli
36 107.2 9.9 1394 3 US-09-395-366-3 Sequence 3, Appli
37 101.2 9.4 1467 4 US-09-826-509-560 Sequence 560, App
38 101.2 9.4 1958 1 US-08-115-365-1 Sequence 1, Appli
39 101.2 9.4 1958 1 US-08-586-897-1 Sequence 1, Appli
40 101.2 9.4 1958 4 US-09-016-434-1380 Sequence 1380, Ap
41 99 9.2 2442 1 US-08-390-162-5 Sequence 5, Appli
42 99 9.2 2442 1 US-08-685-945B-5 Sequence 5, Appli
43 82.6 7.6 2932 4 US-09-016-434-1419 Sequence 1419, Ap
44 82.6 7.6 2932 4 US-09-054-272-5 Sequence 5, Appli
45 71.6 6.6 5688 3 US-09-293-170-7 Sequence 7, Appli

ALIGNMENTS

RESULT 1

US-08-812-203-4
; Sequence 4, Application US/08812203
; Patent No. 5958723
; GENERAL INFORMATION:
; APPLICANT: ABRAMOVITZ, MARK
; APPLICANT: BOIE, YVES
; APPLICANT: SAWYER, NICOLE
; APPLICANT: METTERS, KATHLEEN
; APPLICANT: SLIPETZ, DEBORAH
; TITLE OF INVENTION: DNA ENCODING PROSTAGLANDIN RECEPTOR DP
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: JOHN W. WALLEN, III
; STREET: 126 E. LINCOLN AVE., P.O. BOX 2000
; CITY: RAHWAY
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065-0900
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/812,203
; FILING DATE: 06-MAR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/378,682
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: WALLEN III, JOHN W.
; REGISTRATION NUMBER: 35,403
; REFERENCE/DOCKET NUMBER: MRL 94/185
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908)594-3905
; TELEX: (908)594-4720
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1488 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-812-203-4

Query Match 100.0%; Score 1080; DB 2; Length 1488;
Best Local Similarity 100.0%; Pred. No. 8.4e-256;
Matches 1080; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAAGTCGCGCTTCTACCGCTGCCAGACACCACTCTGTGAAAAAGCAACTCGCGG 60
DB 350 ATGAAGTCGCGCTTCTACCGCTGCCAGACACCACTCTGTGAAAAAGCAACTCGCGG 409
QY 61 GTGATGGCGGGGTGCTCTTTCAGACACCGGCTCTCTGGCAACCTGTGGCCCTGGGGCTG 120
DB 410 GTGATGGCGGGGTGCTCTTTCAGACACCGGCTCTCTGGCAACCTGTGGCCCTGGGGCTG 469
QY 121 CTGGCGCGCTCGGGGTGGGGTGGTGTCTCGGGGTGCACTGGCCCGGTGCGCTCGGTC 180
DB 470 CTGGCGCGCTCGGGGTGGGGTGGTGTCTCGGGGTGCACTGGCCCGGTGCGCTCGGTC 529
QY 181 TTCTACATCTGGTGTGGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT 240
DB 530 TTCTACATCTGGTGTGGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT 589
QY 241 CGGATGGTGTGGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT 300
DB 590 CGGATGGTGTGGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT 649
QY 301 GACAACTGTTGTGCAAGCTTGGCTTCTTCAATGCTCTTCTTCTTCTTCTTCTTCTTCT 360
DB 650 GACAACTGTTGTGCAAGCTTGGCTTCTTCAATGCTCTTCTTCTTCTTCTTCTTCTTCT 709
QY 361 CTGCAACTCTGGCCATGGCACTGGAGTGTGGCTCTCTCTAGGACACCTTCTTCTTCTAC 420
DB 710 CTGCAACTCTGGCCATGGCACTGGAGTGTGGCTCTCTCTAGGACACCTTCTTCTTCTAC 769
QY 421 CGACGACATCACTCTGGCCCTGGCGGCACTGGTGGCCCGGCTGTGAGCGCTTCTTCTTCT 480
DB 770 CGACGACATCACTCTGGCCCTGGCGGCACTGGTGGCCCGGCTGTGAGCGCTTCTTCTTCT 829
QY 481 CTGGCTTCTGGCGCTACTTCTTCAATGAGCTTGGGAGTTCGTGAGTACTGCCCCGGG 540
DB 830 CTGGCTTCTGGCGCTACTTCTTCAATGAGCTTGGGAGTTCGTGAGTACTGCCCCGGG 889
QY 541 ACTGCTGCTTATCCAGATGTCCAGAGGAGGCTGCTCTGCTGCTGCTGCTGCTGCTGCT 600
DB 890 ACTGCTGCTTATCCAGATGTCCAGAGGAGGCTGCTCTGCTGCTGCTGCTGCTGCTGCT 949
QY 601 GTGCTCTACTCAGCCTCATAGCGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
DB 950 GTGCTCTACTCAGCCTCATAGCGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1009
QY 661 GGCATGGCAACTCTATGCGATGCAACCGCGGCTGAGCGGACCCGCGCTCTCTGACCC 720
DB 1010 GGCATGGCAACTCTATGCGATGCAACCGCGGCTGAGCGGACCCGCGCTCTCTGACCC 1069
QY 721 AGGGAATGTGCGAGCGCGCGGACCGGAGGAGCGTCCCTCAGCCCTGGAGGAG 780
DB 1070 AGGGAATGTGCGAGCGCGCGGACCGGAGGAGCGTCCCTCAGCCCTGGAGGAG 1129
QY 781 CTGGATCACTCTCTGCTGCTGCGCTGATGACCGCTGCTCTTCACTATGTTTCTCTGCCC 840
DB 1130 CTGGATCACTCTCTGCTGCTGCGCTGATGACCGCTGCTCTTCACTATGTTTCTCTGCCC 1189
QY 841 GTAATTTATCGCGCTTACTATGAGGATTTAAGGATGTCAGGAGAAAAAGGACCTCT 900
DB 1190 GTAATTTATCGCGCTTACTATGAGGATTTAAGGATGTCAGGAGAAAAAGGACCTCT 1249
QY 901 GAAGAGCAGAGACCTCGAGCCTTGGATTTCTATCTGATTTCAATTCGAGCCCT 960
DB 1250 GAAGAGCAGAGACCTCGAGCCTTGGATTTCTATCTGATTTCAATTCGAGCCCT 1309
QY 961 TGGATTTTATCATTTTTCAGATCTCAGTATTTTCGATATTTTTCACAAAGATTTTCAT 1020
DB 1310 TGGATTTTATCATTTTTCAGATCTCAGTATTTTCGATATTTTTCACAAAGATTTTCAT 1369
QY 1021 AGACCTCTTAGGTACAGGACCGGTGACAGCAATTTCACTAAATGGAATCCAGTCTGTGA 1080
DB 1370 AGACCTCTTAGGTACAGGACCGGTGACAGCAATTTCACTAAATGGAATCCAGTCTGTGA 1429

RESULT 2
US-09-300-864-4
; Sequence 4, Application US/09300864
; Patent No. 6214972
; GENERAL INFORMATION:
; APPLICANT: ABRAMOVITZ, MARK
; APPLICANT: BOIE, YVES
; APPLICANT: SAWYER, NICOLE
; APPLICANT: METTERS, KATHLEEN
; APPLICANT: SLIPETZ, DEBORAH
; TITLE OF INVENTION: DNA ENCODING PROSTAGLANDIN RECEPTOR DP
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: JOHN W. WALLEN, III
; STREET: 126 E. LINCOLN AVE., P.O. BOX 2000
; CITY: RAHWAY
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065-0900
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/300,864
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/378,682
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: WALLEN III, JOHN W.
; REGISTRATION NUMBER: 35,403
; REFERENCE/DOCKET NUMBER: MRL 94/185
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 594-3905
; TELEX: (908) 594-4720
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1488 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-09-300-864-4

Query Match 100.0%; Score 1080; DB 3; Length 1488;
Best Local Similarity 100.0%; Pred. No. 8.4e-258;
Matches 1080; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGAAGTCGCGCTTCTACCGCTGCCAGACACCACTCTGTGAAAAAGCAACTCGCGG 60
DB 350 ATGAAGTCGCGCTTCTACCGCTGCCAGACACCACTCTGTGAAAAAGCAACTCGCGG 409
QY 61 GTGATGGCGGGGTGCTCTTTCAGACACCGGCTCTCTGGCAACCTGTGGCCCTGGGGCTG 120
DB 410 GTGATGGCGGGGTGCTCTTTCAGACACCGGCTCTCTGGCAACCTGTGGCCCTGGGGCTG 469
QY 121 CTGGCGCGCTCGGGGTGGGGTGGTGTCTCGGGGTGCACTGGCCCGGTGCGCTCGGTC 180
DB 470 CTGGCGCGCTCGGGGTGGGGTGGTGTCTCGGGGTGCACTGGCCCGGTGCGCTCGGTC 529
QY 181 TTCTACATCTGGTGTGGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT 240
DB 530 TTCTACATCTGGTGTGGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT 589
QY 241 CGGATGGTGTGGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT 300
DB 590 CGGATGGTGTGGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCT 649
QY 301 GACAACTGTTGTGCAAGCTTGGCTTCTTCAATGCTCTTCTTCTTCTTCTTCTTCTTCT 360


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Db 650 GACAACTCGTGTGGCCAGCCTTCGCTCTTTCATGTCCTCTTTGGGCTCTCTCGACA 709
Qy 361 CTGCAACTCTTGCCCATGGCACTGGAGTGTGGCTCTCCCTAGGCAACCCCTTTCTTCTAC 420
Db 710 CTGCAACTCTTGCCCATGGCACTGGAGTGTGGCTCTCCCTAGGCAACCCCTTTCTTCTAC 769
Qy 421 CGACGGCACAATCACTCTGCGCTTGGGGCACTGGTGGCCCGGCTGGTGGAGCGCTTCTCC 480
Db 770 CGACGGCACAATCACTCTGCGCTTGGGGCACTGGTGGCCCGGCTGGTGGAGCGCTTCTCC 829
Qy 481 CTGGCTTTCTGCGCGTACCTTTTCATGGGCTTCGGGAAGTTCGTGAGTACTGCCCCGGC 540
Db 830 CTGGCTTTCTGCGCGTACCTTTTCATGGGCTTCGGGAAGTTCGTGAGTACTGCCCCGGC 889
Qy 541 ACCTGGTGTCTTATCCAGATGGTCCACGAGAGGGCTCGCTGTGGTGTGGGTACTCT 600
Db 890 ACCTGGTGTCTTATCCAGATGGTCCACGAGAGGGCTCGCTGTGGTGTGGGTACTCT 949
Qy 601 GTGCTCTACTCGACCTCATGGCGCTGTGGTCTCTCGCAACCGTGTGTGCAACCTCGGC 660
Db 950 GTGCTCTACTCGACCTCATGGCGCTGTGGTCTCTCGCAACCGTGTGTGCAACCTCGGC 1009
Qy 661 GCATCGGCACAATCTATCGATGTCACCGCGGCTGCGGGCAACCGCGCTCTCGCAC 720
Db 1010 GCATCGGCACAATCTATCGATGTCACCGCGGCTGCGGGCAACCGCGCTCTCGCAC 1069
Qy 721 AGGAGCTGTGCCAGCGCGCGGAGCGGAGGAGCGTCCCTCAGGCCCTTGGAGGAG 780
Db 1070 AGGAGCTGTGCCAGCGCGCGGAGCGGAGGAGCGTCCCTCAGGCCCTTGGAGGAG 1129
Qy 781 CTGGATCACTCTCTGTGTGGCGCTGTATGACCGTCTCTTCAATGTGTCTTGTGCC 840
Db 1130 CTGGATCACTCTCTGTGTGGCGCTGTATGACCGTCTCTTCAATGTGTCTTGTGCC 1189
Qy 841 GTAATTTATCGCGCTTACTATGAGCATTTAAGGATGTCAGGAGAAACAGGACCTCT 900
Db 1190 GTAATTTATCGCGCTTACTATGAGCATTTAAGGATGTCAGGAGAAACAGGACCTCT 1249
Qy 901 GAAGAAGCAGAAAGACCTCCGAGCCTTTCGATTTCTATCTGTGATTTCAATTTGGACCT 960
Db 1250 GAAGAAGCAGAAAGACCTCCGAGCCTTTCGATTTCTATCTGTGATTTCAATTTGGACCT 1309
Qy 961 TGAATTTTATCAATTTTCAATCTCAGTATTTTCGATATTTTTCACAAAGATTTTCAT 1020
Db 1310 TGAATTTTATCAATTTTCAATCTCAGTATTTTCGATATTTTTCACAAAGATTTTCAT 1369
Qy 1021 AGACCTTTAGTACAGGACCGGTGACGATTTCCACTAAATGGAATCCAGTCTGTGA 1080
Db 1370 AGACCTTTAGTACAGGACCGGTGACGATTTCCACTAAATGGAATCCAGTCTGTGA 1429
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RESULT 3

US-09-598-418-4

; Sequence 4, Application US/09598418

; Patent No. 6395499

; GENERAL INFORMATION:

; APPLICANT: ABRAMOVITZ, MARK

; BOJE, YVES

; SAWYER, NICOLE

; METTERS, KATHLEEN

; SLIPETZ, DEBORAH

; TITLE OF INVENTION: DNA ENCODING PROSTAGLANDIN RECEPTOR DP

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: JOHN W. WALLEN, III

; STREET: 126 E. LINCOLN AVE., P.O. BOX 2000

; CITY: RAHWAY

; STATE: NJ

; COUNTRY: USA

; ZIP: 07065-0900

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/598,418
; FILING DATE: 20-Jun-2000
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: WALLEN III, JOHN W.
; REGISTRATION NUMBER: 35,403
; REFERENCE/DOCKET NUMBER: MRL 94/185
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908)594-3905
; TELEX: (908)594-4720
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1488 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-598-418-4
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Query Match 100.0%; Score 1080; DB 3; Length 1488;

Best Local Similarity 100.0%; Pred. No. 8.4e-258;

Matches 1080; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 ATGAAGTCGCCCTTCTACCGCTGCCAGAACACCACTCTGTGAAAAAGCAACTCGGCG 60
Db 350 ATGAAGTCGCCCTTCTACCGCTGCCAGAACACCACTCTGTGAAAAAGCAACTCGGCG 409
Qy 61 GTGATGGCGGGGTGCTCTTACAGCACCGGCTCTCTGGCAACCTGTGCGCCCTGGGGCTG 120
Db 410 GTGATGGCGGGGTGCTCTTACAGCACCGGCTCTCTGGCAACCTGTGCGCCCTGGGGCTG 469
Qy 121 CTGGCGCGCTCGGGCTGGGGTGGTCTCGCGCGCTGCTGCGCGCGCTGCTGCGCGCTG 180
Db 470 CTGGCGCGCTCGGGCTGGGGTGGTCTCGCGCGCTGCTGCGCGCGCTGCTGCGCGCTG 529
Qy 181 TTCTACATGCTGTGTGGCTGACGGTCAACGCTCTGCGGCAAGTGCCTCTTAAGC 240
Db 530 TTCTACATGCTGTGTGGCTGACGGTCAACGCTCTGCGGCAAGTGCCTCTTAAGC 589
Qy 241 CGCGTGGTGTGGCTGCTTACGCTCAGAACCGGAGTCTCGGGTGTCTGCGCCCGCATTTG 300
Db 590 CGCGTGGTGTGGCTGCTTACGCTCAGAACCGGAGTCTCGGGTGTCTGCGCCCGCATTTG 649
Qy 301 GACAACTGTTGTGCAAGCTTTCGCTTCTTCAATGTCCTTTTGGGCTCTCTCGACA 360
Db 650 GACAACTGTTGTGCAAGCTTTCGCTTCTTCAATGTCCTTTTGGGCTCTCTCGACA 709
Qy 361 CTGCAACTCTCGGCCATGCACTGAGTCTGCTGCTCTCCCTAGGGCACCCCTTTCTTCTAC 420
Db 710 CTGCAACTCTCGGCCATGCACTGAGTGTGCTGCTCTCCCTAGGGCACCCCTTTCTTCTAC 769
Qy 421 CGACGGCACAATCACTCTGCGCTTGGCGCACTGTGTGGCCCGGCTGGTGGAGCGCTTCTCC 480
Db 770 CGACGGCACAATCACTCTGCGCTTGGCGCACTGTGTGGCCCGGCTGGTGGAGCGCTTCTCC 829
Qy 481 CTGGCTTTCTGCGCGTACCTTTTCATGGGCTTTCGGGAAGTTCGTGAGTACTGCCCCGGC 540
Db 830 CTGGCTTTCTGCGCGTACCTTTTCATGGGCTTTCGGGAAGTTCGTGAGTACTGCCCCGGC 889
Qy 541 ACCTGGTGTCTTATCCAGATGGTTCACGAGAGGGCTCGCTGTGGTGTGGGTACTCT 600
Db 890 ACCTGGTGTCTTATCCAGATGGTTCACGAGAGGGCTCGCTGTGGTGTGGGTACTCT 949
Qy 601 GTGCTCTACTCGACCTCATGGCGCTGTGTGTCCTCGCAACCGTGTGTGCAACCTCGGC 660
Db 950 GTGCTCTACTCGACCTCATGGCGCTGTGTGTCCTCGCAACCGTGTGTGCAACCTCGGC 1009
Qy 661 GCATCGGCACAATCTATCGATGTCACCGCGGCTGCGGGCAACCGCGCTCTCGCAC 720
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Db 1010 GCCATGGCAACCTCTATGCGATGCACCGCGGCTGCAGGCGCACCGCGCTCTGCGACC 1069
QY 721 AGGAGCTGCGAGCGCGCGGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 780
Db 1070 AGGAGCTGCGAGCGCGCGGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1129
QY 781 CTGGATCACTCTCTGCTGCTGCGGCTGATGACCGGCTCTTCACTATGTTCTCTGCCC 840
Db 1130 CTGGATCACTCTCTGCTGCTGCGGCTGATGACCGGCTCTTCACTATGTTCTCTGCCC 1189
QY 841 GTAATTATCGGCTTACTATGAGCATTTAAGGATGTCAAGGAGAAAAACAGGACCTCT 900
Db 1190 GTAATTATCGGCTTACTATGAGCATTTAAGGATGTCAAGGAGAAAAACAGGACCTCT 1249
QY 901 GAAGAAGCAAGACCTCGAGCCTTGGGATTTCTATCTGATTTCAATTGTGACCTCT 960
Db 1250 GAAGAAGCAAGACCTCGAGCCTTGGGATTTCTATCTGATTTCAATTGTGACCTCT 1309
QY 961 TGGATTTTATCATTTTCAGATCTCCAGTATTTTCGATATTTTTCAGAAATTTTCATT 1020
Db 1310 TGGATTTTATCATTTTCAGATCTCCAGTATTTTCGATATTTTTCAGAAATTTTCATT 1369
QY 1021 AGACCTTTAGGTACAGGAGCGGTGCAGCAATTCACCTAAATGGAATTCAGTCTGTGA 1080
Db 1370 AGACCTTTAGGTACAGGAGCGGTGCAGCAATTCACCTAAATGGAATTCAGTCTGTGA 1429

RESULT 4

US-09-016-434-1474
; Sequence 1474, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSES: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HERewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1474:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1216 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK

i CLONE: g940378
US-09-016-434-1474
Query Match 78.3%; Score 846; DB 4; Length 1216;
Best Local Similarity 100.0%; Pred. No. 7.5e-200;
Matches 846; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGAAGTCGCGCTTCTACCGCTGCCAGAACACCACTCTGTGGAAGAAAGGCAACTCGGGC 60
Db 350 ATGAAGTCGCGCTTCTACCGCTGCCAGAACACCACTCTGTGGAAGAAAGGCAACTCGGGC 409
QY 61 GTGATGGCGGGGTGCTCTTTCAGCACCGGCTCTTGGGCAACCTCTGTGCGCCCTGGGGCTG 120
Db 410 GTGATGGCGGGGTGCTCTTTCAGCACCGGCTCTTGGGCAACCTCTGTGCGCCCTGGGGCTG 469
QY 121 CTGGCGCCTCGGGCTGGGGTGTGCTCGGGCGCTCCACTGCGGCCCGCTGCCCTCGGTC 180
Db 470 CTGGCGCCTCGGGCTGGGGTGTGCTCGGGCGCTCCACTGCGGCCCGCTGCCCTCGGTC 529
QY 181 TTCTACATGCTGGTGTGGGCTGACGCTCACCGACTTGTGGGCAAGTGCCTCTTAAGC 240
Db 530 TTCTACATGCTGGTGTGGGCTGACGCTCACCGACTTGTGGGCAAGTGCCTCTTAAGC 589
QY 241 CCGGTGTGTGCTGCTGCTACGCTCAGAACCGGAGTCTGCGGGTCTTTCGCGCCCGCATG 300
Db 590 CCGGTGTGTGCTGCTGCTACGCTCAGAACCGGAGTCTGCGGGTCTTTCGCGCCCGCATG 649
QY 301 GACAACTGCTGTGGCAAGCCTTGGCCTTCTTATGCTCTTCTTGGGCTCTCTCGACA 360
Db 650 GACAACTGCTGTGGCAAGCCTTGGCCTTCTTATGCTCTTCTTGGGCTCTCTCGACA 709
QY 361 CTGCAACTCTCGGCGCATGGGCTGAGTGTGGGCTCTCCCTAGGCAACCTTCTTCTAC 420
Db 710 CTGCAACTCTCGGCGCATGGGCTGAGTGTGGGCTCTCCCTAGGCAACCTTCTTCTAC 769
QY 421 CGAGCGCACATCACCTCGGCTGGGCGCACTGTGTGGGCGGCGGTGAGCGCTTCTTCTC 480
Db 770 CGAGCGCACATCACCTCGGCTGGGCGCACTGTGTGGGCGGCGGTGAGCGCTTCTTCTC 829
QY 481 CTGGCTTTCTGGGCTTACCTTTTCATGGGCTTCGGAAGTTCGTGAGTACTGCGCGGC 540
Db 830 CTGGCTTTCTGGGCTTACCTTTTCATGGGCTTCGGAAGTTCGTGAGTACTGCGCGGC 889
QY 541 ACCTGTGCTTTATCCAGATGTCACAGAGGCTCGCTGTGCGGTGTGGGGTACTCT 600
Db 890 ACCTGTGCTTTATCCAGATGTCACAGAGGCTCGCTGTGCGGTGTGGGGTACTCT 949
QY 601 GTGCTTACTCCAGCTCATGGCGCTGTGTGCTTCTCGCCACCGTGTGTGCAACTCTGGC 660
Db 950 GTGCTTACTCCAGCTCATGGCGCTGTGTGCTTCTCGCCACCGTGTGTGCAACTCTGGC 1009
QY 661 GCCATGCGCAACCTCTATGCGATGACCGGGCTGCGAGCGGCGCCCGGCTCTTGGCACC 720
Db 1010 GCCATGCGCAACCTCTATGCGATGACCGGGCTGCGAGCGGCGACCCCGGCTCTTGGCACC 1069
QY 721 AGGAGCTGCGGAGCGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 780
Db 1070 AGGAGCTGTGCGAGCGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1129
QY 781 CTGGATCACTCTGCTGCTGCGGCTGATGACCGGCTCTTCACTATGTTCTCTGCCC 840
Db 1130 CTGGATCACTCTGCTGCTGCGGCTGATGACCGGCTCTTCACTATGTTCTCTGCCC 1189
QY 841 GTAATT 846
Db 1190 GTAATT 1195

RESULT 5

US-08-239-431A-3
; Sequence 3, Application US/08239431A
; Patent No. 5716835
; GENERAL INFORMATION:

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; APPLICANT: Regan, John W.
; APPLICANT: Gil, Daniel W.
; APPLICANT: Woodward, David F.
; TITLE OF INVENTION: NOVEL HUMAN EP PROSTAGLANDIN RECEPTOR
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson and Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: USA
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/239,431A
; FILING DATE: 05-MAY-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Israel, Ned A
; REGISTRATION NUMBER: 29,655
; REFERENCE/DOCKET NUMBER: ALRGN.053A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-235-8550
; TELEFAX: 619-235-0176
;
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2296 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 157...1230
; OTHER INFORMATION:
;
; US-08-239-431A-3
;
; Query Match 20.4%; Score 220.6; DB 1; Length 2296;
; Best Local Similarity 57.8%; Pred. No. 96-45;
; Matches 557; Conservative 0; Mismatches 349; Indels 57; Gaps 7;
;
; QY 48 AGGGAACCTCGGGGTGATGGGGGGGTGCTTTCAGACCGCGCTCTGGGCAACTGCT 107
; DB 219 AGGGAACCTCGGGGTGATGGGGGGGTGCTTTCAGACCGCGCTCTGGGCAACTGCT 278
; QY 108 GCGCTCGGGGTGCTGGGGGGGTGCTGGGGGGGTGCTGGGGGGGTGCTGGGGGGGT 165
; DB 279 AGCATTTGGGGGTGCTGGGGGGGTGCTGGGGGGGTGCTGGGGGGGTGCTGGGGGG 338
; QY 166 CCGCTGCC-CTCGGTCTTTCATCATGCTGGGTGTGGCTTACCGGTACCGGTACCGGT 224
; DB 339 GAGCTCCCTCTCTTGTTCACCGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGG 398
; QY 225 CAAGTGCCTTCAAGCCCGGTGCTGGCTCCCTACGCTAGAACCGGAGTCTGGGGT 284
; DB 399 GACCTGCCTCATCAGCCCACTGTGCTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGT 458
; QY 285 GCTTGGCGCCGATGGGCAACTCGTTGTGCAAGCCTTTCGCTTCTTCATGCTCTTCT 344
; DB 459 ACTGGCGGCC-----GAGAGCGCGCGGTGACCTACTTTCGCTTTCGCTTTCGCTTCT 512
;
; 345 TGGGCTCTCTCGACACTGCAACTCTCTGCGCATGCACTGGAGTGCTGCTCTCCCTAGG 404
; DB 513 CAGCCTGGCCACGATGCTCATGCTCTTGGCCATGCGCCCTGGAGCGCTACTCTTCGATCG 572
; QY 405 GCACCTTTTCTTACACGACGACATCACCTGCGCTGCGCGCACCTGCTGGCGCACCTG 464
; DB 573 GCACCTTCTTCTTACACGACGCGGTCTGCGGCTTCCGGGGGCTGGCGCTGCTGCTGT 632
; QY 465 GGTGAGCGCTTCTCTCGGCTTCTGCGCGCTACTTTTCATGGGCTTCGGGAAAGTCTGT 524
; DB 633 CATCTATGCACTCTCCCTGCTCTTCTGCTGCTGCGCTGCTGCTGCTATGGGCACTGCT 692
; QY 525 GCAGTACTGCGCGCGACCTGCTGCTTTCATCAGATGCTCAGAGGAGGCTGCTGCTGCTC 584
; DB 693 CCAGTACTGCGCGCGACCTGCTGCTTTCATCGGCACTGCTGCTGCTGCTGCTGCTGCT 734
; QY 585 GGTGCTGGGTACTCTGCTGCTTCTACTCCAGCCTCATGCGGCTGCTGCTGCTGCTGCTG 644
; DB 735 ---GACCGCTTACCTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 791
; QY 645 GCTGTGCAACCTCGCGCGACGCAACTCTTATCGGATGCACTGCGCG--GCTGCAAGCG 702
; DB 792 CGCCTGCAACTTCAGTGTCTTCTCAACTCTCATCGCATGCACTGCGCGGAGCGGAGAAG 851
; QY 703 CACCGCGCTCTGCACTGCGGACTGTGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 762
; DB 852 CGCTGCGGACCTTCTGCGGCGGTGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 911
; QY 763 CCTCAGCCCT---GGAGGAGCTGATCACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 818
; DB 912 AAGGTGTCCATGCGGAGGAGACGACCACTCATTTCTCTGCTGCTGCTGCTGCTGCTGCT 971
; QY 819 CTTCATATGTTCTCTGCGCGTAATTTATCGCGCTTACTATGGAGCATTTAAGGATGT 878
; DB 972 CTTCGCGCTGCTGCTCTTTCGCTTTCACGATTTTTCATAT-----1011
; QY 879 CAGGAGAAAAACAGGACCTCTGAAGAAGACGAGAACCTCGAGCGCTTGCAGATTCTATC 938
; DB 1012 -ATGAATGAAACCTCTTCCGAAAGAAAAATGGGACCTCCAAAGCTCTTAGGTTTTATC 1070
; QY 939 TGTGATTTCAATTGAGACCTTGGATTTTATCATTTTATCATTTTTCAGATCTCCAGTAT 998
; DB 1071 AATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1130
; QY 999 ATT 1001
; DB 1131 AAT 1133
;
; RESULT 6
; US-09-267-423-3
; Sequence 3, Application US/09267423
; Patent No. 6395878
; GENERAL INFORMATION:
; APPLICANT: Regan, John W.
; APPLICANT: Gil, Daniel W.
; APPLICANT: Woodward, David F.
; TITLE OF INVENTION: No. 6395878el Human Prostaglandin EP Receptor
; FILE REFERENCE: 17023 DIV CIP
; CURRENT APPLICATION NUMBER: US/09/267,423
; CURRENT FILING DATE: 1999-03-12
; EARLIER APPLICATION NUMBER: 09/019,393
; EARLIER FILING DATE: 1998-02-05
; EARLIER APPLICATION NUMBER: 08/239,431
; EARLIER FILING DATE: 1994-05-05
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 2296
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS

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LOCATION: (157)...(1233)
US-09-267-423-3

Query Match 20.4%; Score 220.6; DB 3; Length 2296;
Best Local Similarity 57.8%; Pred. No. 9e-45;
Matches 557; Conservative 0; Mismatches 349; Indels 57; Gaps 7;

QY 48 AGGCAACTCGGCGGTGATGGGGGGGTGCTCTTACGACCGCGCTCTGGGCAACTGCT 107
DB 219 AGGCAAAAGCCAGCCATCAGTCCGTCACTGCTGCGCGGGGTGCTGGGAACCTCAT 278

QY 108 GGCCTTGGGCGCTGCTGGCGCGCTCGGGGTGGGT--GGTGTCTGGCGGTCCACTGCGC 165
DB 279 ASCACTGGCGCTGCTGGCGCGCGCTGGCGGGGAGCGTGGGTGACGCGCGCGCGAG 338

QY 166 CGCTGTGC--CTCGGTCTTCTACATGCTGTGTGGCTGACGGTACCGACTTGTGG 224
DB 339 GAGCTCCCTCTCTCTTGTTCACGTCTGTGTGACCGAGCTGTGTTCACCGACTGCTCG 398

QY 225 CAAGTGCCTCTAAGCCCGGTGCTGCTGCTACGCTCAGAACCGAGTCTGGGT 284
DB 399 GACCTGCTCTACAGCCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 458

QY 285 GCTTGGCGCGGATGGAACCTCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 344
DB 459 ACTGGCGCC-----GAGAGCGCGCGTGCACCTACTTCTGCTTTCGCACTGCTTCT 512

QY 345 TGGGTCTCTCGACACTGCAACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 404
DB 513 CAGCTTGGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 572

QY 405 GCACCTTCTTCTACCGCGGACACTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 464
DB 573 GCACCTTCTTCTACCGCGGACACTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 632

QY 465 GGTGAGCGCTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 524
DB 633 CATCTATGAGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 692

QY 525 GAGTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 584
DB 693 CCAGTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 734

QY 585 GGTGCTGGGTACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 644
DB 735 ----GACCGTCTTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 791

QY 645 GCTGTGCAACTCGGCGCATCGCAACCTCTATGCTGCTGCTGCTGCTGCTGCTGCTGCT 702
DB 792 CGCTTGCACCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 851

QY 703 CACCGCGCTCTGCAACGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 762
DB 852 CGCTGCGGACCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 911

QY 763 CTTGACCCCT----GGAGGCTGATCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 818
DB 912 AAGGTGTTCATGCGGAGGAGACGACCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 971

QY 819 CTTTCACTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 878
DB 972 CTTTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1011

QY 879 CAAGGAGAAAAACAGACTCTGTAAGAGACGAACTCTGAGCTTGGAGTTCCTATTC 938
DB 1012 -ATGAATGAAACCTCTTCCGAGAAAGAAATGAGACCTTCCAGTCTTTAGGTTTATTC 1070

QY 939 TGTGATTTCAATGTGGACCTTGTGATTTTATTTTATTTTATTTTATTTTATTTTATTTT 998
DB 1071 AATTAAATCAATATGACCCCTGGGTCTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1130

QY 999 ATT 1001

DB 1131 AAT 1133

RESULT 7

US-09-016-434-1441
; Sequence 1441, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1441:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2372 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: G639719
; US-09-016-434-1441

Query Match 20.3%; Score 219; DB 4; Length 2372;
Best Local Similarity 57.7%; Pred. No. 2.3e-44;
Matches 556; Conservative 0; Mismatches 350; Indels 57; Gaps 7;

QY 48 AGGCAACTCGGCGGTGATGGGGGGGTGCTCTTACGACCGCGCTCTGGGCAACTGCT 107
DB 219 AGGCAAAAGCCAGCCATCAGTCCGTCACTGCTGCGCGGGGTGCTGGGAACCTCAT 278

QY 108 GGCCTTGGGCGCTGCTGGCGCGCTCGGGGTGGGT--GGTGTCTGGCGGTCCACTGCGC 165
DB 279 AGCACTGGCGCTGCTGGCGCGCTGCGCGGGGAGCGTGGGTGACGCGCGCGCGAG 338

QY 166 CGCTGTGC--CTCGGTCTTCTACATGCTGTGTGGCTGACGGTACCGACTTGTGG 224
DB 339 GAGCTCCCTCTCTCTTGTTCACGTCTGTGTGACCGAGCTGTGTTCACCGACTGCTCG 398

QY 225 CAAGTGCCTCTTAAAGCCCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 284
DB 399 GACCTGCTCTATCAGCCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 458

QY 285 GCTTGGCGCGGATGGAACCTCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 344

Db 459 ACTGGCGCC-----GAGAGCGCGGCTGCACCTACTTCGCTTTTCGCCATGACCTTCTT 512
Qy 345 TGGGCTCTCTGACACTGCAACTCTGCGCATGCGCACTGGAGTGTGCTCTCCCTAGG 404
Db 513 CAGCTTGGCCAGATGCTATGCTCTTCGCGCATGGCCCTGGAGCGCTACCTCTCGATCG 572
Qy 405 GCACCTTTCTTCTACGAGCGGCACATACCTGCGCGCTGGCGCACTGGTGGCCCGCT 464
Db 573 GCACCCCTACTTCTACAGCGCGGCTCTCGGCTTCGGGCGCTGGCGCTGCTGCTGT 632
Qy 465 GGTGAGCGCTCTCTCCCTGCTTCTGCGCGCTTACCTTTTCATGGGCTTCGGGAAGTTCGT 524
Db 633 CATCTATGAGTCTCTCTGCTCTTCTGCTGCGCTGCTGCTGCTGCTGCTGCTGCT 592
Qy 525 GCAGTACTGCCCGGCACCTGCTGCTTTATCCAGATGCTGCCAGAGAGGCTGCTGTC 584
Db 693 CCAGTACTGCCCGGCACCTGCTGCTTCTATCGGCAACGGCG-----734
Qy 585 GGTGCTGGGTTACTCTGCTCTACTCCAGCCTCATGGCGCTGCTGCTCTGCTGCTGCT 644
Db 735 ---GACCGCTTACCTGACGCTGTACGCCACCTGCTGCTCTCAATTGCTCTGCTGCT 791
Qy 645 GCTGTGCAACCTCGGCGCATGCGCAACCTCTATGCGATGCAACCGCG--GCTGCAAGCG 702
Db 792 CGCTGCAACTTCAGTGTCTATCTCACTCATCGCATGCAACCGCGAAGCGGAGAG 851
Qy 703 CACCGCGCTCTGCAACGAGGACTGTGCGAGCGCGCGCGAGCGGAGGAGCGTCC 762
Db 852 CGCTGCGGACCTTCCCTGGGAGTGCGCGGCGCGCGCGCGCGCGCGCGAGAGGGA 911
Qy 763 CCTCAGCCCT----GGAGGAGTGGATCACTCTGCTGCTGCTGCTGCTGCTGCTGCT 818
Db 912 AAGGAGTGCATGCGGAGGAGACGACCACTCATCTCTGCTGCTGCTGCTGCTGCTGCT 971
Qy 819 CTTCATATGCTCTCTCCCGTAATTATTCGCGCTTACTATGGAGCATTTAAGGATGT 878
Db 972 CTTCGCGTCTGCTCTCTGCTCTTCAGATTTTGCATAT-----1011
Qy 879 CAAGGAGAAAAACAGGACTCTGAAGAACGAGAACCTCGAGCCTTCGCAATTTCTATC 938
Db 1012 -ATGAATGAACCTCTTCCGAAAGGAAAAATGGGACCTCCAAGCTCTTAGGTTTTATC 1070
Qy 939 TGTGATTTCAATTTGGACCTTGAATTTTATCATTTTCAGATCTCCAGTATTTCCGAT 998
Db 1071 AATTAATTAATTAATGACCTTGGGCTCTTGGCCATCTTAGGCTCTCTGCTGAGACT 1130
Qy 999 ATT 1001
Db 1131 AAT 1133

RESULT 8

US-09-293-170-2
; Sequence 2, Application US/09293170
; Patent No. 6383777
; GENERAL INFORMATION:
; APPLICANT: Breyer, Richard M.
; APPLICANT: Ma, Lijun
; APPLICANT: Kennedy, Chris
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR HIGH YIELD
; FILE OF INVENTION: PRODUCTION OF EUKARYOTIC PROTEINS
; FILE REFERENCE: 22000.0094
; CURRENT APPLICATION NUMBER: US/09/293,170
; CURRENT FILING DATE: 1999-04-16
; EARLIER APPLICATION NUMBER: 60/081,989
; EARLIER FILING DATE: 1998-04-16
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 6446
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:

; NAME/KEY: CDS
; LOCATION: (300)...(2126)
; OTHER INFORMATION: Description of Artificial Sequence:/note =
; OTHER INFORMATION: synthetic construct
US-09-293-170-2

Query Match 20.3%; Score 219; DB 3; Length 6446;
Best Local Similarity 57.7%; Pred. No. 3.4e-44;
Matches 556; Conservative 0; Mismatches 350; Indels 57; Gaps 7;

Qy 48 AGCGAACTCGGCGGTGATGGGCGGTGCTCTTACGACCGCGCTCTCGGCAACCTGCT 107
Db 596 AGCGAAAGCCAGCATCAGTCCGTATGTTCTCGGCGGCGGTCTCGGAGAACCTCAT 655
Qy 108 GGCCTTGGGCTGCTGCGCGCTCGGCGGTGGGT--GGTGTGCGGCGGTCCACTGCGC 165
Db 656 AGCACTGGCGCTGCTGGCGCGCGCTGGCGGGGAGGTGGGTGTCAGCGCGCGCGCAG 715
Qy 166 CGCTGTC--CTCGGTCTTCTATCATGCTGCTGCTGCGCTGACGCTCACCAGCTTGTCTGG 224
Db 716 GAGCTCCCTCTCTCTTGTTCACGTGCTGCTGACCGAGCTGCTTCCACGACCTGCTCGG 775
Qy 225 CAAGTGCCTCTTAAGCCCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 284
Db 776 GACCTGCTCTATCAGCCAGTGTACTGCTTCTGATCGCGCGAACCAGACCTTGTGTGC 835
Qy 285 GCTTGGCGCGCATTTGGACAACTCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTT 344
Db 836 ACTGGCGCC-----GAGAGCGCGCTGACCTACTTTCGCTTTCGCCCATGACCTTCT 899
Qy 345 TGGGCTCTCTGCACTGCAACTCTGCGCATGCGACTGGAGTGTGCTGCTCTCCCTAGG 404
Db 890 CAGCCTGGCCAGATGCTCTCTGCGCATGCGCTGCGAGCGCTACTCTCGATCGG 949
Qy 405 GCACCTTTTCTTCTACGAGCGCACATCACCTGCGCTGCGCGCACCTGCTGCGCCCGCT 464
Db 950 GCACCTTCTTCTTCTACGAGCGCGCTCTGCGCTGCGGCGCGCTGCGCGCTGCTGCTGT 1009
Qy 465 GGTGAGCGCTTCTCTGCTGCTTCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 524
Db 1010 CATCTATGAGTCTCTCTGCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1069
Qy 525 CGAGTACTGCGCGCGCACCTGCTGCTTTATCAGATGCTCAGAGGAGGCTGCTGCTGTC 584
Db 1070 CCAGTACTGCGCGCGGACCTGCTGCTTCTATCGGCAACCGCG-----1111
Qy 585 GGTGCTGGGTTACTCTGCTGCTCTACTCCAGCCTCATGGCGCTGCTGCTGCTGCTGCT 644
Db 1112 ---GACCGCTTACCTGCGAGCTGTACGCCACCTGCTGCTGCTGCTGCTGCTGCTGCT 1168
Qy 645 GCTGTGCAACCTCGGCGCATGCGCAACCTCTATGCGATGCAACCGCG--GCTGAGCGG 702
Db 1169 CGCTGCAACTTCAGTGTCTTCTCAACTCATCGCATGCAACCGCGAAGCGGAGAG 1228
Qy 703 CACCGCGCTCTGCAACGAGGACTGTGCGAGCGCGCGCGCGAGCGGAGGAGGAGCTCC 762
Db 1229 CGCTGCGGACCTTCTTGGGAGTGGCGCGCGCGCGCGCGCGCGCGCGCGAGAGGGA 1288
Qy 763 CCTCAGCCCT----GGAGGAGTGGATCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 818
Db 1289 AAGGAGTGCATGCGGAGGAGACGACCTCATCTCTCTGCTGCTGCTGCTGCTGCTGCT 1348
Qy 819 CTTCATATGCTTCTCTGCGCGCTTATTCGCGCTTACTATGGAGCATTTAAGGATGT 878
Db 1349 CTTCGCGCTGCTGCTTCTGCTTTCAGCATTTTGCATAT-----1388
Qy 879 CAAGGAGAAAAACAGGACTCTGAAGAGAGAGAACCTCGAGCTTTCGCAATTTCTATC 938
Db 1389 -ATGAATGAACCTCTTCCGAAAGGAAAAATGGGACCTCCAAGCTCTTAGGTTTTATC 1447
Qy 939 TGTGATTTCAATTTGGAGCCTTGAATTTTATCATTTTCAGATCTCCAGTATTTCCGAT 998
Db 1448 AATTAATTAATTAATGACCTTGGGCTCTTGGCCATCTTAGGCTCTCTGCTGCTGCTGCT 1507

TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-463-081B-29

Query Match 19.5%; Score 211; DB 2; Length 1074;

Best Local Similarity 57.2%; Pred. No. 1.6e-42;
Matches 551; Conservative 0; Mismatches 355; Indels 57; Gaps 7;

QY	48	AGGCAACTCGGCGGTGATGGCGGGTGTCTTCAGACACCGGCTCTCTGGCAACCTGCT	107
DB	63	AGCGGAAGCCAGCATCAGTTCCTCATGTTCTCGCGGGGTCTGGGAACTCAT	122
QY	108	GGCCCTGGGGTGTCTCGCGCTCGGGGTGGGT--GGTGTCTGGGGTCTCACTGC	165
DB	123	AGAACTGGCGTCTGGCGCGCTGGCAGGGGACGTGGGTGAGCGCGCGGTAG	182
QY	166	CGCTGCC-CTGGTCTTCTACATGCTGTGTGTGCGCTGACGGTCAACGACTTGTGG	224
DB	183	GAGCTCCCTCTCTTGTTCACGTGTGTGTGACCGAGCTGGTGTTCACGACCTGCTCG	242
QY	225	CAAGTGCTCTTAAGCCCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	284
DB	243	GACCTGCTCATCAGCCAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	302
QY	285	GCTTGCGCCCGCATTTGACAACTCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	344
DB	303	ACTGGCGCC-----GAGAGCGCGCTCCACCTACTTTCGCTTTCGCGCATGACCTT	356
QY	345	TGGGTCTCTTGACACTGGAATCTCTGGCACTGGCACTGGAGTGTGTGTGTGTGTGT	404
DB	357	CAGCTTGGCGCATGCTCATGCTTTCACCATGGCCCTGGAGCGCTACTCTTCGATCG	416
QY	405	GCACCTTCTTCTACCGAGCGCACATCACCCTGCGCTGGCGCACTGTGGCCCGGT	464
DB	417	GCACCTTCTTCTACCGAGCGCGCTCTCGCGCTCCGGGCGCTGGCGGTGTGTGTGT	476
QY	465	GGTGAGCGCTTCTCCCTGGCTTCTGCGCTTACCTTTTCATGGGCTTCGGGAAGTTC	524
DB	477	CATCTATGAGTCTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	536
QY	525	GCAGTACTCGCGCGCACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	584
DB	537	CCAGTACTCGCGCGCACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	578
QY	585	GGTGTGGGGTACTGTGTCTCTACTCCAGCTCTATGGCGCTGCTGTCTCTCGCACCT	644
DB	579	---GACCGCTTACCTGACGTGTACGCCACCTCTGCTGTCTCTCTCTCTCTCTCT	635
QY	645	GCTGTGCAACCTCGGCGCATCGCAACCTCTATGGATGACACCGCG--GCTGACGCG	702
DB	636	CGCTTGCACTTCACTGTCTATCTCACTCTATCCGCTATGACCGCGGAGCGGAGAG	695
QY	703	CACCGCGCTCTTGACACGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	762
DB	696	CGCTTGGGACCTTCTCTGGGAGTGGCGGGCGCGCGCGCGCGCGCGCGCGCGCGCG	755
QY	763	CTCAGCCCT---GGAGAGTGTATCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	818
DB	756	AAGGTGTCTATGGCGGAGGAGACGACCTTCTCTCTCTCTCTCTCTCTCTCTCTCT	815
QY	819	CTTCACTATGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	878
DB	816	CTTGGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	855
QY	879	CAAGGAGAAAAACAGGACTCTCTGAAGAGCAGAACCTCCGAGCTTCGGAATTTCTAT	938
DB	856	-ATGAATGAACCTCTCTCCGAAAGGAAAAATGGGACCTCCAAGCTCTTAGGTTTTAT	914
QY	939	TGTGATTTCAATGTGACCTTGGATTTTATCATTTTTCAGATCTCCAGTATTTCCGAT	998
DB	915	AATTAATTAATTAATTTGGTCTTTGGCCATCTTTAGCCCTCTCTTCTGAGACT	974

QY 999 ATT 1001
DB 975 AAT 977

RESULT 11

US-08-461-379A-29
Sequence 29, Application US/08461379A
Patent No. 5871961

GENERAL INFORMATION:

APPLICANT: Smith, Kendall A. & Beadling, Carol

TITLE OF INVENTION: Nucleic Acids Encoding CR5 Polypeptide, and

TITLE OF INVENTION: Vector and Transformed Cell Thereof, and

TITLE OF INVENTION: Expression Thereof

NUMBER OF SEQUENCES: 35

CORRESPONDENCE ADDRESS:

ADDRESSEE: Ratner & Prestia

CITY: Valley Forge

STATE: Pennsylvania

COUNTRY: USA

ZIP: 19482

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0,

SOFTWARE: Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/461,379A

FILING DATE: 5-JUNE-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: USSN 08/330,108; 08/104,736

APPLICATION NUMBER: & 07/796,066

FILING DATE: 27-OCT-1994; 10-AUG-1993 & 20-NOV-91

ATTORNEY/AGENT INFORMATION:

NAME: Viviana Amzel, Ph. D.

REGISTRATION NUMBER: 30,930

REFERENCE/DOCKET NUMBER: DART-070

TELECOMMUNICATION INFORMATION:

TELEPHONE: (610)470-0700

TELEFAX: (610)470-0701

INFORMATION FOR SEQ ID NO: 29:

SEQUENCE CHARACTERISTICS:

LENGTH: 1074 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

US-08-461-379A-29

Query Match 19.5%; Score 211; DB 2; Length 1074;

Best Local Similarity 57.2%; Pred. No. 1.6e-42;
Matches 551; Conservative 0; Mismatches 355; Indels 57; Gaps 7;

QY	48	AGGCAACTCGGCGGTGATGGCGGGTGTCTTCAGACACCGGCTCTCTGGCAACCTGCT	107
DB	63	AGCGGAAGCCAGCATCAGTTCCTCATGTTCTCGCGGGGTCTGGGAACTCAT	122
QY	108	GGCCCTGGGGTGTCTGGCGCTCGGGGTGGGT--GGTGTCTGGGGTCTCACTGC	165
DB	123	AGAACTGGCGTCTGGCGCGCTGGCAGGGGACGTGGGTGAGCGCGCGGTAG	182
QY	166	CGCTGCC-CTCGGTCTTCTACATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	224
DB	183	GAGCTCCCTCTCTTGTTCACGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	242
QY	225	CAAGTGCTCTTAAGCCCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	284
DB	243	GACCTGCTCATCAGCCAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	302
QY	285	GCTTGCGCCCGCATTTGGAACAACTCGTGTGTGTGTGTGTGTGTGTGTGTGTGT	344

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Db 303 ACTGGCGCC-----GAGAGCGCGCTCCACCTACTTCGCTTCGCGCATGACCTTCTT 356
Qy 345 TGGGCTCTCTCGACACTGCAACTCTGCGCATGCGACTGGAGTGTGCTCTCCCTAGG 404
Db 357 CAGCCTGGCCAGATGCTCATGCTCTTCAACCATGGCCCTGGAGCGTACCTCTCGATCGG 416
Qy 405 GCACCTTTCTTCTACCGACGACATCACCTGCGCCTGGCGCGCACTGGTGGCCCCGGT 464
Db 417 GCACCTCTACTTCTACCGAGCGCGGTCTCGCGCTCGGGGCGCTGGCGCTGCTGCTGT 476
Qy 465 GGTGAGCGCTTCTCCCTGGCTTTCTGCGCGTACTTTTCATGGCTTCGGAAAGTTCGT 524
Db 477 CATCTATGAGTCTCCCTGCTCTCTGCTCACTGCGCGTGTGGACTATGGGCACTAGCT 536
Qy 525 GCAGTACTGCCCGGCACTGTGCTTTATCCAGATGCTCCAGAGGGGCTCGCTGTC 584
Db 537 CCAGTACTGCCCGGCACTGTGCTTTCATCGGCACTGGCG----- 578
Qy 585 GGTGCTGGGCTACTCTGTGCTCTACTCCAGCTCTGCGGCTGCTGCTCGCCACCGT 644
Db 579 ---GACCGCTTACCTGACGCTGTACGCCACCTGCTGCTGCTTCTCATTTGCTCGGTGCT 635
Qy 645 GCTGTGCAACTCGCGCCATCGCAACTCTTATCGGATGACCGCGG--GCTGAGCGG 702
Db 636 CGCCTGCAACTTCAGTGTCTATTCTCAACCTCATCCGATGCACCGCGGAAGCGGAGAAG 695
Qy 703 CACCGCGCTCTGACACGAGGACTGTGCGAGCGCGCGCGGAGGAGGAGCGTCC 762
Db 696 CGCCTGCGGACCTTCCCTGGGCACTGGCGGGGCGCGCGCGGCGCGGAGGAGGGA 755
Qy 763 CTTGAGCCCT---GGAGGAGCTGATCACCTCTGCTGCTGCTGCTGATCACCGTGT 818
Db 756 AAGGTGTCCATGCGGAGGAGACGCACTCTCATTTCTCTGGCTATCATGACCATCAC 815
Qy 819 CTTCACTATGTTCTTCTGCGCTTAATTATCGCGCTTACTATGAGGACATTTAAGATGT 878
Db 816 CTTGCGGCTGCTCTGCTTCCCTTTCAGGATTTTTCATAT----- 855
Qy 879 CAGGAGAAACAGGACCTCTGAGAGCAGACGACCTCGAGCTTGGGATTTCTATC 938
Db 856 -ATGAATGAACCTCTTCCCGAAGAGAAATGGGACCTTCAAGCTCTTAGGTTTTATC 914
Qy 939 TGTGATTTCAATGTGGACCTTGGATTTTATCATTTTTCAGATCTCCAGTATTTCCGGAT 998
Db 915 AATTATTCATTAATGACCTTGGTCTTTGCCATCTTAGGCTCTCTGTTCTGAGACT 974
Qy 999 ATT 1001
Db 975 AAT 977
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RESULT 12

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US-08-462-390B-29
; Sequence 29, Application US/08462390B
; Patent No. 5882894
; GENERAL INFORMATION:
; APPLICANT: Smith, K. A., & Beadling, C.
; TITLE OF INVENTION: Nucleic Acids Encoding CR8 Polypeptide, Vector and
; TITLE OF INVENTION: Transformed Cell Thereof, and Expression Thereof
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ratner & Prestia
; ADDRESS: (B) STREET:One Westlakes-Berwyn
; CITY: Valley Forge
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/462,390B
; FILING DATE: 5-JUNE-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/330,108
; FILING DATE: 27-OCT-1994
; APPLICATION NUMBER: USSN 08/104,736
; FILING DATE: 10-AUG-1993
; APPLICATION NUMBER: USSN 07/796,066
; FILING DATE: 20-NOV-91
; ATTORNEY/AGENT INFORMATION:
; NAME: Viviana Amzel, Ph. D.
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: DART-040
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610)407-0700
; TELEFAX: (610)407-0701
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1074 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-462-390B-29
```

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Query Match 19.5%; Score 211; DB 2; Length 1074;
Best Local Similarity 57.2%; Pred. No. 1.6e-42;
Matches 551; Conservative 0; Mismatches 355; Indels 57; Gaps 7;

Qy 48 AGGCAACTCGGCGGTGATGGCGGGTGTCTTTACAGCACCGGCTCTCTGGGCAACCTGCT 107
Db 63 AGGCGAAGACCCAGCCATCAGTTCGTCATGTTCTCGGCGGGGTGCTGGGGAACCTCAT 122
Qy 108 GCGCTGGGGTGTGCGGCGCTCGGGGTGGGT--GGTGTGCGGGGTTCATCTGCC 165
Db 123 AGAATGCGCTGTGCGGCGCGCTGGCGGGGACGTGGGGTGCAGCGCGGCGGTAG 182
Qy 166 CGGCTGCC-CTCGGTCTTTCTACATGCTGTGTGGCTGACGCTCAGCGACTTGTGGG 224
Db 183 GAGTCTCCCTCTCTTGTTCACGCTGTGTGACGAGTGGTTCACCGACTGCTCGG 242
Qy 225 CAAGTGCCTCTTAAGCCCGGTGTGCTGCTGTCTACGCTCAGAACCGGAGTCTCGGGT 284
Db 243 GACCTGCTCATCAGCCCACTGCTGCTTCTGCTACGCGGAAACAGACCTGCTGTCG 302
Qy 285 GCTTGGCGCGGATGGACAACCTGTTGTGCAAGCTTTCGCTTCTTCATGCTCTTCT 344
Db 303 ACTGGCGCCC-----GAGAGCGCGCGTTCACCTACTTTCGCTTTCGCGCATGACCTTCT 356
Qy 345 TGGGCTCTCTCGACACTGCAACTCTCGGCGCATGCACTGGAGTGTGCTCTCCCTAGG 404
Db 357 CAGCCTGGCCAGATGCTCATGCTCTTTCACATGCGCTTGGAGCGCTACCTCTCGATCG 416
Qy 405 GCACCTTTTCTTCTACCGACGCGACATCACCTGCGCTGCGCGCACTGGTGGCCCCGGT 464
Db 417 GCACCTCTACTTCTACAGCGCGCGGTCTCGCGCTCCCGGGGCTTGGCGCTGCTGCTGT 476
Qy 465 GGTGAGCGCTTCTCCCTGGCTTCTTGTGCGGCTGCTTTCATGGCTTCGGGAAAGTTCGT 524
Db 477 CATCTATGAGTCTCCCTGCTCTTCTGCTCACTGCGCGCTGCTGGACTATGGGCACTAGCT 536
Qy 525 GCAGTACTGCCCGGCACTGTGCTTTATCCAGATGCTCCAGAGGGGCTCGCTGTC 584
Db 537 CCAGTACTGCCCGGCACTGTGCTTTCATCGGCACTGGCG----- 578
Qy 585 GGTGCTGGGCTACTCTGTGCTCTACTCCAGCTCTGCGGCTGCTGCTCGCCACCGT 644
Db 579 ---GACCGCTTACCTGACGCTGTACGCCACCTGCTGCTGCTTCTCATTTGCTCGGTGCT 635
Qy 645 GCTGTGCAACTCGCGCCATCGCAACTCTTATCGGATGACCGCGG--GCTGAGCGG 702
Db 636 CGCCTGCAACTTCAGTGTCTATTCTCAACCTCATCCGATGCACCGCGGAAGCGGAGAAG 695
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QY 703 CACCCGGCTCTGACACGAGGACTGTGCGAGCGCGCGCGAGCGGAGGAGCGTCC 762
DB 696 CGCTGCGGACCTTCCCTGGGAGTGTGCGGCGCGCGCGCGCGCGCGCGCGCGGGA 755
QY 763 CCTCAGCCCT---GGAGAGCTGGATCATCTCTGCTGCTGCGCTGATGACCGTCT 818
DB 756 AAGGTGTTCATGCGGAGGAGACGACACCTCAITCTCTGCTATCATGACCATCAC 815
QY 819 CTTCACTATGTGTCTCTGCGCGTAATTTATCGCGCTTACTATGAGCATTTAAGGATGT 878
DB 816 CTTGCGGCTGCTCTCTGCTTTCAGATTTTGCATAT----- 855
QY 879 CAAGGAGAAAAACAGGACCTCTGAAGAGCAGAGACCTCCGAGCCTTGCATTTCTATC 938
DB 856 -ATGAATGAACCTCTTCCGAAAGAAAAATGGGACCTCCAGCTCTTAGGTTTTATC 914
QY 939 TGTGATTTCAATGTGAGCCCTTGGATTTTATCAITTTTCAGATCTCCAGTATTTCCGAT 998
DB 915 AATTAATTCATTAATGACCTTGGTCTTTGCGCATCTCTTAGGCCCTCTGTTCTGAGACT 974
QY 999 ATT 1001
DB 975 AAT 977

RESULT 13

US-08-463-074B-29
; Sequence 29, Application US/08463074B
; Patent No. 6020155
; GENERAL INFORMATION:
; APPLICANT: Smith, Kendall A. & Beadling, Carol
; TITLE OF INVENTION: Nucleic Acids Encoding CR1 Fusion Protein, Vector an
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PRETTY, SCHROEDER & POPLAWSKI
; ADDRESS: (B) STREET: 444 South Flower St. - Suite 1900
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0,
; SOFTWARE: Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/463,074B
; FILING DATE: 5-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/104,736
; FILING DATE: 10-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/796,066
; FILING DATE: 20-NOV-91
; ATTORNEY/AGENT INFORMATION:
; NAME: Viviana Amzel, Ph. D.
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: P66 38143 (DART-020)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 622-7700
; TELEFAX: (213) 489-4210
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1074 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-463-074B-29

Query Match

19.5%; Score 211; DB 3; Length 1074;

RESULT 14

Best Local Similarity 57.2%; Pred. No. 1.6e-42;
Matches 551; Conservative 0; Mismatches 355; Indels 57; Gaps 7;
QY 48 AGCGAACTCGGCGGTGATGCGGGGGTGTCTTTACGACCGGCTCTCTGGGCAACCTGCT 107
DB 63 AGCGGAAAGCCAGCCATCAGTCCGTATGTTCTCGGCGGGGTGCTGGGAACTCAT 122
QY 108 GGCCTTGGGGTGTCTGCGCGCTCGGGGCTGGGGT--GGTGTCTCGGGGTTCACGTGCG 165
DB 123 AGAACTGGCGCTGCTGGCGCGCGCTGGCAGGGGAGCTGGGGTGCAGCGCGCGGTAG 182
QY 166 CGCTGCC--CTCGGTCTTCTACATGCTGTGTGTGCGCTGACGGTCAACGACTTGTGGG 224
DB 183 GAGCTCCCTCTCTTGTGTTCCAGCTGCTGTGTGACCGAGCTGGTGTTCACGACCTGTCGG 242
QY 225 CAAGTGCCTCTTAAGCCCGGTGTGTGCTGTCTACGCTCAGAACCGGAGTCTCGCGGT 284
DB 243 GACCTGCCTCATCAGCCAGTGTACTGCTGTGTGACGCGGGAACAGACCTTGTGGG 302
QY 285 GCTTGGCGCGCATTTGGCAACATCGTTGTGCAAGCCTTTCGCTTCTTTCATGTCCTTT 344
DB 303 ACTGGCGCC-----GAGAGCGCGCTCCACTACTTTCGCTTTCGCAATGACCTTCT 356
QY 345 TGGGCTCTCTCGACACTGCAACTCTGTGCGCATGCGACTGCGAGTGTGCTCTCCCTAGG 404
DB 357 CAGCCTGGCCACGATGCTCATGCTCTTCCACCATGCGCCTGGAGCGCTACTCTCGATCGG 416
QY 405 GCACCTTTTCTTACCGAGCGCACATCACCTGCGCCTGGCGGCGACTGTTGCCCCCGGT 464
DB 417 GCACCTTACTTCTACAGCGCGCGGTCTGCGCTCCGGGGGCGCTGGCGTGTGCTGT 476
QY 465 GGTGAGCGCTTCTCCCTGGCTTCTGCGCGCTACCTTTTCATGGGCTTCGGGAAGTTCGT 524
DB 477 CATCTATGAGTCTCCCTGCTCTCTTCTGCTCACTGCGGCTGTGGACTATGGGAGTACGT 536
QY 525 GCAGTACTGCGCGCGCGACTGTGCTTTTATCAGATGCTTCCAGGAGGAGGCTCGCTGTC 584
DB 537 CCAGTACTGCGCGCGCGACTGTGCTTCTCATCGGCGCGCGG----- 578
QY 585 GGTGCTGGGGTACTCTGTGCTCTACTTCCAGCTCTATGCGGCTGTGCTCTCGCCACCGT 644
DB 579 ---GACCGCTTACCTGACGCTGTAGCCACCTGTGCTGCTCTCTCATTTGCTCGGTGCT 635
QY 645 GCTGTGCAACTCGGCGCGCATCGCAACCTCTATGCGATGCAACCGCG--GCTGCAAGCG 702
DB 636 CGCTTGAACCTTCACTGTCTTCTCAACCTCATCGCATGCAACCGCGGAGCGGAGAG 695
QY 703 CACCGCGCTCTCTGACACGAGGACTGTGCGGAGCGCGCGCGCGGAGGAGGAGCTCC 762
DB 696 CCGCTGCGGACCTTCTCGGCGAGTGGCGGGCGCGCGCGCGCGCGCGGAGGAGGGA 755
QY 763 CCTCAGCCCT---GGAGGAGCTGATCACCCTCTGCTGTGCGGCTGATGACCGTCT 818
DB 756 AAGGTGTTCATGCGGAGGAGACGACCACTCATTTCTCTGCTATCATGACCATCAC 815
QY 819 CTTCACTATGTGTCTCTGCGCGTAATTTTATCGCGCTTACTATGAGCATTTAAGGATGT 878
DB 816 CTTGCGGCTGCTCTCTGCGCTTTCAGATTTTGCATAT----- 855
QY 879 CAAGGAGAAAAACAGGACCTCTGAAGAGCAGAGACCTCCGAGCCTTGCATTTCTATC 938
DB 856 -ATGAATGAACCTCTTCCGAAAGAAAAATGGGACCTCCAGCTCTTAGGTTTTATC 914
QY 939 TGTGATTTCAATGTGAGCCCTTGGATTTTATCAITTTTCAGATCTCCAGTATTTCCGAT 998
DB 915 AATTAATTCATTAATGACCTTGGTCTTTGCGCATCTCTTAGGCCCTCTGTTCTGAGACT 974
QY 999 ATT 1001
DB 975 AAT 977

US-08-465-585C-29
; Sequence 29, Application US/08465585C
; Patent No. 6027914
; GENERAL INFORMATION:
; APPLICANT: Smith, K. A., & Beadling, C.
; TITLE OF INVENTION: Nucleic Acids Encoding CR6 Polypeptide, Vector
; TITLE OF INVENTION: Transformed Cell Thereof, and Expression Thereof
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PRETTY, SCHROEDER & POPLAWSKI
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 900071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465,585C
; FILING DATE: 5-JUNE-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/330,108
; FILING DATE: 27-OCT-1994
; APPLICATION NUMBER: USSN 08/104,736
; FILING DATE: 10-AUG-1993
; APPLICATION NUMBER: USSN 07/796,066
; FILING DATE: 20-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Viviana Amzel, Ph. D.
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: P66 38149 (DART-050)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 622-7700
; TELEFAX: (213) 4894210
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1074 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-465-585C-29

Query Match 19.5%; Score 211; DB 3; Length 1074;
Best Local Similarity 57.2%; Pred. No. 1.6e-42;
Matches 551; Conservative 0; Mismatches 355; Indels 57; Gaps 7;

QY	48	AGGCACTCGCGGTGATGGCGGGTGTCTTCAGCACCGGCTCTCGGCAACTGCT	107
DB	63	AGGCGAAAGCCAGGCATCAGTTCCGTCAATTTCTGCGCGGGGTGCTGGGAACTCAT	122
QY	108	GGCCCTCGGGCTGCTGGCGCGCTCGGGGTGGGT--GGTGTGCGGGGTCCACTGGCG	165
DB	123	AGAACTGGCGCTGTGGCGCGCGCTGGCGAGGGGACGTGGGTGAGCGCGCGGTAG	182
QY	166	CGCTGCCC--CTGGTCTTCTACATGCTGTGTGTGGCTGACGGTACCGACTTGTGGG	224
DB	183	GAGCTCCCTCTCTCTGTTCCAGGTGTGTGACCGAGCTGGTGTTCACCGACTGCTCG	242
QY	225	CAAGTGCCTCTTAAGCCCGGTGTGTGCTGCTGCTAGCTCAGAACCGGAGTCTCGGGT	284
DB	243	GACCTGCTCTATAGCCCGAGTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	302
QY	285	GCTTGGCGCGGATGGACAACTCGTGTGTGCAAGCTTTCGCTTCTTCTCATGCTCTTT	344
DB	303	ACTGGGCGCC-----GAGAGCGCGCGTCCACTTCTGCTTTCGCTGCACTGCTT	356
QY	345	TGGGTCTCTCGACACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	404
DB	357	CAGCTGGCGCAGGTGCTCATGCTCTTTCACCTGCTGCTGCTGCTGCTGCTGCTGCTG	416

QY	405	GCACCTTTCTTTACGACGGCACATCACCTCGGCTCGGCGCACCTGGTGGCCCCCGGT	464
DB	417	GCACCTTACTTCTACAGCGCGGGTCTCGGGTCCGGGGCTGGCGTGTGCTGCTGT	476
QY	465	GCTGAGCGCTTCTCCCTGGGCTTTCTGCGCTACCTTTTCATGGCTTTCGGAAGTCT	524
DB	477	CATCTATGACGTCTCCCTGCTCTTCTGCTCACTGCGCTGCTGGACTATGGGCACTGT	536
QY	525	GCAGTACTGCGCGCGCACTGCTGCTTTATCCAGATGCTCCAGAGGAGGCTGCTGTC	584
DB	537	CCAGTACTGCGCGCGCACTGCTGCTTTATCCAGATGCTCCAGAGGAGGCTGCTGTC	578
QY	585	GCTGCTGGGTACTCTGCTGCTTACTCCAGCTCATGCGCTGCTGCTGCTGCTGCTGCT	644
DB	579	---GACCGCTTACTGCGAGCTGTACCGCACCTGCTGCTGCTGCTGCTGCTGCTGCT	635
QY	645	GCTGTCAACCTCGCGCGCATGCGCAACTCTATGCGATGACCGCG--GCTGAGCGG	702
DB	636	CGCTGCAACTTCACTGCTGCTTCTCAACTCATCGCATGCACTGCGCGGAGGAGG	695
QY	703	CACCGCGCTCTGCAACGAGGACTGTGCGGAGCGCGCGGCGGAGGAGGAGGAGGAG	762
DB	696	CGCTGCGGACTTCTTCTGCGAGTGTGCGGCGGCGCGCGGCGGCGGCGGCGGCGG	755
QY	763	CTCAGCCCTT---GGAGGAGCTGGATCACCTCTGCTGCTGCTGCTGCTGCTGCTGCT	818
DB	756	AAGGTGTCTATGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	815
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QY	879	CAAGGAGAAACAGGAGCTCTGAGAGCAGAGAGGAGGAGGAGGAGGAGGAGGAGG	938
DB	856	-ATGAATGAACCTTCTCCGAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	914
QY	939	TGTGATTTCAATTTGGACCTTGGATTTTATCATTTTTCAGATCTCCAGTATTTTGG	998
DB	915	AATTAATTCATTAATGACCTTGGTCTTTGGCCATCTTAGGCTCTCTGTTCTGAG	974
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DB	975	AAT 977	

RESULT 15
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; Sequence 29, Application US/08652446
; Patent No. 6057427
; GENERAL INFORMATION:
; APPLICANT: Smith, Kendall A. & Beadling, Carol
; TITLE OF INVENTION: Nucleic Acids Encoding CRS
; TITLE OF INVENTION: Polypeptide, Vector and Transformed Cell Thereof, and
; TITLE OF INVENTION: Expression Thereof
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PRETTY, SCHROEDER & POPLAWSKI
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0,
; SOFTWARE: Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/652,446
; FILING DATE:
; PRIOR APPLICATION DATA:

444 South Flower St. - Suite 1900

APPLICATION NUMBER: EP App. # 96921319.8
FILING DATE: 5-JAN-1998
APPLICATION NUMBER: PCT/US/96/09194
FILING DATE: 5-JUN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,108
FILING DATE: 27-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/463,074
FILING DATE: 5-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/462,337
FILING DATE: 5-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/462,390
FILING DATE: 5-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/465,585
FILING DATE: 5-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/463,081
FILING DATE: 5-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/461,379
FILING DATE: 5-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/739,523
FILING DATE: 29-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Viviana Amzel, Ph. D.
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: FP66 40035
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 622-7700
TELEFAX: (213) 489-4210
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 1074 base pairs
TYPE: nucleic acid
STRAINEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-652-446-29

Query Match 19.5%; Score 211; DB 3; Length 1074;
Best Local Similarity 57.2%; Pred. No. 1.6e-42;
Matches 551; Conservative 0; Mismatches 355; Indels 57; Gaps 7;
QY 48 AGGCAACTCGGGGATGATGGGGGGGTGCTTTTCAGCACCGGCTCTCGGGCAACCTGCT 107
DB 63 AGGCGAAAGCCAGCCATCAGTTCCGTCATGTTCTCGGCGGGGTGCTGGGAAACCTCAT 122
QY 108 GGCCTGGGGCTGCGCGGCTCGGGCTGGGT--GGTGTGCGGGGCTCACTGCGC 165
DB 123 AGAATGGCGCTGCTGGCGCGCGCTGGCAGGGGACGTGGGTGGCAGCGCGCGCGGTAG 182
QY 166 CCGCTGCC--CTCGGTCTTCTACATGCTGTGTGCGCTGACGGTCAACCGACTTGTGGG 224
DB 183 GAGTCTCTCTCTTCTTCCAGTGTGTGTGACCGAGCTGTGTTTCAACCGACTGTCTCG 242
QY 225 CAAATGCTCTTAAGCCCGGTGTGTGCTGCTACGCTCAGAACCGGAGTCTGCGGT 284
DB 243 GACCTGCTCATCAGCCCACTGCTGCTGCTTCTGTTACGCGCGGAAACAGACCTTGTGGC 302
QY 285 GCTTGGCGCGCATTTGGAACATCTGTTTGCAGGCTTTCGCTTCTTATGCTCTTCTT 344
DB 303 ACTGGCGCCC-----GAGAGCGCGCGTCCACTACTTCTGCTTTCGCCATGACCTTCT 356
QY 345 TGGGCTCTCTCGACATGCAACTCTCTGGCCATGGCACTGGAGTGTGGTCTTCCCTAGG 404
DB 357 CAGCTGGGCCAGATGCTATGCTCTTACCATGGCCCTGGAGCGTACTCTCGATCG 416
QY 405 GCACCCCTTTCTTACCGACGGCACAATCACCTGTGCGCTTGGGCGCACTGTTGGCCCCGT 464

Db 417 GCACCCCTACTTCTTACAGCGCGGTCTCGCGCTCCGGGGGCTTGCGCGTGTCTGCTGT 476
QY 465 GGTGAGCGCTTCTCCCTGGCTTTCGCGCGTACCTTTTCATGCGGCTTCGGGAAGTTCTGT 524
DB 477 CATCTATGAGTCTCCCTGCTCTTCTGCTCACTGCGGCTGCTGGACTATGGGCACTACGT 536
QY 525 GCAGTACTGCCCCGCGCACCTGTGTGCTTTATCAGATGTTCCAGAGAGGCTTCGCTGTC 584
DB 537 CCAGTACTGCCCGGAGACCTGTGTGCTTTCATCCGCGACGGCG----- 578
QY 585 GGTGTGGGGTACTCTGTGCTCTACTCCAGCGCTCATGGCGCTGCTGCTGCTCTGCCACCGT 644
DB 579 ---GACCGCTTACCTGCGAGCTGTAGCCACCTGTGCTGCTCTCATTTGCTCTCGGTGCT 635
QY 645 GCTGTGCAACCTCGCGCCCATCGCAACCTCTATGCGATGCAACCGCGC--GCTGCAGCGG 702
DB 636 CGCCTGCAACTTCAGTGTCTATTCTCAACCTCATCCGATGCAACCGCGCGGAGAG 695
QY 703 CACCGCGCTCTGCAACAGGAGCTGTGCGAGCGCGCGCGGACCGGAGGAGGAGCTGCC 762
DB 696 CCGCTCGGACCTTCCCTGGGCGAGTGGCGGGCGCGCCCGGGGCGCGCAGGAGAGGGA 755
QY 763 CCTCAGCCCT---GGAGGAGCTGATCACCTCTGCTGCTGCTGCTGCTGATGACCGTCT 818
DB 756 AAGGGTGTCCATGGCGGAGGAGACCGACCTCATTTCTCTGCTGCTCATGACCATCAC 815
QY 819 CTTCACTATGTTCTCTGCGCGTAATTTATCGCGCTTACTATGGAGCATTTAAGGATGT 878
DB 816 CTTGCGCGCTGCTCTCTGCGCTTTCAGGATTTTGCATAT----- 855
QY 879 CAAGGAGAAAAACAGGACCTCTGAAGAGAGAAAGACCTCCGAGCCTTCGATTTCTATC 938
DB 856 -ATGAATGAACCTCTTCCCGAAAGGAAATGGGACCTCCAAGCTCTTAGGTTTTTATC 914
QY 939 TGTGATTTCAATTTGGACCTTGGATTTTATCATTTCAGATCTCCAGTATTTCCGAT 998
DB 915 AATTAATTAATAATTAATGACCTTGGGTCTTTGCCATCTTAGGCTCTCTTCTGAGACT 974
QY 999 ATT 1001
DB 975 AAT 977

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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(without alignments)
9208.852 Million cell updates/sec

Title: US-10-689-861-3

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Searched: 5633728 seqs, 3035525691 residues

Total number of hits satisfying chosen parameters: 11267456

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	1080	100.0	1253	US-10-128-558-263	Sequence 263, App
3	900.4	83.4	1505	US-10-128-558-24	Sequence 24, App1
4	846	78.3	1216	US-10-305-720-1474	Sequence 1474, App
5	829	76.8	964	US-10-029-386-24136	Sequence 24136, A
6	829	76.8	964	US-10-029-386-10081	Sequence 10081, A
7	436	40.4	597	US-10-225-567A-286	Sequence 286, App
8	436	40.4	597	US-10-029-386-23781	Sequence 23781, A
9	220.6	20.4	2296	US-10-108-714-3	Sequence 3, App1
10	220.6	20.4	2395	US-10-684-206-37	Sequence 37, App1
11	219	20.3	2372	US-10-225-567A-290	Sequence 290, App

12	219	20.3	2372	US-10-352-684A-35	Sequence 35, App1
13	219	20.3	2372	US-10-366-288-35	Sequence 35, App1
14	219	20.3	2372	US-10-305-720-1441	Sequence 1441, App
15	219	20.3	2372	US-10-755-889-91	Sequence 91, App1
16	219	20.3	6446	US-10-139-686A-2	Sequence 2, App1
17	214.2	19.8	1077	US-09-826-509-558	Sequence 558, App
18	214.2	19.8	1077	US-10-925-095-558	Sequence 558, App
19	208	19.3	501	US-10-029-386-10432	Sequence 10432, A
20	203.4	18.8	2824	US-10-108-260A-1464	Sequence 1464, App
21	201.8	18.7	1417	US-10-305-720-1403	Sequence 1403, App
22	201.8	18.7	1417	US-10-225-567A-284	Sequence 284, App
23	200.6	18.6	1360	US-09-917-800A-1482	Sequence 1482, App
24	186.4	17.3	1342	US-10-349-528-3	Sequence 3, App1
25	108.8	10.1	1209	US-10-472-362-2	Sequence 2, App1
26	108.8	10.1	1209	US-10-681-029-7	Sequence 7, App1
27	108.8	10.1	3918	US-09-781-311-1	Sequence 1, App1
28	107.2	9.9	1140	US-10-681-029-1	Sequence 1, App1
29	107.2	9.9	1209	US-09-826-509-556	Sequence 556, App
30	107.2	9.9	1209	US-10-925-095-556	Sequence 556, App
31	107.2	9.9	1376	US-10-225-567A-288	Sequence 288, App
32	107.2	9.9	1376	US-10-305-720-1361	Sequence 1361, App
33	107.2	9.9	1376	US-10-473-974-119	Sequence 179, App
34	107.2	9.9	1473	US-10-243-501-1	Sequence 1, App1
35	107.2	9.9	1473	US-10-243-501-2	Sequence 2, App1
36	103.4	9.6	1473	US-10-243-351-1	Sequence 1, App1
37	101.2	9.4	1467	US-09-826-509-560	Sequence 560, App
38	101.2	9.4	1467	US-10-925-095-560	Sequence 560, App
39	101.2	9.4	1554	US-10-320-351-1	Sequence 1, App1
40	101.2	9.4	1554	US-10-320-351-2	Sequence 2, App1
41	101.2	9.4	1558	US-10-225-567A-295	Sequence 295, App
42	101.2	9.4	1558	US-10-295-027-1109	Sequence 1109, App
43	101.2	9.4	1558	US-10-305-720-1380	Sequence 1380, App
44	101.2	9.4	1558	US-10-755-889-169	Sequence 169, App
45	101.2	9.4	1558	US-10-755-889-169	Sequence 38, App1

ALIGNMENTS

RESULT 1
US-10-276-774-1020
; Sequence 1020, Application US/10276774
; Publication No. US20040053245A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: No. US20040053245A1 Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-030
; CURRENT APPLICATION NUMBER: US/10/276,774
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 09/496,914
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 2700
; SOFTWARE: Custom
; SEQ ID NO 1020
; LENGTH: 1253
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-276-774-1020

Query Match 100.0%; Score 1080; DB 17; Length 1253;
Best Local Similarity 100.0%; Pred. No. 2.5e-306;
Matches 1080; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAAGTCGCGGTCCTTACGCGCCAGAACACACCTGTGGAAGCAACTGGCG 60
DB 122 ATGAAGTCGCGGTCCTTACGCGCCAGAACACACCTGTGGAAGCAACTGGCG 181
QY 61 GTGATGGGCGGGGTCCTTACGCGCCAGAACACACCTGTGGAAGCAACTGGCG 120
DB 182 GTGATGGGCGGGGTCCTTACGCGCCAGAACACACCTGTGGAAGCAACTGGCG 241

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QY 121 CTGGCGCGCTCGGGGCTGGGGTGTGCTGCGCGGCTGCACTGGCCCGCTGCGCTGCTG 180
Db 242 CTGGCGCGCTCGGGGCTGGGGTGTGCTGCGCGGCTGCACTGGCCCGCTGCGCTGCTG 301
QY 181 TTCTACATGCTGTGTGTGTGCTGACGCTGCACTGCTGCTGCTGCTGCTGCTGCTG 240
Db 302 TTCTACATGCTGTGTGTGTGCTGACGCTGCACTGCTGCTGCTGCTGCTGCTGCTG 361
QY 241 CCGGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTG 300
Db 362 CCGGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTG 421
QY 301 GACAACTGCTGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 360
Db 422 GACAACTGCTGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 481
QY 361 CTGCAACTCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTG 420
Db 482 CTGCAACTCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTG 541
QY 421 CGACGGCAGATCACTCGGCGCTGGGGGCTGGGGGCTGGGGGCTGGGGGCTGGGGGCTG 480
Db 542 CGACGGCAGATCACTCGGCGCTGGGGGCTGGGGGCTGGGGGCTGGGGGCTGGGGGCTG 601
QY 481 CTGGGCTTTCTGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540
Db 602 CTGGGCTTTCTGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 661
QY 541 ACTGTGTGCTTTTATCCAGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 600
Db 662 ACTGTGTGCTTTTATCCAGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 721
QY 601 GTGCTCTTACTCCAGCTTATGAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 660
Db 722 GTGCTCTTACTCCAGCTTATGAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 781
QY 721 GGCATCGGCACTCTATGAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 780
Db 782 GGCATCGGCACTCTATGAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 841
QY 781 AGGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 780
Db 842 AGGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 901
QY 841 CTGGATCCTCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 840
Db 902 CTGGATCCTCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 961
QY 901 GATTAATTTATCGGCTTATGAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 900
Db 962 GATTAATTTATCGGCTTATGAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 1021
QY 961 GAAAGAGCAGAGAGCTCGAGGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 960
Db 1022 GAAAGAGCAGAGAGCTCGAGGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 1081
QY 1021 TGAGATTTTATCATTTTTCAGATCTCCAGATTTTTCAGATTTTTCAGATTTTTCAGAT 1020
Db 1082 TGAGATTTTATCATTTTTCAGATCTCCAGATTTTTCAGATTTTTCAGATTTTTCAGAT 1141
QY 1141 AGACCTCTTATGATGAGAGCGGCTGAGGCTTCCAGATTAAGATTAAGATTAAGATTA 1201

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RESULT 2
US-10-128-558-263
; Sequence 263, Application US/10128558
; Publication No. US20040219521A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Wang, Zhiwei

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; APPLICANT: Weng, Gezhai
; APPLICANT: Boyle, Bryan J
; APPLICANT: Drmanac, Radolje T
; TITLE OF INVENTION: Novel Nucleic Acids and
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 812A
; CURRENT APPLICATION NUMBER: US/10/128,558
; PRIOR FILING DATE: 2002-04-22
; PRIOR APPLICATION NUMBER: US 60/339,453
; PRIOR FILING DATE: 2001-12-11
; PRIOR APPLICATION NUMBER: US 09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: PCT/US00/35017
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: PCT/US01/02623
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: US 09/496,914
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: US 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: PCT/US01/03800
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: US 09/515,126
; PRIOR FILING DATE: 2000-02-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 412
; SOFTWARE: pc_fl_genes Version 6.0
; SEQ ID NO 263
; LENGTH: 1253
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-128-558-263

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Query Match 100.0%; Score 1080; DB 18; Length 1253;
Best Local Similarity 100.0%; Pred. No. 2,5e-306;
Matches 1080; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ATGAGTGTGCGGCTTTTCTTACCGCTGCGGAGAACACACCTCTGTGTGAAAGGCACTGCGG 60
Db 122 ATGAGTGTGCGGCTTTTCTTACCGCTGCGGAGAACACACCTCTGTGTGAAAGGCACTGCGG 181
QY 61 GTGATGGGGGGGGGTGCTTTTACAGACCGGCTCTGTGGGCAACTGTGTGCGGCTGCGGCTG 120
Db 182 GTGATGGGGGGGGGTGCTTTTACAGACCGGCTCTGTGGGCAACTGTGTGCGGCTGCGGCTG 241
QY 121 CTGGCGCGCTCGGGGCTGGGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 180
Db 242 CTGGCGCGCTCGGGGCTGGGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 301
QY 241 TTCTACATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 240
Db 302 TTCTACATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 361
QY 301 CCGGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 300
Db 362 CCGGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 421
QY 421 GACAACTGCTGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTG 360
Db 422 GACAACTGCTGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTG 481
QY 481 CTGCAACTCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTG 420
Db 541 CTGCAACTCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTG 541
QY 541 CGACGGCAGATCACTCGGCGCTGGGGGCTGGGGGCTGGGGGCTGGGGGCTGGGGGCTG 480
Db 601 CGACGGCAGATCACTCGGCGCTGGGGGCTGGGGGCTGGGGGCTGGGGGCTGGGGGCTG 601

```

QY 481 CTGGCTTCTGCGCGCTACCTTTTCATGAGGCTTCGGGAAGTTCTGTGACAGTACTGCCCCG 540
Db 602 CTGGCTTCTGCGCGCTACCTTTTCATGAGGCTTCGGGAAGTTCTGTGACAGTACTGCCCCG 661
QY 541 ACCTGCTGCTTATCCAGATGCTTCACAGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
Db 662 ACCTGCTGCTTATCCAGATGCTTCACAGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 721
QY 601 GTGCTTACTCCAGCGCTCATGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
Db 722 GTGCTTACTCCAGCGCTCATGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 781
QY 661 GCCATGCGCAACCTCTATGCGATGCAACCGCGCTGCGAGGCAACCCGCTGCTGCTGCTGCTGCTGCT 720
Db 782 GCCATGCGCAACCTCTATGCGATGCAACCGCGCTGCGAGGCAACCCGCTGCTGCTGCTGCTGCTGCT 841
QY 721 AGGGAATGTCGCGAGCGCGCGCGCGAGAGGGAAGCGTCCCTCAGCCCTGAGAGAG 780
Db 842 AGGGAATGTCGCGAGCGCGCGCGAGAGGGAAGCGTCCCTCAGCCCTGAGAGAG 901
QY 781 CTGATCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840
Db 902 CTGATCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 961
QY 841 GTAATTATCGCGCTTACTATGAGAGATTTAAGATGTCAAGAGAGAGAGAGAGAGAGAGAGAGAG 900
Db 962 GTAATTATCGCGCTTACTATGAGAGATTTAAGATGTCAAGAGAGAGAGAGAGAGAGAGAGAGAG 1021
QY 901 GAAGAAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960
Db 1022 GAAGAAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1081
QY 961 TGGATTTTATCATTTTTCAGATCTCCAGATTTTTCAGATTTTTCAGATTTTTCAGATTTTTCAGAT 1020
Db 1082 TGGATTTTATCATTTTTCAGATCTCCAGATTTTTCAGATTTTTCAGATTTTTCAGATTTTTCAGAT 1141
QY 1021 AGAGCTCTTATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1080
Db 1142 AGAGCTCTTATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1201

RESULT 3
US-10-128-558-24
; Sequence 24, Application US/10128558
; Publication No. US20040219521A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wang, Gezhi
; APPLICANT: Boyle, Bryan J
; APPLICANT: Drmanac, Radoje T
; TITLE OF INVENTION: Novel Nucleic Acids and
; FILE REFERENCE: 812A
; CURRENT APPLICATION NUMBER: US/10128,558
; PRIOR FILING DATE: 2002-04-22
; PRIOR APPLICATION NUMBER: US 60/339,453
; PRIOR FILING DATE: 2001-12-11
; PRIOR APPLICATION NUMBER: US 09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: PCT/US00/35017
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: PCT/US01/02623
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: US 09/496,914
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: US 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: PCT/US01/03800

; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: US 09/515,126
; PRIOR FILING DATE: 2000-02-28
; Remaining Prior Application data removed - See File Wrapper or PAM.
; NUMBER OF SEQ ID NOS: 412
; SOFTWARE: pc_fl_genes Version 6.0
; SEQ ID NO 24
; LENGTH: 1505
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (231)..(1505)
US-10-128-558-24

Query Match 83.4%; Score 900.4; DB 18; Length 1505;
Best Local Similarity 89.3%; Pred. No. 1,5e-253;
Matches 1034; Conservative 0; Mismatches 1; Indels 123; Gaps 1;

QY 1 ATGAATGCGCGCTTCTACCGCTGCGAGAAACACCACTCTGTGAGAAAGAGCACTGCGCG 60
Db 231 ATGAATGCGCGCTTCTACCGCTGCGAGAAACACCACTCTGTGAGAAAGAGCACTGCGCG 230
QY 61 GTGATGCGCGCGCTTCTACCGCTGCGAGAAACACCACTCTGTGAGAAAGAGCACTGCGCG 120
Db 291 GTGATGCGCGCGCTTCTACCGCTGCGAGAAACACCACTCTGTGAGAAAGAGCACTGCGCG 350
QY 121 CTGCGCGCGCTGCGCGCTGCGCGCTGCGCGCTGCGCGCTGCGCGCTGCGCGCTGCGCGCTGCGCG 180
Db 351 CTGCGCGCGCTGCGCGCTGCGCGCTGCGCGCTGCGCGCTGCGCGCTGCGCGCTGCGCGCTGCGCG 410
QY 181 TTCTACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
Db 411 TTCTACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 470
QY 241 CCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
Db 471 CCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 530
QY 301 GACAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
Db 531 GACAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 590
QY 361 CTGCAACTCTGCGCAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
Db 591 CTGCAACTCTGCGCAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 650
QY 421 CGACGCGCAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
Db 651 CGACGCGCAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 710
QY 481 CTGCGCTTCTGCGCGCTTCTGCGCGCTTCTGCGCGCTTCTGCGCGCTTCTGCGCGCTTCTGCGCGCT 540
Db 711 CTGCGCTTCTGCGCGCTTCTGCGCGCTTCTGCGCGCTTCTGCGCGCTTCTGCGCGCTTCTGCGCGCT 770
QY 541 ACCTGCTTATATCCAGATGCTTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600
Db 771 ACCTGCTTATATCCAGATGCTTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 830
QY 601 GTGCTTACTCCAGCGCTCATGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
Db 831 GTGCTTACTCCAGCGCTCATGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 890
QY 661 GCCATGCGCAACCTCTATGCGATGCAACCGCGCTGCGAGGCAACCCGCTGCTGCTGCTGCTGCTGCT 720
Db 891 GCCATGCGCAACCTCTATGCGATGCAACCGCGCTGCGAGGCAACCCGCTGCTGCTGCTGCTGCTGCT 950
QY 721 AGGGAATGTCGCGAGCGCGCGCGAGAGGGAAGCGTCCCTCAGCCCTGAGAGAGAG 780
Db 951 AGGGAATGTCGCGAGCGCGCGCGAGAGGGAAGCGTCCCTCAGCCCTGAGAGAGAG 1010
QY 781 CTGATCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840

Db 1011 CTGGATCACCCTCTGCTGCTGCGCGCTGANGACCGTCTCTTCACTAATGTTCTCTGCCC 1070
QY 841 GTAATT----- 846
Db 1071 GTAAATTGTAGTCCCGGCGCCCGAGGACGACGACTGATGCTCCGGCCGGGATG 1130
QY 847 ----- 846
Db 1131 CGGGGCGGGAAGGTGAGCGGATCGGGAATGACGCGCGCCGACGAGCTGCGCCCTG 1190
QY 847 -----TATGCGCCTTACTATGAGCATTTTAAGATGTCAGAGGAAAAAGAGAC 897
Db 1191 GCCAGAGATGCGCCTTACTATGAGCATTTTAAGATGTCAGAGGAAAAAGAGAC 1250
QY 898 TCTGAAGACGAGAAACCTCCGAGCCTTGCGATTTCTATCTGATTTCAATTGAGAC 957
Db 1251 TCTGAAGACGAGAAACCTCCGAGCCTTGCGATTTCTATCTGATTTCAATTGAGAC 1310
QY 958 CCTGGATTTTATCATATTTTCAGATCTCGAGATTTTCGATATTTTTCAGAAATTTTC 1017
Db 1311 CCTGGATTTTATCATATTTTCAGATCTCCAGATTTTCGATATTTTTCAGAAATTTTC 1370
QY 1018 ATTAGACCTCTTAGGTAC 1035
Db 1371 ATTAGACCTCTTAGGTAC 1388

RESULT 4

US-10-305-720-1474
Sequence 1474, Application US/10305720
Publication No. US20040010136A1
GENERAL INFORMATION:
APPLICANT: Au-Young, Janice K.; Seilhamer, Jeffrey J.
TITLE OF INVENTION: Composition for the Detection of Signaling Pathway Gene Expression
FILE REFERENCE: PA-0002-1 CON
CURRENT APPLICATION NUMBER: US/10/305,720
CURRENT FILING DATE: 2002-11-26
PRIOR APPLICATION NUMBER: 09/016,434
PRIOR FILING DATE: 1998-01-30
NUMBER OF SEQ ID NOS: 1490
SOFTWARE: PERL Program
SEQ ID NO 1474
LENGTH: 1216
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: GenBank ID No. US20040010136A1 g940378
US-10-305-720-1474

Query Match 78.3%; Score 846; DB 17; Length 1216;
Best Local Similarity 100.0%; Pred. No. 1.3e-237;
Matches 846; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAAGTCCCGCTTCTACCGCTGCCAGAACACCACTCTGTGAAAAAGGCAACTCGGCG 60
Db 350 ATGAAGTCCCGCTTCTACCGCTGCCAGAACACCACTCTGTGAAAAAGGCAACTCGGCG 409
QY 61 GTGATGGGGGGGGTGTCTTACGACACCGGCTCTCTG3GCAACTGTGCGCCCTG3G3CTG 120
Db 410 GTGATGGGGGGGGTGTCTTACGACACCGGCTCTCTG3GCAACTGTGCGCCCTG3G3CTG 469
QY 121 CTGCGCGCGCTCGGGGCTGGGGTGTGCTCGCGCGCTCACTGCGCCGCTGCGCTCGGTC 180
Db 470 CTGCGCGCGCTCGGGGCTGGGGTGTGCTCGCGCGCTCACTGCGCCGCTGCGCTCGGTC 529
QY 181 TTCTACATCTGCTGTGTGTGCGCTGACGCTCAACGACTTGTGTG3CAAGTGTCTCTAACG 240
Db 530 TTCTACATCTGCTGTGTGTGCGCTGACGCTCAACGACTTGTGTG3CAAGTGTCTCTAACG 589
QY 241 CCGGTGTGTCTGCTGCTGCTACGCTACGAAACCGGAGTCTGCGGGTCTTGGCCCGGATG 300
Db 590 CCGGTGTGTCTGCTGCTGCTACGCTACGAAACCGGAGTCTGCGGGTCTTGGCCCGGATG 649

QY 301 GACAACCTGTTGNGCCAGACCTTGGCTTCTTATGTCCTTCTTTGGGCTCTCTGACA 360
Db 650 GACAACCTGTTGNGCCAGACCTTGGCTTCTTATGTCCTTCTTTGGGCTCTCTGACA 709
QY 361 CTGCAACTCTCTGGCCATGACACTGAGAGTGTGCTCTCTCTAGGGGACCTTTCTTAC 420
Db 710 CTGCAACTCTCTGGCCATGACACTGAGAGTGTGCTCTCTCTAGGGGACCTTTCTTAC 769
QY 421 CGACGGCATATCACCTTGGCGCTGGGCGCATGAGTGGCCCGGATGAGCCCTTCTCC 480
Db 770 CGACGGCATATCACCTTGGCGCTGGGCGCATGAGTGGCCCGGATGAGCCCTTCTCC 829
QY 481 CTGCTTTCTGCGCGCTACCTTTCATGAGGCTTGGGAAATTCGTGACATCTGCCC 540
Db 830 CTGCTTTCTGCGCGCTACCTTTCATGAGGCTTGGGAAATTCGTGACATCTGCCC 889
QY 541 ACCTGTGCTTTATTCAGATGTTCCACGAGAGGCTGCTGTGCTGTGCTGAGTACTCT 600
Db 890 ACCTGTGCTTTATTCAGATGTTCCACGAGAGGCTGCTGTGCTGTGCTGAGTACTCT 949
QY 601 GTGCTCTACTCCAGCCTCATGGCGCTGCTGTGCTGTGCTGACCGTGTGCAACTCGGC 660
Db 950 GTGCTCTACTCCAGCCTCATGGCGCTGCTGTGCTGTGCTGACCGTGTGCAACTCGGC 1009
QY 661 GCCATGCGCAACCTCTATGCGATGACCGCGCGCTGACGCGCACCCGCGCTCTGAC 720
Db 1010 GCCATGCGCAACCTCTATGCGATGACCGCGCGCTGACGCGCACCCGCGCTCTGAC 1069
QY 721 AGGAGTGTGCGGAGCGCGCGCGCGGAGGAGGAGGCTCCCTTCAGCCCTTGAGAG 780
Db 1070 AGGAGTGTGCGGAGCGCGCGCGGAGGAGGAGGCTCCCTTCAGCCCTTGAGAG 1129
QY 781 CTGATACACTCTCTGCTGCTGCGCTGATGACCGTGTCTTCACTATGTTCTGCCC 840
Db 1130 CTGATACACTCTCTGCTGCTGCGCTGATGACCGTGTCTTCACTATGTTCTGCCC 1189
QY 841 GTAATT 846
Db 1190 GTAATT 1195

RESULT 5

US-10-029-386-24136/c
Sequence 24136, Application US/10029386
Publication No. US2003019470A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR GENE EXPRESSION ANALYSIS
FILE REFERENCE: AEWICA-X-2
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 24136
LENGTH: 964
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AL355833.1
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.9
OTHER INFORMATION: EXPRESSED IN LIVER, SIGNAL = 0.96
OTHER INFORMATION: EST_HUMAN HIT: A1460323.1, EVALUATE 1.00e-108
OTHER INFORMATION: SWISSPROT HIT: Q13258, EVALUATE 1.00e-128
OTHER INFORMATION: NT HIT: U31332.1, EVALUATE 0.00e+00
US-10-029-386-24136

Query Match 76.8%; Score 829; DB 16; Length 964;
Best Local Similarity 100.0%; Pred. No. 1.2e-232;
Matches 829; Conservative 0; Mismatches 0; Indels 0; Gaps 0;


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18 CCCTGTCAGAACCACTCTGTGAAAAAGCACTCGGCGGTGATGGGCGGGTGT 77
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664 CCCTGTCAGAACCACTCTGTGAAAAAGCACTCGGCGGTGATGGGCGGGTGT 905
   |||
QY 78 CTTGACGACCGGCTCTCTGAGGCACTGTGCGCTGAGGCTGTGCGGCTCGGAGCT 137
   |||
Db 904 CTTGACGACCGGCTCTCTGAGGCACTGTGCGCTGAGGCTGTGCGGCTCGGAGCT 845
   |||
QY 138 GGGGTGTGTGCGGCGGTGATGCGGCGGCTGCGCTGCTTCTTCACTGCTGTG 197
   |||
Db 844 GGGGTGTGTGCGGCGGTGATGCGGCGGCTGCGCTGCTTCTTCACTGCTGTG 785
   |||
QY 198 TGGCTGACGAGTACGAGTGTGCGGCAAGTGTCTTAAGCCCGGAGTGTGCTG 257
   |||
Db 784 TGGCTGACGAGTACGAGTGTGCGGCAAGTGTCTTAAGCCCGGAGTGTGCTG 725
   |||
QY 258 CTAAGCTCAGAACCGAGTGTGCGGCTGTGCGCGCGCATTTGACAACTGTTGCA 317
   |||
Db 724 CTAAGCTCAGAACCGAGTGTGCGGCTGTGCGCGCGCATTTGACAACTGTTGCA 665
   |||
QY 318 AGCTTGGCTTTTCTTATGCTCTTCTTGTGGCTCTCTGCACTGCACTCTGCGCAT 377
   |||
Db 664 AGCTTGGCTTTTCTTATGCTCTTCTTGTGGCTCTCTGCACTGCACTCTGCGCAT 605
   |||
QY 378 GGCACGTGAGTGTGCTCTCTCTAGGAGCACTCTTCTTCTTACGAGCAATCACT 437
   |||
Db 604 GGCACGTGAGTGTGCTCTCTCTAGGAGCACTCTTCTTCTTACGAGCAATCACT 545
   |||
QY 438 GCGCCTGAGCGCACTGATGCGCCCGGTGTGAGCGCTTCTCTGCTTCTGCGGCT 497
   |||
Db 544 GCGCCTGAGCGCACTGATGCGCCCGGTGTGAGCGCTTCTCTGCTTCTGCGGCT 485
   |||
QY 498 ACCTTTCATGAGCTTTGGGAAATTCTGCACTGCACTGCGCGGCACTGCTGCTTATCA 557
   |||
Db 484 ACCTTTCATGAGCTTTGGGAAATTCTGCACTGCACTGCGCGGCACTGCTGCTTATCA 425
   |||
QY 558 GATGTCACAGAGAGGCTGCTGTGCGGTGAGGCTGCTGCTGCTGCTGCTGCTGCT 617
   |||
Db 424 GATGTCACAGAGAGGCTGCTGTGCGGTGAGGCTGCTGCTGCTGCTGCTGCTGCT 365
   |||
QY 618 CATGCGCTGCTGCTGCTGCTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 677
   |||
Db 364 CATGCGCTGCTGCTGCTGCTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 305
   |||
QY 678 TCGATGCAACCGGCGGCTGCACTGCGGCTCTCTGCACTGCGGCACTGCTGCTGCT 737
   |||
Db 304 TCGATGCAACCGGCGGCTGCACTGCGGCTCTCTGCACTGCGGCACTGCTGCTGCT 245
   |||
QY 738 GCGCGGGAAGGAGGAGGCTGCTGCTGCACTGCGGCTCTCTGCACTGCGGCACTGCTGCT 797
   |||
Db 244 GCGCGGGAAGGAGGAGGCTGCTGCTGCACTGCGGCTCTCTGCACTGCGGCACTGCTGCT 185
   |||
QY 798 GCTGCGCTGATGACCGTGTCTTCTTCACTATGTTCTGCGCGGTATT 846
   |||
Db 184 GCTGCGCTGATGACCGTGTCTTCTTCACTATGTTCTGCGCGGTATT 136
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RESULT 6
US-10-029-386-10081
; Sequence 10081, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
; FILE REFERENCE: AEOMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029, 386
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Anomax Sequence Listing Engine Vers. 1.1

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; SEQ ID NO 10081
; LENGTH: 597
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO CHR14.3
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.5
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.6
; OTHER INFORMATION: EXPRESSED IN LIVER, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.3
; OTHER INFORMATION: NT HIT: U31332.1, EVALUE 0.00e+00
; OTHER INFORMATION: EST HUMAN HIT: A1460323.1, EVALUE 1.00e-108
; OTHER INFORMATION: SWISSPROT HIT: Q13258, EVALUE 1.00e-92
US-10-029-386-10081

Query Match 54.5%; Score 589; DB 16; Length 597;
Best Local Similarity 100.0%; Pred. No. 2.9e-162;
Matches 589; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 258 CTAAGCTCAGAACCGGAGTGTGCGGCTGTGCGCGCGCATTTGACAACTGTTGCA 317
   |||
Db 1 CTAAGCTCAGAACCGGAGTGTGCGGCTGTGCGCGCGCATTTGACAACTGTTGCA 60
   |||
QY 318 AGCTTGGCTTTTCTTATGCTCTTCTTGTGGCTCTCTGCACTGCACTCTGCGCAT 377
   |||
Db 61 AGCTTGGCTTTTCTTATGCTCTTCTTGTGGCTCTCTGCACTGCACTCTGCGCAT 120
   |||
QY 378 GGCACGTGAGTGTGCTCTCTCTAGGAGCACTCTTCTTCTTACGAGCAATCACT 437
   |||
Db 121 GGCACGTGAGTGTGCTCTCTCTAGGAGCACTCTTCTTCTTACGAGCAATCACT 180
   |||
QY 438 GCGCCTGAGCGCACTGATGCGCCCGGTGTGAGCGCTTCTCTGCTTCTGCGGCT 497
   |||
Db 181 GCGCCTGAGCGCACTGATGCGCCCGGTGTGAGCGCTTCTCTGCTTCTGCGGCT 240
   |||
QY 498 ACCTTTCATGAGCTTTGGGAAATTCTGCACTGCACTGCGCGGCACTGCTGCTTATCA 557
   |||
Db 241 ACCTTTCATGAGCTTTGGGAAATTCTGCACTGCACTGCGCGGCACTGCTGCTTATCA 300
   |||
QY 558 GATGTCACAGAGAGGCTGCTGTGCGGTGAGGCTGCTGCTGCTGCTGCTGCTGCT 617
   |||
Db 301 GATGTCACAGAGAGGCTGCTGTGCGGTGAGGCTGCTGCTGCTGCTGCTGCTGCT 360
   |||
QY 618 CATGCGCTGCTGCTGCTGCTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 677
   |||
Db 361 CATGCGCTGCTGCTGCTGCTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
   |||
QY 678 TCGATGCAACCGGCGGCTGCACTGCGGCTCTCTGCACTGCGGCACTGCTGCTGCT 737
   |||
Db 421 TCGATGCAACCGGCGGCTGCACTGCGGCTCTCTGCACTGCGGCACTGCTGCTGCT 480
   |||
QY 738 GCGCGGGAAGGAGGAGGCTGCTGCTGCACTGCGGCTCTCTGCACTGCGGCACTGCTGCT 797
   |||
Db 481 GCGCGGGAAGGAGGAGGCTGCTGCTGCACTGCGGCTCTCTGCACTGCGGCACTGCTGCT 540
   |||
QY 798 GCTGCGCTGATGACCGTGTCTTCTTCACTATGTTCTGCGCGGTATT 846
   |||
Db 541 GCTGCGCTGATGACCGTGTCTTCTTCACTATGTTCTGCGCGGTATT 589
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RESULT 7
US-10-225-567A-286
; Sequence 286, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: Lifespan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burner, Glenna C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225, 567A

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;; CURRENT FILING DATE: 2001-12-19
;; PRIOR APPLICATION NUMBER: 60/257,144
;; PRIOR FILING DATE: 2000-12-19
;; NUMBER OF SEQ ID NOS: 2292
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 286
;; LENGTH: 495
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-10-225-567A-286

Query Match 40.4%; Score 436; DB 15; Length 495;
Best Local Similarity 100.0%; Pred. No. 2,3e-117;
Matches 436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 645 GGTGTCACCTCGGCGCATGCGCAACTCTATGAGATGACCGCGGCTGAGCGGA 704
DB 1 GCTGTGCAACCTCGGCGCATGCGCAACTCTATGAGATGACCGCGGCTGAGCGGA 60
QY 705 CCGCGCTCTGACACGAGGACTGTGCGAGCGCGCGGAGCGGAGGGAAGCCGCCCC 764
DB 61 CCGCGCTCTGACACGAGGACTGTGCGAGCGCGCGGAGCGGAGGGAAGCCGCCCC 120
QY 765 TCAGCCCCCTGAGAGAGCTGATCACTCTGCTGCTGCGGCTGATGACCGCTCTTAC 824
DB 121 TCAGCCCCCTGAGAGAGCTGATCACTCTGCTGCTGCGGCTGATGACCGCTCTTAC 180
QY 825 TATGTTCTCTGCGCGTATTTATGCGCTTACTATGAGCATTTAAGGATGCAAGA 884
DB 181 TATGTTCTCTGCGCGTATTTATGCGCTTACTATGAGCATTTAAGGATGCAAGA 240
QY 885 GAAAAACAGAGCTCTGAAGAAGCAGAGACCTCCAGCGCTTGCATTTCTATCTGTAT 944
DB 241 GAAAAACAGAGCTCTGAAGAAGCAGAGACCTCCAGCGCTTGCATTTCTATCTGTAT 300
QY 945 TTCAATTTGAGACCTTGGATTTTATCATTTTCAATCTCCAGTATTTGCGATTTT 1004
DB 301 TTCAATTTGAGACCTTGGATTTTATCATTTTCAATCTCCAGTATTTGCGATTTT 360
QY 1005 TCACAAGATTTTCATTAAGACCTCTTATGATGATGAGAGCGGATGAGCAATTCACATACT 1064
DB 361 TCACAAGATTTTCATTAAGACCTCTTATGATGATGAGAGCGGATGAGCAATTCACATACT 420
QY 1065 GGAATCCAGCTGTGTA 1080
DB 421 GGAATCCAGCTGTGTA 436

RESULT 8

US-10-029-386-23781
;; Sequence 23781, Application US/10029386
;; Publication No. US20030194704A1
;; GENERAL INFORMATION:
;; APPLICANT: Penn, Sharon G.
;; APPLICANT: Rank, David R.
;; APPLICANT: Hanzel, David K.
;; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
;; FILE REFERENCE: AEWICA-X-2
;; CURRENT APPLICATION NUMBER: US/10/029,386
;; CURRENT FILING DATE: 2001-12-20
;; NUMBER OF SEQ ID NOS: 34288
;; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
;; SEQ ID NO 23781
;; LENGTH: 371
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE:
;; OTHER INFORMATION: MAP TO CHR14.3
;; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.2
;; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.5
;; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.6
;; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.1

;; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.3
;; OTHER INFORMATION: SWISSPROT HIT: Q13258, EVALUE 7.00e-59
;; OTHER INFORMATION: NT HIT: U1332.1, EVALUE 0.00e+00
;; OTHER INFORMATION: EST_HUMAN HIT: A146032.1, EVALUE 2.00e-16
US-10-029-386-23781

Query Match 34.4%; Score 371; DB 16; Length 371;
Best Local Similarity 100.0%; Pred. No. 2.5e-98;
Matches 371; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 322 TTGCGCTTCTTATGATGCTCTTTGGGCTCTCTGAGACATGCACTCCTGGCATGGA 381
DB 1 TTGCGCTTCTTATGATGCTCTTTGGGCTCTCTGAGACATGCACTCCTGGCATGGA 60
QY 382 CTGAGATGCTGCTCTCTCCCTTACGAGCACTCTTCTTACGAGGACATCACTCCGCGC 441
DB 61 CTGAGATGCTGCTCTCTCCCTTACGAGCACTCTTCTTACGAGGACATCACTCCGCGC 120
QY 442 CTGGGCGCATGCTGAGCGCGGCTGTGAGCGCTTCTCTGCTTCTGCGGCTACT 501
DB 121 CTGGGCGCATGCTGAGCGCGGCTGTGAGCGCTTCTCTGCTTCTGCGGCTACT 180
QY 502 TTCAATGAGCTTGGGAGATGCTGAGCATGCTGCGGAGCACTGAGCTTTATCCAGATG 561
DB 181 TTCAATGAGCTTGGGAGATGCTGAGCATGCTGCGGAGCACTGAGCTTTATCCAGATG 240
QY 562 GTCCAGAGAGAGGCTGCTGCTGCTGAGGATCTGTGCTCTACTCCAGCTCATG 621
DB 241 GTCCAGAGAGAGGCTGCTGCTGCTGAGGATCTGTGCTCTACTCCAGCTCATG 300
QY 622 GCGCTGCTGCTCTGCGCACCGTCTGTGCAACTCTGCGGCAATGCGCACTCTATGG 681
DB 301 GCGCTGCTGCTCTGCGCACCGTCTGTGCAACTCTGCGGCAATGCGCACTCTATGG 360
QY 682 ATGCACCGGCG 692
DB 361 ATGCACCGGCG 371

RESULT 9

US-10-108-714-3
;; Sequence 3, Application US/10108714
;; Publication No. US20020128445A1
;; GENERAL INFORMATION:
;; APPLICANT: Regan, John W.
;; APPLICANT: Gil, Daniel W.
;; APPLICANT: Woodward, David F.
;; TITLE OF INVENTION: No. US20020128445A1el Human Prostaglandin EP Receptor
;; FILE REFERENCE: 17023 DIV CIP
;; CURRENT APPLICATION NUMBER: US/10/108,714
;; CURRENT FILING DATE: 2002-03-28
;; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/267,423
;; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-12
;; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/239,431
;; NUMBER OF SEQ ID NOS: 10
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 3
;; LENGTH: 2296
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: (157) ... (1233)
US-10-108-714-3

Query Match 20.4%; Score 220.6; DB 13; Length 2296;
Best Local Similarity 57.8%; Pred. No. 7.6e-54;
Matches 557; Conservative 0; Mismatches 349; Indels 57; Gaps 7;

QY 48 AGGCACTGGGGGGGATGGGGGGGCTCTTACGACACGGGCTCTGGGCAACCTGCT 107
DB 219 AGGCAACGCCAGCCATCAGCTCCCTCATGTTCTCGGCGGGGCTGGGCAACCTCAT 278


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; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/390,965
; PRIOR FILING DATE: 2002-06-24
; PRIOR APPLICATION NUMBER: US 60/392,480
; PRIOR FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: US 60/394,128
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 60/399,783
; PRIOR FILING DATE: 2002-07-31
; PRIOR APPLICATION NUMBER: US 60/403,221
; PRIOR FILING DATE: 2002-08-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 35
; LENGTH: 2372
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (157)...(1233)
US-10-352-684A-35

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Query Match      20.3%; Score 219; DB 17; Length 2372;
Best Local Similarity 57.7%; Pred. No. 2.3e-53;
Matches 556; Conservative 0; Mismatches 350; Indels 57; Gaps 7;

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QY 48 AGGCACTGCGGCGGTATGGGCGGGGCTCTTTCAGACCGGCGCTCTGAGCAACTGCT 107
DB 219 AGCGGAAAGCCGACCATGCTCCGTCGATGTTCTCGCGGGGTGTGGGAACTCAT 278
QY 108 GGGCTGCGGCGCTGCTGCGCGGCTCGGGGCTGGGGT--GGTCTCGCGGCGTCCACTGCG 165
DB 279 AGACATGGGCGCTGCTGCGCGGCTCGGGGAGAGTGGGGTGCAGCGCCGCGCGAG 338
QY 166 CCGCTGCC-CTCGGTCTTCAATGCTGTGTGTGCGCTGACGCGTACCGACTTGTGG 224
DB 339 GAGCTCCCTCTCTGTTCCAGTGTGTCGAGCCGAGCTGTGTTCACGACCTGCTCG 398
QY 225 CAAGTCCCTCTTAAGCCCGGTGTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 284
DB 399 GACCTCCCTCATAGCCCACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 458
QY 285 GCTTGGCGCGCATGTGGAACAATCGTTGTGCAAGCGCTTCTTCAATGCTCTT 344
DB 459 ACTGGGCGCC-----GAGAGCGCGCGGTGCACTTCTTGGCCTTGTGCACTTCTT 512
QY 345 TGGGCTCTCTGACACTGCACTCTGCGCATGAGCACTGAGTGTGCTCTCTCTAGG 404
DB 513 CAGCTGGGCGACGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 572
QY 405 GCACTCTTCTTTCAGAGGCAATCACTGCGCTGCGGCGCTGAGGCGACTGTGCGCG 464
DB 573 GCACTCTTCTTTCAGAGGCAATCACTGCGCTGCGGCGCTGAGGCGACTGTGCGCT 632
QY 465 GGTGAGCGCTTCTCTGCTGCTTGTGCGGCTACCTTTCATAGGGGCTTGGGAAATTG 524
DB 633 CATCTATGAGTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 692
QY 525 GCACTCTGCGCGGCGCACTGCTGCTTTCATGAGTGTGCAAGAGAGGCGCTGCTG 584
DB 693 CCACTGCTGCGCGGCGCACTGCTGCTTTCATGAGTGTGCAAGAGAGGCGCTGCTG 734
QY 585 GGTGCTGCGGCTGCTGCTGCTTTCATGAGTGTGCAAGAGAGGCGCTGCTGCTG 644
DB 735 ---GACCGCTTCTCTGCTGCTGCTTTCATGAGTGTGCAAGAGAGGCGCTGCTG 791
QY 645 GGTGCTGCGGCTGCTGCGGCACTGCTTTCATGAGTGTGCAAGAGAGGCGCTGCTG 702
DB 792 CCGCTGCACTTATGATGCTTTCATGAGTGTGCAAGAGAGGCGCTGCTGCTGCTG 851
QY 703 CACCCGCGCTCTGCAAGAGGAGTGTGCGGCGCGCGGCGGAGGAGGAGGCTGCTG 762

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DB 852 CCGCTGCGGACTTCTCTGCGAGTGGCCGCGGCGCGCGCGCGCGCGCGCGAGAGGGA 911
QY 763 CTCAGGCCCT----GAGAGAGCTGGATCACTCTGCTGCTGCGGCTGATGACCGTGT 818
DB 912 AAGGTGTCCATGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 971
QY 819 CTTCATGATGCTGCTGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 878
DB 972 CTTCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1011
QY 879 CAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 938
DB 1012 -ATGAATGAAACCTCTTCCGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1070
QY 939 TGTGATTTCAATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 998
DB 1071 AATTAATTCATATTAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1130
QY 999 ATT 1001
DB 1131 AAT 1133

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RESULT 13
US-10-366-288-35
; Sequence 35, Application US/10366288
; Publication No. US20030216288A1
; GENERAL INFORMATION:
; APPLICANT: Powell, Douglas
; APPLICANT: Welch, Nadine S.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: AIDS AND HIV-RELATED DISORDERS USING
; TITLE OF INVENTION: 34021, 1720, 1683, 1557, 1682, 1675, 12825, 5816,
; TITLE OF INVENTION: 10002, 1611, 1371, 14324, 126, 270, 312, 167, 326, 18926,
; TITLE OF INVENTION: 6747, 1793, 1784 OR 2045 MOLECULES
; FILE REFERENCE: MP102-025P1RNMNM
; CURRENT APPLICATION NUMBER: US/10/366,288
; PRIOR APPLICATION NUMBER: 60/357,391
; PRIOR FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: 60/380,249
; PRIOR FILING DATE: 2002-05-13
; PRIOR APPLICATION NUMBER: 60/391,306
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: 60/406,297
; PRIOR FILING DATE: 2002-08-27
; PRIOR APPLICATION NUMBER: 60/412,007
; PRIOR FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: 60/417,508
; PRIOR FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: 60/432,318
; PRIOR FILING DATE: 2002-12-10
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 35
; LENGTH: 2372
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-366-288-35

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Query Match      20.3%; Score 219; DB 17; Length 2372;
Best Local Similarity 57.7%; Pred. No. 2.3e-53;
Matches 556; Conservative 0; Mismatches 350; Indels 57; Gaps 7;

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```

QY 48 AGGCACTGCGGCGGTATGGGCGGGGCTCTTTCAGACCGGCGCTCTGAGCAACTGCT 107
DB 219 AGCGGAAAGCCGACCATGCTCCGTCGATGTTCTCGCGGGGTGTGGGAACTCAT 278
QY 108 GGGCTGCGGCGCTGCTGCGCGGCTCGGGGCTGGGGT--GGTCTCGCGGCGTCCACTGCG 165
DB 279 AGACATGGGCGCTGCTGCGCGGCTCGGGGAGAGTGGGGTGCAGCGCCGCGCGAG 338
QY 166 CCGCTGCC-CTCGGTCTTCAATGCTGTGTGTGCGCTGACGCGTACCGACTTGTGCG 224

```


Oy		939	TGTGATTTCAATTGGAGCCCTGGATTTTTATCATTTTCAGATCTCCAGATAATTCGAT	998
Db		1071	AATTAATTCAATTAATTGACCCCTTGGSGTCTTTGCCATCCTTAGCGCTCCTGTGTTTGAGACT	1130
Oy		999	ATT	1001
Db		1131	AAT	1133

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RESULT 15
US-10-755-889-91
: Sequence 91, Application US/10755889
: Publication No. US20040171823A1
: GENERAL INFORMATION:
: APPLICANT: Bristol-Myers Squibb Company
: TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ASSOCIATED WITH THE NF-KB
: TITLE OF INVENTION: PATHWAY
: FILE REFERENCE: D0284 NP
: CURRENT APPLICATION NUMBER: US/10/755,889
: CURRENT FILING DATE: 2004-01-13
: PRIOR APPLICATION NUMBER: U.S. 60/440,068
: PRIOR FILING DATE: 2003-01-14
: PRIOR APPLICATION NUMBER: U.S. 60/469,757
: PRIOR FILING DATE: 2003-05-12
: NUMBER OF SEQ ID NOS: 823
: SOFTWARE: PatentIn version 3.2
: SEQ ID NO 91
: LENGTH: 2372
: TYPE: DNA
: ORGANISM: Homo sapiens
US-10-755-889-91

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Query Match	20.3%;	Score 219;	DB 18;	Length 2372;
Best Local Similarity	57.7%;	Pred. No. 2.3e-53;		
Matches 556; Conservative	0;	Mismatches 350;	Indels 57;	Gaps 7;

QY	48	AGGCAATCGGCGGGGATGAGGCGGGGTGCTTCAACAACCGGCTCTGGAGCAACTGCT	107
Dp	219	AGGCAAAAGCCAGCCATAGCTCCGTCAATGTTCTTGCGCGGGGTCTGGGAACCTCAT	278
QY	108	GGCCCTGAGGCTGTGGCGCGCTCGGGGCTGAGGGT--GGTGTCTCGCGCGTCACTGGCC	165
Dp	279	AGCAATGGCGGCTGCTGCGCGCGCTGGCGGGGGAGACGTGGGGTGTACAGCGCCCGCGCAG	338
QY	166	CCGCTGCC-CTCGGCTTCTACATGCTGGTGGTGGTGGCTGAGGGTCAACGACCTTGGTGGG	224
Dp	339	GAGCTCCCTCTCTTGTTCACGTGTGTGTGACCGAGCTGGTGTATACGAACTGTCTCG	398
QY	225	CAAGTGCCTCTTAACCCCGGCTGGCTGCTGCTCAACGCTCAACCCGAGTCTGGCGGT	284
Dp	399	GACCTGCTCATCAGCCCGAGTGGTACTGGCTTGTGTGCGCGGGAACAGACCTGGTGGC	458
QY	285	GCTTGGCGCCGATGGACAATCTGTTGGTGGCAAGCTTGGCTTTCATGTCCTTCTT	344
Dp	459	ACTGGCGGCC-----GAGAGCGCGCGTGCACCTACTTGTGCTTGGCAATGACCTTCTT	512
QY	345	TGGGCTCTCTCGACACTGCAATCTCTGGCCATATGGCACTGAGTGTGGCTTCCCTAGG	404
Dp	513	CAGCTGGCAACGATGCTCATGCTCTTGGCAATGGCCCTGGAAGCGTTACTCTGCATCGG	572
QY	405	GCACTCTTCTTCTACCGACGAGCAATACCTCTGCGCTCTGGGCGCACTGTGACCCCGGT	464
Dp	573	GCACCCCTACTTCTACAGAGCGCGCGCTCTCGGCTTCGGGGGCTGAGCGCTGTGCTGT	632
QY	465	GGTGAAGCGCTTCTCCCTGGCTTCTTCTGCGCGCTACTTTCATGGGCTCTGGGAAGTTCGT	524
Dp	633	CATCATAGAGTCTCCCTGCTCTTCTGCTCGCTGCGCGCTGTGAGCTATAGGAGATACGT	692
QY	525	GCACTACTGCCCCCGGCACTGCTGTGCTTATCCAGATGCTTCACAGAGAGGGCTCGCTGTC	584
Dp	693	CCAGTACTGCCCCCGGACCTGGGTGCTTCAATCCGACGGAGCG-----	734

QY	585	GGTCTGGGGGACTCTGTGCTCTACTCCAGCTTCATGGCGTGTGGTCTGGCACCGT	644
Db	735	---GACCGCTTACCCTGCAGCGTGTACGCCAACCCCTGCTGCTTCTCATTTGCTCGTGTCT	791
QY	645	GCTGTGCACCTCGGCGCCATGCGCAACCTTATGCAATGCACCGGG--GCTGCACGG	702
Db	792	CGCCTGCACACTTCGATGTCAATTTCAACCTTCATCCGATGCACCGCCGGAAGCCGGAAMG	851
QY	703	CACCCGGCGCTCTGCACACAGGAGCTGTGCCGAGCCGGCGCGAGCGGAGGGAAGCGTCC	762
Db	852	CCGCTGCGGACCTTCTCCTGGGCAATGGCCGGGCGCGCCCGGGGCCCCGACGAGAGGGGA	911
QY	763	CCTCAGCCCT----GGAGAGCTGATTCACCTTCTGCTGTGGCGCTGATGACCGTGTCT	818
Db	912	AAGGGTGCCATGCGGAGGAGACGGACCACTCATTTCTCCTGGCTATCATGACCACTCAC	971
QY	819	CTTCACTATGTGTTCTCTGCCCCGTAATTTATGCGGCTTACTATGAGACATTTAAGATGT	878
Db	972	CTTGGCGCTGTCTCTTGGCTTTCACGATTTTGCATAT-----1011	
QY	879	CAAGGAGAAAAACAGACCTCTGAAGAGCAGAAAGACCTCGAGCCTTTCGATTTCTATC	938
Db	1012	-ATGAATGAACCTCTTCCGGAAGGAAAAATGGAACCTCCACAGCTCTTAGGTTTTATC	1070
QY	939	TGTGATTTCAATTGTGACCTTGGATTTTTTATCATTTTCAGATCTCCAGATTTTGGAT	998
Db	1071	AATTATTCATTAATGACCTCTGGGTCTTTCGCATCCTTAGGCGCTCTGTTCGAGACT	1130
QY	999	ATT 1001	
Db	1131	AAT 1133	

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Job time : 716.004 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 22, 2005, 21:00:43 ; Search time 21.3756 Seconds
(without alignments)
1253.721 Million cell updates/sec

Title: US-10-689-861-4
Perfect score: 1864
Sequence: 1 MKSPFYRCQNTSVKGNLSA.....IRPLRYRCSNSTMSSL 359

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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4: /cgn2_6/ptodata/1/1aa/6A_COMB.pep: *
5: /cgn2_6/ptodata/1/1aa/6B_COMB.pep: *
6: /cgn2_6/ptodata/1/1aa/PTCUS_COMB.pep: *
7: /cgn2_6/ptodata/1/1aa/PTCUS_COMB.pep: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1864	100.0	359	2	US-08-812-203-3
2	1864	100.0	359	3	US-09-300-864-3
3	1864	100.0	359	3	US-09-598-418-3
4	688	36.9	358	1	US-08-239-431A-4
5	688	36.9	358	1	US-09-267-423-4
6	683	36.6	358	4	US-09-826-509-559
7	667	35.8	358	2	US-08-463-081B-6
8	667	35.8	358	2	US-08-461-379A-6
9	667	35.8	358	2	US-08-462-390B-6
10	667	35.8	358	3	US-08-463-074B-6
11	667	35.8	358	3	US-08-465-585C-6
12	667	35.8	358	3	US-08-652-446-6
13	597	32.0	386	1	US-08-134-012-3
14	597	32.0	386	1	US-08-520-519-3
15	597	32.0	386	1	US-09-039-798-3
16	458.5	24.6	513	1	US-08-390-162-6
17	458.5	24.6	513	1	US-08-685-945B-6
18	443	23.8	488	1	US-08-115-365-2
19	443	23.8	488	1	US-08-586-897-2
20	440	23.6	488	4	US-09-826-509-561
21	308	16.5	365	1	US-08-390-162-2
22	308	16.5	365	1	US-08-685-945B-2
23	307.5	16.5	361	1	US-08-390-162-4
24	307.5	16.5	361	1	US-08-685-945B-4
25	302	16.2	385	1	US-08-416-756A-3
26	302	16.2	385	4	US-08-880-865-3
27	297.5	16.0	390	3	US-08-155-005A-4

28	297.5	16.0	390	3	US-08-155-005A-17	Sequence 17, Appl
29	297.5	16.0	390	3	US-09-363-783-4	Sequence 4, Appl
30	297.5	16.0	390	3	US-09-363-783-17	Sequence 17, Appl
31	297.5	16.0	390	4	US-09-661-758A-4	Sequence 4, Appl
32	297.5	16.0	390	4	US-09-661-758A-17	Sequence 17, Appl
33	294	15.8	388	3	US-08-155-005A-6	Sequence 6, Appl
34	294	15.8	388	3	US-09-363-783-6	Sequence 6, Appl
35	294	15.8	388	4	US-09-661-758A-6	Sequence 6, Appl
36	293.5	15.7	365	3	US-08-155-005A-8	Sequence 8, Appl
37	293.5	15.7	365	3	US-09-363-783-8	Sequence 8, Appl
38	293.5	15.7	365	3	US-09-661-758A-8	Sequence 8, Appl
39	289.5	15.5	343	4	US-09-054-272-6	Sequence 4, Appl
40	267	14.3	378	4	US-08-416-756A-4	Sequence 4, Appl
41	267	14.3	378	4	US-08-880-865-4	Sequence 4, Appl
42	255.5	13.7	402	2	US-08-068-729-4	Sequence 4, Appl
43	255.5	13.7	402	3	US-09-255-671-4	Sequence 4, Appl
44	255.5	13.7	402	4	US-09-395-366-4	Sequence 4, Appl
45	252.5	13.5	402	4	US-09-826-509-557	Sequence 557, App

ALIGNMENTS

RESULT 1
US-08-812-203-3
; Sequence 3, Application US/08812203
; Patent No. 5958723
GENERAL INFORMATION:
APPLICANT: ABRAMOVITZ, MARK
APPLICANT: BOIE, YVES
APPLICANT: SAWYER, NICOLE
APPLICANT: METTERS, KATHLEEN
APPLICANT: SLIBETZ, DEBORAH
TITLE OF INVENTION: DNA ENCODING PROSTAGLANDIN RECEPTOR DP
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: JOHN W. WALLEN, III
STREET: 126 E. LINCOLN AVE., P.O. BOX 2000
CITY: RAHWAY
STATE: NJ
COUNTRY: USA
ZIP: 07065-0900
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/812,203
FILING DATE: 06-MAR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/378,682
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: WALLEN III, JOHN W.
REGISTRATION NUMBER: 35,403
REFERENCE/DOCKET NUMBER: MRL 94/185
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908)594-3905
TELEX: (908)594-4720
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 359 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-812-203-3
Query Match 100.0%; Score 1864; DB 2; Length 359;
Best Local Similarity 100.0%; Pred. No. 16-166;
Matches 359; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query 1 MKSPFRCONTTSVEKNSAVMGVLFSTGLGNLALGLIASSGIGWCSRRPLRPLPSV 60
Best Local Similarity 100.0%; Pred. No. 1e-166;
Matches 359; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MKSPFRCONTTSVEKNSAVMGVLFSTGLGNLALGLIASSGIGWCSRRPLRPLPSV 60
QY 61 FYMLVCGLTITDILGKCLSPVLAAYAQRSLRVLAIPALDNLSCQAFAPFMSFFGLSST 120
DB 61 FYMLVCGLTITDILGKCLSPVLAAYAQRSLRVLAIPALDNLSCQAFAPFMSFFGLSST 120
QY 121 LQILAMALECWLISLGHFFPYRRHITRLGALVAPVSAFSLAFCAIPMGFGKPVQYCPG 180
DB 121 LQILAMALECWLISLGHFFPYRRHITRLGALVAPVSAFSLAFCAIPMGFGKPVQYCPG 180
QY 181 TWCFIQWHEGSLSVIGSVLYSSLMALLVATVLCNIGAMRNLVAMHRRLOHPRSC 240
DB 181 TWCFIQWHEGSLSVIGSVLYSSLMALLVATVLCNIGAMRNLVAMHRRLOHPRSC 240
QY 241 RDCAEPADGRASPOPLELDHLLALMTVLFTMCSLPVYRAYYGAFDYKRNRTS 300
DB 241 RDCAEPADGRASPOPLELDHLLALMTVLFTMCSLPVYRAYYGAFDYKRNRTS 300
QY 301 EEAEDLRALRFLSVISIVDPWIFIFRSVPVRIFFHKIFIRPLRYRSCNSTMESSL 359
DB 301 EEAEDLRALRFLSVISIVDPWIFIFRSVPVRIFFHKIFIRPLRYRSCNSTMESSL 359

RESULT 2

US-09-300-864-3
Sequence 3, Application US/09300864
Patent No. 6214972

GENERAL INFORMATION:

APPLICANT: ABRAMOVITZ, MARK

APPLICANT: BOLE, YVES

APPLICANT: SAWYER, NICOLE

APPLICANT: METTERS, KATHLEEN

APPLICANT: SLIPETZ, DEBORAH

TITLE OF INVENTION: DNA ENCODING PROSTAGLANDIN RECEPTOR DP

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: JOHN W. WALLEN, III

STREET: 126 E. LINCOLN AVE., P.O. BOX 2000

CITY: RAHWAY

STATE: NJ

COUNTRY: USA

ZIP: 07065-0900

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/300,864

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/378,682

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: WALLEN III, JOHN W.

REGISTRATION NUMBER: 35,403

REFERENCE/DOCKET NUMBER: MRL 94/185

TELECOMMUNICATION INFORMATION:

TELEPHONE: (908)594-3905

TELEX: (908)594-4720

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 359 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-300-864-3

Query Match 100.0%; Score 1864; DB 3; Length 359;
Best Local Similarity 100.0%; Pred. No. 1e-166;
Matches 359; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MKSPFRCONTTSVEKNSAVMGVLFSTGLGNLALGLIASSGIGWCSRRPLRPLPSV 60
QY 61 FYMLVCGLTITDILGKCLSPVLAAYAQRSLRVLAIPALDNLSCQAFAPFMSFFGLSST 120
DB 61 FYMLVCGLTITDILGKCLSPVLAAYAQRSLRVLAIPALDNLSCQAFAPFMSFFGLSST 120
QY 121 LQILAMALECWLISLGHFFPYRRHITRLGALVAPVSAFSLAFCAIPMGFGKPVQYCPG 180
DB 121 LQILAMALECWLISLGHFFPYRRHITRLGALVAPVSAFSLAFCAIPMGFGKPVQYCPG 180
QY 181 TWCFIQWHEGSLSVIGSVLYSSLMALLVATVLCNIGAMRNLVAMHRRLOHPRSC 240
DB 181 TWCFIQWHEGSLSVIGSVLYSSLMALLVATVLCNIGAMRNLVAMHRRLOHPRSC 240
QY 241 RDCAEPADGRASPOPLELDHLLALMTVLFTMCSLPVYRAYYGAFDYKRNRTS 300
DB 241 RDCAEPADGRASPOPLELDHLLALMTVLFTMCSLPVYRAYYGAFDYKRNRTS 300
QY 301 EEAEDLRALRFLSVISIVDPWIFIFRSVPVRIFFHKIFIRPLRYRSCNSTMESSL 359
DB 301 EEAEDLRALRFLSVISIVDPWIFIFRSVPVRIFFHKIFIRPLRYRSCNSTMESSL 359

RESULT 3

US-09-598-418-3
Sequence 3, Application US/09598418
Patent No. 6395499

GENERAL INFORMATION:

APPLICANT: ABRAMOVITZ, MARK

APPLICANT: BOLE, YVES

APPLICANT: SAWYER, NICOLE

APPLICANT: METTERS, KATHLEEN

APPLICANT: SLIPETZ, DEBORAH

TITLE OF INVENTION: DNA ENCODING PROSTAGLANDIN RECEPTOR DP

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: JOHN W. WALLEN, III

STREET: 126 E. LINCOLN AVE., P.O. BOX 2000

CITY: RAHWAY

STATE: NJ

COUNTRY: USA

ZIP: 07065-0900

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/598,418

FILING DATE: 20-Jun-2000

CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: WALLEN III, JOHN W.

REGISTRATION NUMBER: 35,403

REFERENCE/DOCKET NUMBER: MRL 94/185

TELECOMMUNICATION INFORMATION:

TELEPHONE: (908)594-3905

TELEX: (908)594-4720

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 359 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 3:

US-09-598-418-3

Query Match 100.0%; Score 1864; DB 3; Length 359;
 Best Local Similarity 100.0%; Pred. No. 1e-166;
 Matches 359; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKSPFRQNTTSVEKGNASVAVGVLFTSTGLLGNLALGLLARSGLGCSRRLPLPSPV 60
 DB 1 MKSPFRQNTTSVEKGNASVAVGVLFTSTGLLGNLALGLLARSGLGCSRRLPLPSPV 60
 QY 61 FYMLVCGITVTYDILGKCLISPVLAAYNONSRLVLAALNLSLQAFAPFMSFFGLSST 120
 DB 61 FYMLVCGITVTYDILGKCLISPVLAAYNONSRLVLAALNLSLQAFAPFMSFFGLSST 120
 QY 121 LQILAMLECLSLGHPFFRYRHTLRGLAVAPVSAFSLAFCLPFGKGFQYQCPG 180
 DB 121 LQILAMLECLSLGHPFFRYRHTLRGLAVAPVSAFSLAFCLPFGKGFQYQCPG 180
 QY 181 TWCFIQVHEEGSLSVLGYSVLVSLMALVLAIVLCNLGAMRNLVAMHRLQHRPSCCT 240
 DB 181 TWCFIQVHEEGSLSVLGYSVLVSLMALVLAIVLCNLGAMRNLVAMHRLQHRPSCCT 240
 QY 241 RDCAPRADGRBASPOPLEEDHLLALMTVLFTMCSLPYIYAYYGAFDVKEKRTS 300
 DB 241 RDCAPRADGRBASPOPLEEDHLLALMTVLFTMCSLPYIYAYYGAFDVKEKRTS 300
 QY 301 EEAEDLALRPLSYISIVDPWIFIIFRSPVPRIFPKIFIRPLRYSRCSNSTMMESL 359
 DB 301 EEAEDLALRPLSYISIVDPWIFIIFRSPVPRIFPKIFIRPLRYSRCSNSTMMESL 359

RESULT 4

US-08-239-431A-4
 ; Sequence 4, Application US/08239431A
 ; Patent No. 5716835

GENERAL INFORMATION:
 APPLICANT: Regan, John W.
 APPLICANT: Gil, Daniel W.
 APPLICANT: Woodward, David F.
 TITLE OF INVENTION: NOVEL HUMAN EP PROTAGLANDIN RECEPTOR
 NUMBER OF SEQUENCES: 10
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Knobbe, Martens, Olson and Bear
 STREET: 620 Newport Center Drive 16th Floor
 CITY: Newport Beach
 STATE: CA
 COUNTRY: USA
 ZIP: 92660
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSeq Version 1.5
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/239,431A
 FILING DATE: 05-MAY-1994
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Israelien, Ned A
 REGISTRATION NUMBER: 29,655
 REFERENCE/DOCKET NUMBER: ALRGN.053A
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 619-235-8550
 TELEFAX: 619-235-0176
 TELEX:
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 358 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear

MOLECULE TYPE: protein
 ;
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: NO
 ; FRAGMENT TYPE: internal
 ; ORIGINAL SOURCE:
 US-08-239-431A-4

Query Match 36.9%; Score 688; DB 1; Length 358;
 Best Local Similarity 43.7%; Pred. No. 1.9e-56;
 Matches 157; Conservative 54; Mismatches 118; Indels 30; Gaps 10;

QY 8 QNTTSVEKGNASVAVGVLFTSTGLLGNLALGLLARSGLG--WCSRRLPLPSPVFMV 65
 DB 13 CETRQWLPBGSPSAISSVMSAGVLAIVLALALARRWRGDCSAGRSSL-SLFVLY 71
 QY 66 CGLTVTDILGKCLISPVLAAYNONSRLVLAALNLSLQAFAPFMSFFGLSSTLQILA 125
 DB 72 TELVFTDLGTCCLISPVLAAYNONSRLVLAALNLSLQAFAPFMSFFGLSSTLQILA 129
 QY 126 MALECWLSLGHPPFFRYRHTLRGLAVAPVSAFSLAFCLPFGKGFQYQCPGTCFI 185
 DB 130 MALERYSLGHPFFRYRHTLRGLAVAPVSAFSLAFCLPFGKGFQYQCPGTCFI 189
 QY 186 QVHEEGSLSVLGYSVLVSLMALVLAIVLCNLGAMRNLVAMHRLQHRPSCCTRCAE 245
 DB 190 R-HGR-----TAVLQVATLILLIYSLACNFSVILIRHRRRR--SRCGPSLGS 240
 QY 246 ----PRADGRBASPOPLEEDHLLALMTVLFTMCSLPYIYAYYGAFDVKEKRTSE 301
 DB 241 GRGGPGARRRGERVSMAEETDHLILAMITTFVAVCSLPFTIFAY-----MNETSS 291
 QY 302 EAE--DLRALRPLSYISIVDPWIFIIFRSPVPRIFPKIFIRPLRYSRCSNSTMMES 357
 DB 292 RKEKMDLQALRPLSYISIVDPWIFIIFRSPVPRIFPKIFIRPLRYSRCSNSTMMES 350

RESULT 5

US-09-267-423-4
 ; Sequence 4, Application US/09267423
 ; Patent No. 6395878

GENERAL INFORMATION:
 APPLICANT: Regan, John W.
 APPLICANT: Gil, Daniel W.
 APPLICANT: Woodward, David F.
 TITLE OF INVENTION: No. 6395878el Human Prostaglandin EP Receptor
 FILE REFERENCE: 17023 DIV CIP
 CURRENT APPLICATION NUMBER: US/09/267,423
 CURRENT FILING DATE: 1999-03-12
 EARLIER APPLICATION NUMBER: 09/019,393
 EARLIER FILING DATE: 1998-02-05
 EARLIER APPLICATION NUMBER: 08/239,431
 EARLIER FILING DATE: 1994-05-05
 NUMBER OF SEQ ID NOS: 10
 SOFTWARE: FastSeq for Windows Version 3.0
 SEQ ID NO 4
 LENGTH: 358
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-267-423-4

Query Match 36.9%; Score 688; DB 3; Length 358;
 Best Local Similarity 43.7%; Pred. No. 1.9e-56;
 Matches 157; Conservative 54; Mismatches 118; Indels 30; Gaps 10;

QY 8 QNTTSVEKGNASVAVGVLFTSTGLLGNLALGLLARSGLG--WCSRRLPLPSPVFMV 65
 DB 13 CETRQWLPBGSPSAISSVMSAGVLAIVLALALARRWRGDCSAGRSSL-SLFVLY 71
 QY 66 CGLTVTDILGKCLISPVLAAYNONSRLVLAALNLSLQAFAPFMSFFGLSSTLQILA 125
 DB 72 TELVFTDLGTCCLISPVLAAYNONSRLVLAALNLSLQAFAPFMSFFGLSSTLQILA 129
 QY 126 MALECWLSLGHPPFFRYRHTLRGLAVAPVSAFSLAFCLPFGKGFQYQCPGTCFI 185

Db 130 MALERYLSIGHPIYQGRVRSGLAVLPVYAVSLFCSPLLDYQGYOYCGTWCFI 189
QY 186 QMHEESLSVLGVSYSMLLVATVLCNIGAMRNLYAMHRLQHRSCSTRCAE 245
Db 190 R--HGR-----TAYLQYATLTLILVSVLACNFSVLINLRMRSSR--SRCGSLGS 240
QY 246 ----PRADGASQPLEEDLHLLALMTVLFTMCSLPVYRAYGAFKDVKEKNTSE 301
Db 241 GRGGPGARRRGERVSMABETDHLILAMITTFVCSLPFTIFAY-----MNETSS 291
QY 302 EAE--DIRALRFLSVISIVDPWIFIRSPVFRIFPKIFIR-PLRYRSRCSNTNMS 357
Db 292 RKEKMDIQLARFLSINSIIDPWVFAIRPVLRLMRSVLCRISLRQDATQTSCTOS 350

RESULT 6
US-09-826-509-559
; Sequence 559, Application US/09826509
; Patent No. 6806054
; GENERAL INFORMATION:
; APPLICANT: Lehmann-Brinnsma, Karin
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: No. 6806054-Endogenous, Constitutively Activated Known G
; TITLE OF INVENTION: Protein-Coupled Receptors
; FILE REFERENCE: AREN-207
; CURRENT APPLICATION NUMBER: US/09/826,509
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/195,747
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 589
; SOFTWARE: Patentin Version 2.1
; SEQ ID NO 559
; LENGTH: 358
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-826-509-559

Query Match 36.6%; Score 683; DB 4; Length 358;
Best Local Similarity 43.5%; Pred. No. 5.7e-56;
Matches 156; Conservative 54; Mismatches 119; Indels 30; Gaps 10;
QY 8 CQNTSVKNSAVMGVLFSTGLGNLALGLIARSLG--WCSRRLRPLPSVFTMLV 65
Db 13 CETRQMPPEGPSPAISSVMSAGVGNLILALILARRMGDVGCSAGRSSL-SLFHVLV 71
QY 66 CGLTVDLLGKCLSPVLAAYANRSLRVLAAPALDNLCOAFPFMSFGLSSTLQLLA 125
Db 72 TELVFTDLGLCLISPVLAAYANRSLRVLAAPALDNLCOAFPFMSFGLSSTLQLLA 129
QY 126 MALECWLSLGHPPFYRRHITRLGALVAPVVSASFALFCAFPWGFQKFOYCGTWCFI 185
Db 130 MALERYLSIGHPIYQGRVRSGLAVLPVYAVSLFCSPLLDYQGYOYCGTWCFI 189
QY 186 QMHEESLSVLGVSYSMLLVATVLCNIGAMRNLYAMHRLQHRSCSTRCAE 245
Db 190 R--HGR-----TAYLQYATLTLILVSVLACNFSVLINLRMRSSR--SRCGSLGS 240
QY 246 ----PRADGASQPLEEDLHLLALMTVLFTMCSLPVYRAYGAFKDVKEKNTSE 301
Db 241 GRGGPGARRRGERVSMABETDHLILAMITTFVCSLPFTIFAY-----MNETSS 291
QY 302 EAE--DIRALRFLSVISIVDPWIFIRSPVFRIFPKIFIR-PLRYRSRCSNTNMS 357
Db 292 RKEKMDIQLARFLSINSIIDPWVFAIRPVLRLMRSVLCRISLRQDATQTSCTOS 350

RESULT 7
US-08-463-081B-6
; Sequence 6, Application US/08463081B

; Patent No. 5871960
; Patent No. 5871960 5837487
; GENERAL INFORMATION:
; APPLICANT: Smith, Kendall A. & Beadling, Carol
; TITLE OF INVENTION: Nucleic Acids Encoding CR5 Polypeptide.
; TITLE OF INVENTION: Vector and Transformed Cell Thereof, and Expression Thereof
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PRETTY, SCHROEDER & POPLAWSKI
; STREET: 444 South Flower St. - Suite 1900
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0,
; SOFTWARE: Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/463,081B
; FILING DATE: 5-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/104,736
; FILING DATE: 10-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/796,066
; FILING DATE: 20-NOV-91
; ATTORNEY/AGENT INFORMATION:
; NAME: Viviana Amzel, Ph. D.
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: P66 38150 (DART-060)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 622-7700
; TELEFAX: (213) 489-4210
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 358 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-463-081B-6

Query Match 35.8%; Score 667; DB 2; Length 358;
Best Local Similarity 42.9%; Pred. No. 1.8e-54;
Matches 154; Conservative 53; Mismatches 122; Indels 30; Gaps 10;
QY 8 CQNTSVKNSAVMGVLFSTGLGNLALGLIARSLG--WCSRRLRPLPSVFTMLV 65
Db 13 CETRQMPPEGPSPAISSVMSAGVGNLILALILARRMGDVGCSAGRSSL-SLFHVLV 71
QY 66 CGLTVDLLGKCLSPVLAAYANRSLRVLAAPALDNLCOAFPFMSFGLSSTLQLLA 125
Db 72 TELVFTDLGLCLISPVLAAYANRSLRVLAAPALDNLCOAFPFMSFGLSSTLQLLA 129
QY 126 MALECWLSLGHPPFYRRHITRLGALVAPVVSASFALFCAFPWGFQKFOYCGTWCFI 185
Db 130 MALERYLSIGHPIYQGRVRSGLAVLPVYAVSLFCSPLLDYQGYOYCGTWCFI 189
QY 186 QMHEESLSVLGVSYSMLLVATVLCNIGAMRNLYAMHRLQHRSCSTRCAE 245
Db 190 R--HGR-----TAYLQYATLTLILVSVLACNFSVLINLRMRSSR--SRCGSLGS 240
QY 246 ----PRADGASQPLEEDLHLLALMTVLFTMCSLPVYRAYGAFKDVKEKNTSE 301
Db 241 GRGGPGARRRGERVSMABETDHLILAMITTFVCSLPFTIFAY-----MNETSS 291
QY 302 EAE--DIRALRFLSVISIVDPWIFIRSPVFRIFPKIFIR-PLRYRSRCSNTNMS 357
Db 292 RKEKMDIQLARFLSINSIIDPWVFAIRPVLRLMRSVLCRISLRQDATQTSCTOS 350

RESULT 8
US-08-461-379A-6
Sequence 6, Application US/08461379A
Patent No. 5871961
GENERAL INFORMATION:
APPLICANT: Smith, Kendall A. & Beadling, Carol
TITLE OF INVENTION: Nucleic Acids Encoding CR5 Polypeptide,
VECTOR OF INVENTION: Vector and Transformed Cell Thereof, and
TITLE OF INVENTION: Expression Thereof
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ratner & Prestia
CITY: Valley Forge
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19482
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,379A
FILING DATE: 5-JUNE-1995
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: USSN 08/330,108; 08/104,736
FILING DATE: 27-OCT-1994; 10-AUG-1993 & 20-NOV-91
ATTORNEY/AGENT INFORMATION:
NAME: Viviana Amzel, Ph. D.
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: DART-070
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610)470-0700
TELEFAX: (610)470-0701
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 358 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-461-379A-6

Query Match 35.8%; Score 667; DB 2; Length 358;
Best Local Similarity 42.9%; Pred. No. 1.8e-54;
Matches 154; Conservative 53; Mismatches 122; Indels 30; Gaps 10;

QY 8 CQNTTSVEKNSAMVGVLPTSTGLGNLALGLIARSGLG--WCSRRPLRLPSPVFMV 65
DB 13 CETRQWPPPESSPAISSVMSAGVLGNLIELALARRWQDVGCSAGRSSL-SLFLV 71
QY 66 CGLTVDLKGKCLSPVLAAYVQNSRLVAPALDNLSCQAFPFMSFGSLSTLQLA 125
DB 72 TELVFTDLSTCLISPVLAAYVQNSRLVAPALDNLSCQAFPFMSFGSLSTLQLA 129
QY 126 MALECWLSLGHPPFYRRHITRLGALVAPVSAFSLAFCAIPMGFGKPYQYCGTWC 185
DB 130 MALERYLSIGHPPFYRRHITRLGALVAPVSAFSLAFCAIPMGFGKPYQYCGTWC 189
QY 186 QMVEHESGLSVLGYVSYSSLMALVLAIVLCNGAMRNLYAMHRLQHRPSTRCDAE 245
DB 190 R--HGR-----TAYLQIYATLLILLIVSLACNFSVLTNLRHRSRR--SRGSP 240
QY 246 ----PRADGEASPPLEEDHLLALMTVLFTMCSLPVIRAYYGAFDVKEKNTSE 301
DB 241 GGGPGARRRGERVSAEEDHLLALMTVLFTMCSLPVIRAYYGAFDVKEKNTSE 301
QY 302 EAE--DLRALFLSVISVDPWFIIFRSVPFRIFFHKIFIR--PLRYRSRCSNTNMS 357
DB 292 RKEKMDLQALRFLSVISVDPWFIIFRSVPFRIFFHKIFIR--PLRYRSRCSNTNMS 357

RESULT 9
US-08-462-390B-6
Sequence 6, Application US/08462390B
Patent No. 5882894
GENERAL INFORMATION:
APPLICANT: Smith, K. A., & Beadling, C.
TITLE OF INVENTION: Nucleic Acids Encoding CR8 Polypeptide, Vector and
TITLE OF INVENTION: Transformed Cell Thereof, and Expression Thereof
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ratner & Prestia
CITY: Valley Forge
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19482
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,390B
FILING DATE: 5-JUNE-1995
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: USSN 08/330,108
FILING DATE: 27-OCT-1994
APPLICATION NUMBER: USSN 08/104,736
FILING DATE: 10-AUG-1993
APPLICATION NUMBER: USSN 07/796,066
FILING DATE: 20-NOV-91
ATTORNEY/AGENT INFORMATION:
NAME: Viviana Amzel, Ph. D.
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: DART-040
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610)407-0700
TELEFAX: (610)407-0701
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 358 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-462-390B-6

Query Match 35.8%; Score 667; DB 2; Length 358;
Best Local Similarity 42.9%; Pred. No. 1.8e-54;
Matches 154; Conservative 53; Mismatches 122; Indels 30; Gaps 10;

QY 8 CQNTTSVEKNSAMVGVLPTSTGLGNLALGLIARSGLG--WCSRRPLRLPSPVFMV 65
DB 13 CETRQWPPPESSPAISSVMSAGVLGNLIELALARRWQDVGCSAGRSSL-SLFLV 71
QY 66 CGLTVDLKGKCLSPVLAAYVQNSRLVAPALDNLSCQAFPFMSFGSLSTLQLA 125
DB 72 TELVFTDLSTCLISPVLAAYVQNSRLVAPALDNLSCQAFPFMSFGSLSTLQLA 129
QY 126 MALECWLSLGHPPFYRRHITRLGALVAPVSAFSLAFCAIPMGFGKPYQYCGTWC 185
DB 130 MALERYLSIGHPPFYRRHITRLGALVAPVSAFSLAFCAIPMGFGKPYQYCGTWC 189
QY 186 QMVEHESGLSVLGYVSYSSLMALVLAIVLCNGAMRNLYAMHRLQHRPSTRCDAE 245
DB 190 R--HGR-----TAYLQIYATLLILLIVSLACNFSVLTNLRHRSRR--SRGSP 240
QY 246 ----PRADGEASPPLEEDHLLALMTVLFTMCSLPVIRAYYGAFDVKEKNTSE 301
DB 241 GGGPGARRRGERVSAEEDHLLALMTVLFTMCSLPVIRAYYGAFDVKEKNTSE 301
QY 302 EAE--DLRALFLSVISVDPWFIIFRSVPFRIFFHKIFIR--PLRYRSRCSNTNMS 357
DB 292 RKEKMDLQALRFLSVISVDPWFIIFRSVPFRIFFHKIFIR--PLRYRSRCSNTNMS 357

Db 292 RKERMDLQALRFLSINSIIDPWVFAILRPVLRILMRSLCCRISLRQTQATQTSCTOS 350

RESULT 10

US-08-463-074B-6
Sequence 6, Application US/08463074B
Patent No. 6020155
GENERAL INFORMATION:
APPLICANT: Smith, Kendall A. & Beadling, Carol
TITLE OF INVENTION: Nucleic Acids Encoding Crl Fusion Protein, Vector and
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: PRETTY, SCHROEDER & POPLAWSKI
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90071
444 South Flower St. - Suite 1900
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,074B
FILING DATE: 5-JUN-1995
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/104,736
FILING DATE: 10-AUG-1993
PRIOR APPLICATION NUMBER:
APPLICATION DATA:
APPLICATION NUMBER: US 07/796,066
FILING DATE: 20-NOV-91
ATTORNEY/AGENT INFORMATION:
NAME: Viviana Amzel, Ph. D.
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: P66 38143 (DART-020)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 622-7700
TELEFAX: (213) 489-4210
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 358 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-463-074B-6

Query Match 35.8%; Score 667; DB 3; Length 358;
Best Local Similarity 42.9%; Pred. No. 1.8e-54;
Matches 154; Conservative 53; Mismatches 122; Indels 30; Gaps 10;

QY 8 CQNTTSVEKNSAVMGVLPSTGLGNLALGLIARSGLG--WCSRRLRLPLDSVFMV 65
DB 13 CTRQWPPPPSPAISSVMSFAGVGLNLIETALARRWQDVCSSAGRSSL-SLFHVLV 71
QY 66 CGLVTDLIGKCLISPVLAAYANRSLRVAPALDNLSCQAFPMSEFGSLSTQLOLA 125
DB 72 TELVFTDLIGTCLISPVLAAYANRSLRVAPALDNLSCQAFPMSEFGSLSTQLOLA 129
QY 126 MALECMWLSLGHPPFYRRHITRLGALVAPVVSASFALFCALPFMGFGKPVQYCGTWC 185
DB 130 MALERYLSIGHPPFYQRRVRSRSGGLAVLPVIVAVSLFCSLPILDYQYQYCGTWC 189
QY 186 QMHEBSLSVLGVSIVSYSLMALVLAIVLCNIGAMRNLYAMHRLQHRPSTRCAC 245
DB 190 R--HGR-----TAYLQIYATLILLIIVSVLACNFSVLNIRHRRSR--SRGSPSIG 240
QY 246 ----PRADGRASQPLLEEDHLLALLMTVLFTMCSLPVIRAYYGAFAVDKXKNTSE 301
DB 241 GRGPGARRRGERVSMABETDHLILALMTITPAVCSLPPTIFAY-----METSS 291
QY 302 EAE--DRAALRFLSVISIVDPWIFIRSPSPVIRIFHKKIFIR-DIARYSRCSNSTNMS 357

Db 292 RKERMDLQALRFLSINSIIDPWVFAILRPVLRILMRSLCCRISLRQTQATQTSCTOS 350

RESULT 11

US-08-465-585C-6
Sequence 6, Application US/08465585C
Patent No. 6027914
GENERAL INFORMATION:
APPLICANT: Smith, K. A., & Beadling, C.
TITLE OF INVENTION: Nucleic Acids Encoding CR6 Polypeptide, Vector
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: PRETTY, SCHROEDER & POPLAWSKI
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 900071
444South Flower St. - Suite 1900
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,585C
FILING DATE: 5-JUNE-1995
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: USN 08/330,108
FILING DATE: 27-OCT-1994
APPLICATION NUMBER: USN 08/104,736
FILING DATE: 10-AUG-1993
APPLICATION NUMBER: USN 07/796,066
FILING DATE: 20-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: Viviana Amzel, Ph. D.
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: P66 38149 (DART-050)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 622-7700
TELEFAX: (213) 4894210
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 358 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-465-585C-6

Query Match 35.8%; Score 667; DB 3; Length 358;
Best Local Similarity 42.9%; Pred. No. 1.8e-54;
Matches 154; Conservative 53; Mismatches 122; Indels 30; Gaps 10;

QY 8 CQNTTSVEKNSAVMGVLPSTGLGNLALGLIARSGLG--WCSRRLRLPLDSVFMV 65
DB 13 CTRQWPPPPSPAISSVMSFAGVGLNLIETALARRWQDVCSSAGRSSL-SLFHVLV 71
QY 66 CGLVTDLIGKCLISPVLAAYANRSLRVAPALDNLSCQAFPMSEFGSLSTQLOLA 125
DB 72 TELVFTDLIGTCLISPVLAAYANRSLRVAPALDNLSCQAFPMSEFGSLSTQLOLA 129
QY 126 MALECMWLSLGHPPFYRRHITRLGALVAPVVSASFALFCALPFMGFGKPVQYCGTWC 185
DB 130 MALERYLSIGHPPFYQRRVRSRSGGLAVLPVIVAVSLFCSLPILDYQYQYCGTWC 189
QY 186 QMHEBSLSVLGVSIVSYSLMALVLAIVLCNIGAMRNLYAMHRLQHRPSTRCAC 245
DB 190 R--HGR-----TAYLQIYATLILLIIVSVLACNFSVLNIRHRRSR--SRGSPSIG 240
QY 246 ----PRADGRASQPLLEEDHLLALLMTVLFTMCSLPVIRAYYGAFAVDKXKNTSE 301
DB 241 GRGPGARRRGERVSMABETDHLILALMTITPAVCSLPPTIFAY-----METSS 291

QY 302 EAE--DURALFSLVSIIVPMIFIRSPVFRIFPKIFIR-PLRYRSCSNSTNMES 357
Db 292 RKEMDQLALRFLSINSLIDPMWFAILRPVLRMLRSVLCRISLRTQDATQTSCTOS 350

RESULT 12

US-08-652-446-6
Sequence 6, Application US/08652446
Patent No. 6057427
GENERAL INFORMATION:
APPLICANT: Smith, Kendall A. & Beadling, Carol
TITLE OF INVENTION: Nucleic Acids Encoding CRS
TITLE OF INVENTION: Polypeptide, Vector and Transformed Cell Thereof, and
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: PRETTY, SCHROEDER & POPLAWSKI
ADDRESS: (B) STREET:
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90071
444 South Flower St. - Suite 1900
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,446
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP App. # 96921319.8
FILING DATE: 5-JAN-1998
APPLICATION NUMBER: PCT/US/96/09194
FILING DATE: 5-JUN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/330,108
FILING DATE: 27-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/463,074
FILING DATE: 5-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/462,337
FILING DATE: 5-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/462,390
FILING DATE: 5-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/465,585
FILING DATE: 5-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/463,081
FILING DATE: 5-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/461,379
FILING DATE: 5-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/739,523
FILING DATE: 29-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: VIVIANA AMZEL, PH. D.
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: FP66 40035
TELEPHONE: (213) 622-7700
TELEFAX: (213) 489-4210
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 358 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: protein
US-08-652-446-6

Query Match 35.8%; Score 667; DB 3; Length 358;
Best Local Similarity 42.9%; Pred. No. 1,8e-54;
Matches 154; Conservative 53; Mismatches 122; Indels 30; Gaps 10;

QY 8 CONTTSVEKGNASAVMGVFLSTGLGNLALGLARSGLG--WCSRRPLRLPSVFMVLY 65
Db 13 CETRQWFPPEBPSPAISSVMFSAGVLTGLILALLARRWQDVGCASARRSSL-SLFVLY 71
QY 66 CGLTVTDLGGKCLSPVLAAYQNSRLVLPALDNLCOAFAPFMSFFGLSTQLLA 125
Db 72 TELVFTDLGTCLISPVLAAYANGLVALAP--ESRASTYAFAMTFSLATMLLFT 129
QY 126 MALECWLSLGHPPFYRRHITLRIGALVAPVVSASFALCPMFGPKFYQYCGTWCFI 185
Db 130 MALERYLSIGHPPFYRRVRSGLAVLPVYAVSLFCSLPILDVQYQYQYCGTWCFI 189
QY 186 QMHEEGSLSLGVSYSLSMALVLAIVLCNIGAMRNLYAMHRLQRPSCTRDCAE 245
Db 190 R--HGR-----TAYLQIYATLLILLIVSLACNFSVLTNLRHRRRR--SRGSPSLG 240
QY 246 ----PRADGEASPPLELDHLLLLMTVLFMCSLPVIYRAYGAFDVAEKNTSE 301
Db 241 GGGPGARRRGERVSMAEETDHLILLAIMTITFVCSLPFTIRAY-----MNETSS 291
QY 302 EAE--DURALFSLVSIIVPMIFIRSPVFRIFPKIFIR-PLRYRSCSNSTNMES 357
Db 292 RKEMDQLALRFLSINSLIDPMWFAILRPVLRMLRSVLCRISLRTQDATQTSCTOS 350

RESULT 13

US-08-134-012-3
Sequence 3, Application US/08134012
Patent No. 5516652
GENERAL INFORMATION:
APPLICANT: Abramovitz, Mark
APPLICANT: Boie, Yves
APPLICANT: Grygorczyk, Richard
APPLICANT: Metters, Kathleen
APPLICANT: Rushmore, Thomas H.
APPLICANT: Slipeitz, Deborah M.
TITLE OF INVENTION: DNA ENCODING PROSTAGLANDIN RECEPTOR IP
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: John Wallen
STREET: 126 E. Lincoln Avenue
CITY: Rahway
STATE: New Jersey
COUNTRY: USA
ZIP: 07065
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/134,012
FILING DATE: 06-OCT-1993
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Wallen, John W
REGISTRATION NUMBER: 35,403
REFERENCE/DOCKET NUMBER: 19098
TELEPHONE: (908) 594-3905
TELEFAX: (908) 594-3905
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 386 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

LENGTH: 386 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-09-039-798-3

Query Match 32.0%; Score 597; DB 3; Length 386;
 Best local Similarity 42.3%; Pred. No. 7,2e-48;
 Matches 141; Conservative 46; Mismatches 102; Indels 44; Gaps 9;

QY	8	CONTTSYEKNSAVMGVLFSTGLGNLALGLIARSGLGWCSRRPLPLPSVFYMLVCG	67
DB	5	CRNLTYYRGSVGPATSTLMFVAGVGNGLALGILS-----ARRPAR--PSAPAVLVTG	55
QY	68	LVTYDILGKCLLSFVLAAYANRSLAVLA---PALDNLCOAFAPFMSFPGLSSTIQLL	124
DB	56	LAATDILGTSFLSPAVFVAAYARNSSLGLARGPA---LCDAPAFAMTFEGLASMLILF	111
QY	125	AMALECWLISGHPFYYRHITLRLGALVAPVSAFSLAFCALPFMGFGKFVQYCPGTWCF	184
DB	112	AMAVERTLASHPIYLAQDGPRCARLALPAIYAFCVLPCLPLIGLGHQYCPGSMCF	171
QY	185	IQN--VHEEGSLSVLGYSLYSIMALLVATVLCNLGAMENLYAMHRLQRHPRSCTRD	242
DB	172	LRRWMAQPGGA---AFSLAYAGLVALLVAIFLCNGSVTLSLCRMVROQKRHGS----	223
QY	243	CAEPRADGRASPOPL---EELDHLLALMTVLFTWCSPVIYRAYYGAFKDYKEKRT	299
DB	224	-----LQPRPRGTGEVDHLILLALMTVMVAVCSLPLTIRCTQAVAP-----DS	268
QY	300	SEEAEDLRALRPLSVISIVDPWIFLIRSPVER	332
DB	269	SSEMGDLARFYAFNPILDPWVILPRKAVFQ	301

Search completed: April 22, 2005, 21:30:47
 Job time: 21.3756 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 22, 2005, 17:53:08 ; Search time 65.771 Seconds
(without alignments)
2111.067 Million cell updates/sec

Title: US-10-689-861-4

Perfect score: 1864

Sequence: 1 MKSPFVRCNTTSVEKNGSA.....IRPLVRSRCSNTNMESSL 359

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: Geneseqp1980s:*
- 2: Geneseqp1990s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003as:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1864	100.0	359	2	AAW03516 Prostagla
2	1864	100.0	359	4	AAW79009 Human pro
3	1864	100.0	359	6	ABP81901 Human pro
4	1864	100.0	359	7	ADD48182 Human pro
5	1864	100.0	359	8	ADO29614 Human GPC
6	1864	100.0	359	4	ABB12000 Human pro
7	1864	100.0	359	4	AAW79993 Human pro
8	1864	100.0	359	7	ADE09040 Novel pro
9	1757.5	94.3	424	7	ADE07993 Novel pro
10	1580	84.8	369	3	AAV94346 Human cel
11	1386.5	74.4	357	7	ADD48180 Rat Prote
12	1347.5	72.3	357	8	ADO29615 Mouse GPC
13	1346.5	72.2	357	2	AAW84708 Prostagla
14	752	40.3	144	8	ADP55149 Human PRO
15	707.5	38.0	362	8	ADO29619 Mouse GPC
16	689	37.0	358	6	ABP81903 Human pro
17	689	37.0	358	7	ADE40457 Human pro
18	689	37.0	358	7	ADK32578 Hematolog
19	689	37.0	358	8	ADO29618 Human GPC
20	689	37.0	358	8	ADRI4091 Human NF-
21	689	37.0	358	8	ADR43385 Prostagla
22	689	37.0	609	2	AAV41279 Fusion pr
23	688	36.9	358	2	AAW44246 Human HP4
24	688	36.9	358	5	ABG30499 Human HP4
25	688	36.9	358	8	ADO05738 Human pro

26	683	36.6	358	4	ABB56383	Abb56383 Non-endog
27	667	35.8	358	2	AAW08135	Aaw08135 Human cyt
28	667	35.8	358	3	AAW87954	Aay87954 Human CR3
29	597	32.0	386	2	AAW81979	Aar81979 Human pro
30	597	32.0	386	2	AAW81980	Aar81980 Human pro
31	597	32.0	386	6	ABP81900	Abp81900 Human pro
32	597	32.0	386	7	ADP03580	Adp03580 Human GPC
33	597	32.0	386	8	ADO29626	Ado29626 Human GPC
34	597	32.0	386	8	ADO29627	Ado29627 Mouse GPC
35	596.5	32.0	415	8	ADO29627	Ado29627 T cell ac
36	592	31.8	386	2	AAW74915	Aar74915 Prostagla
37	585.5	31.4	416	2	AAW81981	Aar81981 Rat proest
38	519.5	27.9	256	8	ADQ95984	Adq95984 T cell ac
39	518.5	27.8	284	8	ADQ95982	Adq95982 T cell ac
40	518.5	27.8	289	7	ADM05222	Adm05222 Human pro
41	516	27.7	253	8	ADP29755	Adp29755 Human sec
42	458.5	24.6	513	2	AAW42282	Aar42282 PGE2 rece
43	458.5	24.6	513	8	ADO29623	Ado29623 Mouse GPC
44	443	23.8	480	8	ADR46683	Adr46683 Cancer-as
45	443	23.8	488	2	AAW02271	Aaw02271 Human pro

ALIGNMENTS

RESULT 1

AAW03516

ID AAW03516 standard; protein; 359 AA.

XX AC AAW03516;

XX DT 11-MAR-1997 (first entry)

XX DE Prostaglandin DP receptor.

XX KW Prostaglandin DP receptor; human; prostanoid receptor; blood platelet;

XX KW smooth muscle; nervous tissue; G protein-coupled receptor; modulator;

XX KW mouse; prostaglandin-related disease; therapy.

XX OS Homo sapiens.

XX PN WO9623066-A2.

XX PD 01-AUG-1996.

XX PF 23-JAN-1996; 96WO-CA000047.

XX PR 26-JAN-1995; 95US-00378682.

XX PA (MERI) MERCK FROSST CANADA INC.

XX PI Abramovitz M, Boie Y, Metters K, Sawyer N, Slipetz DM;

XX DR WPI; 1996-362690/36.

XX DR N-PSDB; AAT37402.

XX PT Human prostaglandin DP receptor and related DNA - used to identify

XX PS receptor modulators to treat prostaglandin-related diseases.

XX PS Claim 2; Page 41; 49pp; English.

XX CC This sequence represents the human prostaglandin DP receptor. The DP receptor is the least ubiquitous and least abundant of the prostanoid receptors. The DP receptors are thought to be distributed mainly in blood platelets, smooth muscle of various tissues, and nervous tissue (including the central nervous system). However, many of the actions and distribution of the DP receptor is species dependent. This receptor is a G protein-coupled receptor which can specifically bind prostaglandin molecules. The DNA encoding this sequence was isolated using primers (see AAT37403 and AAT37404) based on the N-terminal sequence, and an internal sequence from purified mouse DP. The human prostaglandin DP receptor can be used to identify modulators of the receptor. The identified modulators can then be used to treat prostaglandin-related diseases, and for

CC modulating the effects of prostaglandins on the DP receptor
XX Sequence 359 AA;
SQ

Query Match 100.0%; Score 1864; DB 2; Length 359;
Best Local Similarity 100.0%; Pred. No. 8.1e-187;
Matches 359; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKSPFYRCQNTTSVEKGN SAVMGVLFSTGLGNLLALGLLARSGLGWCRRRLPLPSV 60
DB 1 MKSPFYRCQNTTSVEKGN SAVMGVLFSTGLGNLLALGLLARSGLGWCRRRLPLPSV 60
QY 61 FYMLVCGLTVDLLGKCLLSPVLAAYQNRSLRVLPALDNLSCQAFAPFMSFFGLSST 120
DB 61 FYMLVCGLTVDLLGKCLLSPVLAAYQNRSLRVLPALDNLSCQAFAPFMSFFGLSST 120
QY 121 LQLLMALECWLSLGHFFFYRRHITLRIGALVAPVVSFAFLAFALPFGMGFGKVFQYCPG 180
DB 121 LQLLMALECWLSLGHFFFYRRHITLRIGALVAPVVSFAFLAFALPFGMGFGKVFQYCPG 180
QY 181 TWCFIQWVHEGSLVGLGYSLVSSLMALLVLTATVLCNLAGMRNLYAMHRRLOHPRSC 240
DB 181 TWCFIQWVHEGSLVGLGYSLVSSLMALLVLTATVLCNLAGMRNLYAMHRRLOHPRSC 240
QY 241 RDCAEPADGREGASPOPLELDHLLALMTVLFTWCSLPVIYRAYYGAFKDVKEKNRTS 300
DB 241 RDCAEPADGREGASPOPLELDHLLALMTVLFTWCSLPVIYRAYYGAFKDVKEKNRTS 300
QY 301 EEAEEDLRALRFLSVISIVDPWIFIRFSPVFRIFHKKIFIRPLRYRSCSNSTNMESSL 359
DB 301 EEAEEDLRALRFLSVISIVDPWIFIRFSPVFRIFHKKIFIRPLRYRSCSNSTNMESSL 359

RESULT 2
AA79009
ID AA79009 standard; protein; 359 AA.
XX
AC AA79009;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human protein SEQ ID NO 1671.
XX
KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorder; arthritis; inflammation.
XX
OS Homo sapiens.
XX
PN WO200157190-A2.
XX
PD 09-AUG-2001.
XX
PF 05-FEB-2001; 2001WO-US004098.
XX
PR 03-FEB-2000; 2000US-00496914.
PR 27-APR-2000; 2000US-00560875.
PR 20-JUN-2000; 2000US-00598075.
PR 19-JUL-2000; 2000US-00620325.
PR 01-SEP-2000; 2000US-00654936.
PR 15-SEP-2000; 2000US-00663561.
PR 20-OCT-2000; 2000US-00693325.
PR 30-NOV-2000; 2000US-00728422.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y;
PI Ma Y, Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;
XX
DR WPI; 2001-476283/51.
XX
DR N-PSDB; AAK52142.

XX Nucleic acids encoding polypeptides with cytokine-like activities, useful
PT in diagnosis and gene therapy.
XX
XX Claim 20; Page 4016-4017; 6221pp; English.
XX
XX The invention relates to polynucleotides (AAK51456-AAK53435) and the
CC encoded polypeptides (AAW78323-AAW80302) that exhibit activity relating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111
CC (AAK52582) and 3666 (AAW80020) are omitted as the relevant pages from the
CC sequence listing were missing at the time of publication
XX
SQ Sequence 359 AA;
Query Match 100.0%; Score 1864; DB 4; Length 359;
Best Local Similarity 100.0%; Pred. No. 8.1e-187;
Matches 359; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKSPFYRCQNTTSVEKGN SAVMGVLFSTGLGNLLALGLLARSGLGWCRRRLPLPSV 60
DB 1 MKSPFYRCQNTTSVEKGN SAVMGVLFSTGLGNLLALGLLARSGLGWCRRRLPLPSV 60
QY 61 FYMLVCGLTVDLLGKCLLSPVLAAYQNRSLRVLPALDNLSCQAFAPFMSFFGLSST 120
DB 61 FYMLVCGLTVDLLGKCLLSPVLAAYQNRSLRVLPALDNLSCQAFAPFMSFFGLSST 120
QY 121 LQLLMALECWLSLGHFFFYRRHITLRIGALVAPVVSFAFLAFALPFGMGFGKVFQYCPG 180
DB 121 LQLLMALECWLSLGHFFFYRRHITLRIGALVAPVVSFAFLAFALPFGMGFGKVFQYCPG 180
QY 181 TWCFIQWVHEGSLVGLGYSLVSSLMALLVLTATVLCNLAGMRNLYAMHRRLOHPRSC 240
DB 181 TWCFIQWVHEGSLVGLGYSLVSSLMALLVLTATVLCNLAGMRNLYAMHRRLOHPRSC 240
QY 241 RDCAEPADGREGASPOPLELDHLLALMTVLFTWCSLPVIYRAYYGAFKDVKEKNRTS 300
DB 241 RDCAEPADGREGASPOPLELDHLLALMTVLFTWCSLPVIYRAYYGAFKDVKEKNRTS 300
QY 301 EEAEEDLRALRFLSVISIVDPWIFIRFSPVFRIFHKKIFIRPLRYRSCSNSTNMESSL 359
DB 301 EEAEEDLRALRFLSVISIVDPWIFIRFSPVFRIFHKKIFIRPLRYRSCSNSTNMESSL 359

RESULT 3
ABP81901
ID ABP81901 standard; protein; 359 AA.
XX
AC ABP81901;
XX
DT 04-MAR-2003 (first entry)
XX
DE Human prostaglandin D2 receptor protein SEQ ID NO:287.
XX
KW G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
KW G protein-coupled receptor modulator; antibody; immune-related disease;
KW growth-related disease; cell regeneration-related disease; AIDS; cancer;
KW immunological-related cell proliferative disease; autoimmune disease;
KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;
KW osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;
KW graft versus host disease; Parkinson's disease; multiple sclerosis; pain;
KW psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
KW hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
XX

OS Homo sapiens.
 XX W0200261087-A2.
 XX 08-AUG-2002.
 XX 19-DEC-2001; 2001WO-US050107.
 XX 19-DEC-2000; 2000US-0257144P.
 XX (LIFE-) LIFESPAN BIOSCIENCES INC.
 XX Burmer GC, Roush CL, Brown JP;
 XX WPI; 2003-046718/04.
 XX N-PSDB; ABZ42748.
 XX New isolated antigenic peptides e.g., for G protein-coupled receptors
 PT (GPCR), useful for diagnosing and designing drugs for treating conditions
 PT in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or
 PT autoimmune diseases.
 XX Disclosure; Fig 1; 523pp; English.
 XX The present invention describes antigenic peptides (I) comprising: (a)
 CC any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino
 CC acids. Also described: (1) an assay for the detection of a particular G
 CC protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;
 CC and (2) an isolated antibody having high specificity and high affinity or
 CC avidity for a particular GPCR. (I) can be used as GPCR modulators and in
 CC gene therapy. The antigenic peptides for GPCRs are useful in detecting an
 CC antibody against a particular GPCR, and in the production of specific
 CC antibodies. The peptides and antibodies are also useful for detecting the
 CC presence or absence of corresponding GPCRs. The antigenic peptides for
 CC GPCRs and antibodies are useful for diagnosing and designing drugs for
 CC treating immune-related diseases, growth-related diseases, cell
 CC regeneration-related disease, immunological-related cell proliferative
 CC diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,
 CC atherosclerosis, bacterial, fungal, protozoan or viral infections,
 CC osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute
 CC inflammation, allergies, Crohn's disease, diabetes, graft versus host
 CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis, memory
 CC anxiety, depression, schizophrenia, dementia, mental retardation, memory
 CC loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,
 CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or
 CC any other disorder in which GPCRs are involved. The antibodies may be
 CC used in immunoassays and immunodiagnosis. ABZ42523 to ABZ42869 encode
 CC GPCR proteins given in ABP81675 to ABP82018, which are used in the
 CC exemplification of the present invention
 XX Sequence 359 AA;
 XX Query Match 100.0%; Score 1864; DB 6; Length 359;
 XX Best Local Similarity 100.0%; Pred No. 8.1e-187;
 XX Matches 359; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MKSPFYRCQNTTSVEKGNAGVGGVLFSTGLLGNLLALGLLARSGLGWCRRRLPLPSV 60
 DB 1 MKSPFYRCQNTTSVEKGNAGVGGVLFSTGLLGNLLALGLLARSGLGWCRRRLPLPSV 60
 QY 61 FYMLVGLTVDLLGKLLSPVLAAYQNRSLRVLPALDNLSCQAPAFMSFGLSST 120
 DB 61 FYMLVGLTVDLLGKLLSPVLAAYQNRSLRVLPALDNLSCQAPAFMSFGLSST 120
 QY 121 LQLLMALECNLSLGHFFVRRHITLRLGALVAPVVSFAFLAFCLPFMGFGKFCVYCPG 180
 DB 121 LQLLMALECNLSLGHFFVRRHITLRLGALVAPVVSFAFLAFCLPFMGFGKFCVYCPG 180
 QY 181 TWCFIQMVHEEGSLVGLSVLYSSLMALLVTLVLCNLGAMENLYAMHRRRLQHRPSRCT 240
 DB 181 TWCFIQMVHEEGSLVGLSVLYSSLMALLVTLVLCNLGAMENLYAMHRRRLQHRPSRCT 240
 QY 241 RDCAEPADGASPOLELDHLLALLMTVLFTWCSSLFVIYRAYYGAFKVDKVKRNTS 300

Db 241 RDCAEPADGASPOLELDHLLALLMTVLFTWCSSLFVIYRAYYGAFKVDKVKRNTS 300
 QY 301 EEAEEDLRALRFLSVISIVDPWFIIFRSPVFRIFFFHKIFIRPLRYRSCNSTNWESSL 359
 Db 301 EEAEEDLRALRFLSVISIVDPWFIIFRSPVFRIFFFHKIFIRPLRYRSCNSTNWESSL 359
 RESULT 4
 ADD48182
 ID ADD48182 standard; protein; 359 AA.
 XX AC ADD48182;
 XX 02-DEC-2004 (revised)
 DT 29-JAN-2004 (first entry)
 XX Human Protein Q13258, SEQ ID NO 13980.
 XX Human; pain; neuronal tissue; gene therapy;
 KW spinal segmental nerve injury; chronic constriction injury; CCI;
 KW spared nerve injury; SNI; Chung.
 XX Homo sapiens.
 OS Unidentified.
 XX WO2003016475-A2.
 XX 27-FEB-2003.
 XX 14-AUG-2002; 2002WO-US025765.
 XX 14-AUG-2001; 2001US-0312147P.
 PR 01-NOV-2001; 2001US-0346382P.
 PR 26-NOV-2001; 2001US-0333347P.
 XX (GEHO) GEN HOSPITAL CORP.
 PA (FARB) BAYER AG.
 XX Woolf C, D'urso D, Befort K, Costigan M;
 WPI; 2003-268312/26.
 DR GENBANK; Q13258.
 XX New composition comprising two or more isolated polypeptides, useful for
 PT preparing a medicament for treating pain in an animal.
 XX Example 1; Page; 1017pp; English.
 CC The invention discloses a composition comprising two or more isolated rat
 CC or human polynucleotides or a polynucleotide which represents a fragment,
 CC derivative or allelic variation of the nucleic acid sequence. Also
 CC claimed are a vector comprising the novel polynucleotide, a host cell
 CC comprising the vector, a method for identifying a nucleotide sequence
 CC which is differentially regulated in an animal subjected to pain and a
 CC kit to perform the method, an array, a method for identifying an agent
 CC that increases or decreases the expression of the polynucleotide sequence
 CC that is differentially expressed in neuronal tissue of a first animal
 CC subjected to pain, a method for identifying a compound which regulates
 CC the expression of a polynucleotide sequence which is differentially
 CC expressed in an animal subjected to pain, a method for identifying a
 CC compound that regulates the activity of one or more of the
 CC polynucleotides, a method for producing a pharmaceutical composition, a
 CC method for identifying a compound or small molecule that regulates the
 CC activity in an animal of one or more of the polypeptides given in the
 CC specification, a method for identifying a compound useful in treating
 CC pain and a pharmaceutical composition comprising the one or more
 CC polypeptides or their antibodies. The polynucleotide or the compound that
 CC modulates its activity is useful for preparing a medicament for treating
 CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
 CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
 CC therapy). The sequence presented is a human protein (described in Table 3
 CC of the specification) which is differentially expressed during pain.

CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.

```
XX SQ Sequence 359 AA;
Query Match 100.0%; Score 1864; DB 7; Length 359;
Best Local Similarity 100.0%; Pred. No. 8.1e-187;
Matches 359; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKSPFYRCQNTTSVEKNSAVMGVLFSTGLGNLLALGALLARSGLWCRRRLPLPSV 60
DB 1 MKSPFYRCQNTTSVEKNSAVMGVLFSTGLGNLLALGALLARSGLWCRRRLPLPSV 60

QY 61 FYMLVGLTVTDLGKLLSPVLAAYQNRSLRVLPALDNLSCQAFPMFFGLSST 120
DB 61 FYMLVGLTVTDLGKLLSPVLAAYQNRSLRVLPALDNLSCQAFPMFFGLSST 120

QY 121 LQLLMALECWLSLGHPPFFYRRHITLRLGALVAPVVSFAFLAFPMFGFKFVQYCPG 180
DB 121 LQLLMALECWLSLGHPPFFYRRHITLRLGALVAPVVSFAFLAFPMFGFKFVQYCPG 180

QY 181 TWCFIQWVHEGSLVGLSVLYSSLMALLVTLVLCNIGAMNLYAMHRRRLQHRPSCT 240
DB 181 TWCFIQWVHEGSLVGLSVLYSSLMALLVTLVLCNIGAMNLYAMHRRRLQHRPSCT 240

QY 241 RDCAEPRADGRASPOPLELDHLLALMTVLFTWCSPVIYRAYYGAFAKDKVKNRTS 300
DB 241 RDCAEPRADGRASPOPLELDHLLALMTVLFTWCSPVIYRAYYGAFAKDKVKNRTS 300

QY 301 EEAEEDRALRFLSVISIVDPWIFIIFRSPVFRIFFFHKIFIRPLRYRSRCSNSTNMESSL 359
DB 301 EEAEEDRALRFLSVISIVDPWIFIIFRSPVFRIFFFHKIFIRPLRYRSRCSNSTNMESSL 359

RESULT 5
AD029614
ID AD029614 standard; protein; 359 AA.
XX AC AD029614;
XX DT 29-JUL-2004 (first entry)
XX DE Human GPCR PTGDR, SEQ ID NO:716.
XX

KW G protein-coupled receptor; GPCR; drug screening; diagnosis;
KW transgenic mouse; neurological disorder; adrenal gland disorder;
KW colon disorder; intestinal disorder; cardiovascular disorder;
KW muscular disorder; blood disorder; immune disorder; bone disorder;
KW joint disorder; metabolic disorder; nutritive disorder; cancer;
KW kidney disorder; liver disorder; lung disorder; breast disorder;
KW ovary disorder; uterus disorder; prostate disorder; testis disorder;
KW skin disorder; stomach disorder; pancreas disorder; spleen disorder;
KW thymus disorder; thyroid disorder; antiparkinsonian; antinemic;
KW cytostatic; antiinflammatory; vasotropic; antidiabetic;
KW CNS; central nervous system; respiratory; antidiarrhoeic; antidiabetic;
KW virucide; hepatotropic; antibacterial; antianaemic; antiseborrhoeic;
KW dermatological; antiulcer; antichryoid; antiallergic; anorectic;
KW immunosuppressive; nephrotropic; gene therapy; GPCR modulator; human;
KW receptor.
XX OS Homo sapiens.
XX PN WO2004040000-A2.
XX PD 13-MAY-2004.
XX PF 09-SEP-2003; 2003WO-US028226.
XX PR 09-SEP-2002; 2002US-0409303P.
XX PR 09-APR-2003; 2003US-0461329P.
XX PA (PRIM-) PRIMAL INC.
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XX PI Gaitanaris GA, Bergmann JE, Gragerov A, Hohmann J, Li F;
PI Madisen L, Meilwain KL, Pavlova MN, Vassiliadis D, Zeng H;
XX WPI; 2004-390329/36.
DR N-PSDB; ADO30026.
XX Novel mammalian G protein coupled receptors, useful for identifying
PT compounds that modulates diagnosing and treating disease condition
PT associated with GPCR dysfunction e.g. autoimmune diseases, angina
PT pectoris, Parkinson's disease.
XX Claim 151; SEQ ID NO 716; 542pp: English.
XX The invention relates to human and mouse G protein-coupled receptors
CC (GPCRs) and nucleic acids encoding them. The invention also relates to
CC sequences at least 90% identical to the GPCR proteins and nucleic acids
CC of the invention; methods of treating, preventing or diagnosing diseases
CC associated with GPCRs of the invention; methods of screening for
CC compounds useful in the treatment of GPCR-related diseases; a transgenic
CC mouse comprising a GPCR gene of the invention; a mouse comprising a
CC mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived
CC from the transgenic mice; kits comprising several mice, each of which has
CC a mutation in a different GPCR gene of the invention; and kits comprising
CC probes which hybridise to GPCR polynucleotides of the invention. The
CC invention further discloses variants of the GPCR polypeptides and vectors
CC comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may
CC be used in the diagnosis, treatment or prevention of a wide variety of
CC diseases including neurological disorders (e.g., Alzheimer's disease,
CC depression, diabetic neuropathy, Parkinson's disease or schizophrenia);
CC disorders of the adrenal gland; disorders of the colon or intestine
CC (e.g., Crohn's disease, diarrhoea, food poisoning or irritable bowel
CC syndrome); cardiovascular disorders (e.g., angina, cardiac arrhythmia or
CC myocardial infarction); muscular disorders; blood disorders (e.g.,
CC anaemia or leukaemia); immune disorders (e.g., autoimmune disorders or
CC AIDS); bone and joint disorders (e.g., osteoarthritis, rheumatoid
CC arthritis, gout or osteoporosis); metabolic or nutritive disorders (e.g.,
CC obesity, enzyme deficiency-related diseases or vitamin deficiency-related
CC diseases); and disorders of the kidney, liver, lung, breast, ovary,
CC uterus, prostate, testis, skin, stomach, pancreas, spleen, thymus and
CC thyroid (e.g., cancers). The present sequence represents a GPCR of the
CC invention. Note: The full sequence data for this patent did not form part
CC of the printed specification; those sequences not shown were obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX SQ Sequence 359 AA;
Query Match 100.0%; Score 1364; DB 8; Length 359;
Best Local Similarity 100.0%; Pred. No. 8.1e-187;
Matches 359; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKSPFYRCQNTTSVEKNSAVMGVLFSTGLGNLLALGALLARSGLWCRRRLPLPSV 60
DB 1 MKSPFYRCQNTTSVEKNSAVMGVLFSTGLGNLLALGALLARSGLWCRRRLPLPSV 60

QY 61 FYMLVGLTVTDLGKLLSPVLAAYQNRSLRVLPALDNLSCQAFPMFFGLSST 120
DB 61 FYMLVGLTVTDLGKLLSPVLAAYQNRSLRVLPALDNLSCQAFPMFFGLSST 120

QY 121 LQLLMALECWLSLGHPPFFYRRHITLRLGALVAPVVSFAFLAFPMFGFKFVQYCPG 180
DB 121 LQLLMALECWLSLGHPPFFYRRHITLRLGALVAPVVSFAFLAFPMFGFKFVQYCPG 180

QY 181 TWCFIQWVHEGSLVGLSVLYSSLMALLVTLVLCNIGAMNLYAMHRRRLQHRPSCT 240
DB 181 TWCFIQWVHEGSLVGLSVLYSSLMALLVTLVLCNIGAMNLYAMHRRRLQHRPSCT 240

QY 241 RDCAEPRADGRASPOPLELDHLLALMTVLFTWCSPVIYRAYYGAFAKDKVKNRTS 300
DB 241 RDCAEPRADGRASPOPLELDHLLALMTVLFTWCSPVIYRAYYGAFAKDKVKNRTS 300

QY 301 EEAEEDRALRFLSVISIVDPWIFIIFRSPVFRIFFFHKIFIRPLRYRSRCSNSTNMESSL 359
```

||||| 301 EEADLRALRFLSVISIVDPWIFIRFSPVRIFFHKIFIRPLRYRSCSNSTNMESSL 359

RESULT 6

ABB12000

ID ABB12000 standard; peptide; 399 AA.

AC ABB12000;

XX

DT 11-JAN-2002 (first entry)

XX

DE Human prostaglandin DP receptor homologue, SEQ ID NO:2370.

XX

Human; cytokine; cell proliferation; cell differentiation; growth factor;

KW haematopoiesis regulation; tissue growth; immunomodulator; activin;

KW inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis;

KW proliferation; metastasis; cancer; tumour; haematopoietic disorder;

KW myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;

KW chronic inflammatory condition; proliferative retinopathy;

KW atherosclerosis; coronary heart disease; arterial ischaemia;

KW bone disorder; osteoporosis; vascular growth disorder;

KW tissue regeneration; wound healing; infection; immune disorder;

KW cell culture; drug screening; gene therapy; anti-inflammatory;

KW antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic;

KW cytostatic; osteopathic; vasotropic; cardiant; virucide; antibacterial;

KW antifungal; vulnery; antiulcer.

XX

OS Homo sapiens.

XX

PN W0200157188-A2.

XX

09-AUG-2001.

XX

05-FEB-2001; 2001WO-US003800.

XX

03-FEB-2000; 2000US-00496914.

PR

27-APR-2000; 2000US-00560875.

XX

(HYSE-) HYSEQ INC.

XX

PA Tang YT, Liu C, Drmanac RT;

PI

XX

WPI; 2001-457740/49.

DR

N-PSDB; ABA09244.

XX

Human proteins and DNA encoding sequences useful for preventing, treating

PT or ameliorating a medical condition in a mammalian subject e.g. arthritis

PT and cancer.

XX

Claim 20; Page 294; 1963pp; English.

PS

XX

Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and

CC sequences ABA08225-ABA09574 represent nucleic acids encoding them. The

CC invention also relates to vectors and recombinant host cells comprising a

CC nucleotide of the invention, methods of producing the novel polypeptides,

CC antibodies against the polypeptides, methods of detecting the nucleotides

CC or polypeptides in a sample, and methods of identifying compounds which

CC bind to polypeptides of the invention. Although novel, many of the

CC polypeptides of the invention have homology to known proteins, thereby

CC giving an insight into their probable biological activities, and hence

CC potential therapeutic applications. The polypeptides of the invention may

CC have various activities, including cytokine, cell proliferation or cell

CC differentiation activities; stem cell growth factor activity;

CC haematopoiesis regulatory activity; tissue growth activity;

CC immunomodulatory activity; activin- or inhibin-related activities;

CC chemotactic or chemokinetic activities; haemostatic, thrombotic or

CC thrombolytic activities; receptor or ligand activities; or may be

CC involved in oncogenesis, cancer cell proliferation or metastasis.

CC Depending on their biological activities, polypeptides and nucleotides of

CC the invention are useful for preventing, treating or ameliorating medical

CC conditions, e.g., by protein or gene therapy. Such conditions include

CC cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell

CC disorders), chronic inflammatory conditions (e.g., asthma or arthritis),

CC proliferative retinopathy, atherosclerosis, coronary heart disease,

CC arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal

CC vascular growth. Polypeptides involved with tissue regeneration and

CC repair (or nucleic acids encoding them) may be used to promote wound

CC healing (e.g., of burns, incisions and ulcers), while those with

CC immunomodulatory activities may be used in the treatment of viral,

CC bacterial and fungal infections in addition to immune disorders.

CC Polypeptides with growth factor activity may be used in cell cultures to

CC promote cell growth. For example, such polypeptides may be used to

CC manipulate stem cells in culture to give rise to neuroepithelial cells

CC that can be used to augment or replace cells damaged by illness,

CC autoimmune disease or accidental damage. The polypeptides and nucleotides

CC may also be used in the diagnosis of the above conditions, and in drug

CC screening techniques. The present sequence represents a novel human

CC polypeptide of the invention

XX

SQ Sequence 399 AA;

Query Match 100.0%; Score 1864; DB 4; Length 399;

Best Local Similarity 100.0%; Pred. No. 9.3e-187;

Matches 359; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKSPFTRCQNTTSVEKGNQAVMGVLFSTGLGNLLALGLLARSGLGWCSSRRPLRPLPSV 60

Db 41 MKSPFTRCQNTTSVEKGNQAVMGVLFSTGLGNLLALGLLARSGLGWCSSRRPLRPLPSV 100

Qy 61 FYMLVCGLTVDLLGKCLLSPVLAAYQNRSLRVLAAPALDNLSCQAFAPFMSFFGLSST 120

Db 101 FYMLVCGLTVDLLGKCLLSPVLAAYQNRSLRVLAAPALDNLSCQAFAPFMSFFGLSST 160

Qy 121 LQLLMALECWLSLGHPPFFYRRHITLRLGALVAPVVSFAFLAFALPFMGFGFVQYCPG 180

Db 161 LQLLMALECWLSLGHPPFFYRRHITLRLGALVAPVVSFAFLAFALPFMGFGFVQYCPG 220

Qy 181 TWCFIQWVHEEGSLVGYSLVSSLMALLVLTATVLCNIGMRNLVAMHRRRLQHPRSCT 240

Db 221 TWCFIQWVHEEGSLVGYSLVSSLMALLVLTATVLCNIGMRNLVAMHRRRLQHPRSCT 280

Qy 241 RDCABPRADGREASPOPLELDHLLALMTVLFTWCSLPVIYRAYYGAFKDVKEKRTS 300

Db 281 RDCABPRADGREASPOPLELDHLLALMTVLFTWCSLPVIYRAYYGAFKDVKEKRTS 340

Qy 301 EEADLRALRFLSVISIVDPWIFIRFSPVRIFFHKIFIRPLRYRSCSNSTNMESSL 359

Db 341 EEADLRALRFLSVISIVDPWIFIRFSPVRIFFHKIFIRPLRYRSCSNSTNMESSL 399

RESULT 7

AAW79993

ID AAW79993 standard; protein; 399 AA.

XX

AC AAW79993;

XX

DT 06-NOV-2001 (first entry)

XX

DE Human protein SEQ ID NO 3639.

XX

KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;

KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;

KW tissue growth factor; immunomodulatory; cancer; leukaemia;

KW nervous system disorder; arthritis; inflammation.

OS Homo sapiens.

XX

PN W0200157190-A2.

XX

09-AUG-2001.

XX

05-FEB-2001; 2001WO-US004098.

PF

03-FEB-2000; 2000US-00496914.

XX

27-APR-2000; 2000US-00560875.

PR

PR 20-JUN-2000; 2000US-00598075.
 PR 19-JUL-2000; 2000US-00620325.
 PR 01-SEP-2000; 2000US-00654936.
 PR 15-SEP-2000; 2000US-00663561.
 PR 20-OCT-2000; 2000US-00693325.
 PR 30-NOV-2000; 2000US-00728422.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 XX Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y;
 PI Ma Y, Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
 PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;
 XX
 DR WPI: 2001-476283/51.
 DR N-PSDB; AAK53126.
 XX
 XX Nucleic acids encoding polypeptides with cytokine-like activities, useful
 PT in diagnosis and gene therapy.
 XX
 PS Claim 20; Page 403-404; 6221pp; English.
 XX
 CC The invention relates to polynucleotides (AAK51456-AAK53435) and the
 CC encoded polypeptides (AAM78323-AAM80302) that exhibit activity relating to
 CC cytokine, cell proliferation or cell differentiation or which may induce
 CC production of other cytokines in other cell populations. The
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,
 CC e.g. stem cell growth factor activity, haematopoiesis regulating
 CC activity, tissue growth factor activity, immunomodulatory activity and
 CC activin/inhibin activity and may be useful in the diagnosis and/or
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
 CC inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111
 CC (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the
 CC sequence listing were missing at the time of publication
 XX
 SQ Sequence 399 AA;
 Query Match 100.0%; Score 1864; DB 4; Length 399;
 Best Local Similarity 100.0%; Pred. No. 9.3e-187;
 Matches 359; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MKSPFYRCQNTTSVEKGNQAVMGVLFSTGLGNLLALGLLARSGLGWCSSRRRLPLPSV 60
 DB 41 MKSPFYRCQNTTSVEKGNQAVMGVLFSTGLGNLLALGLLARSGLGWCSSRRRLPLPSV 100
 QY 61 FYMLVCGLTVDLLGKCLLSPVLAAYAQNRSLRVLAAPALDNLSCQAFAPFMSFFGLSST 120
 DB 101 FYMLVCGLTVDLLGKCLLSPVLAAYAQNRSLRVLAAPALDNLSCQAFAPFMSFFGLSST 160
 QY 121 LQLLMALECWLSLGHGHPFFYRRHITLRLGALVAPVVSFAFLAFALPFMGFGKVFQYCPG 180
 DB 161 LQLLMALECWLSLGHGHPFFYRRHITLRLGALVAPVVSFAFLAFALPFMGFGKVFQYCPG 220
 QY 181 TWCFIQWVHEEGSLVGLSVLYSSLMALLVATVLCNLAGMRLYAMHRRRLQHRPSCT 240
 DB 221 TWCFIQWVHEEGSLVGLSVLYSSLMALLVATVLCNLAGMRLYAMHRRRLQHRPSCT 280
 QY 241 RDCAEPRADGRASPOPLELDHLLALMTVLFTWCSLPVIYRAYGAFKQVKEKNRTS 300
 DB 281 RDCAEPRADGRASPOPLELDHLLALMTVLFTWCSLPVIYRAYGAFKQVKEKNRTS 340
 QY 301 EEAEEDLRALRFLSVISIVDPWIFIRPSVPFRIFFFHKKIFIRPLRYRSCSNSTNMESSL 359
 DB 341 EEAEEDLRALRFLSVISIVDPWIFIRPSVPFRIFFFHKKIFIRPLRYRSCSNSTNMESSL 399
 RESULT 8
 ADE09040
 ID ADE09040 standard; protein; 399 AA.
 XX
 AC ADE09040;
 XX
 DT 29-JAN-2004 (first entry)

XX Novel protein-related contig polypeptide sequence #106.
 DE novel gene; novel protein; tissue marker; molecular weight marker;
 KW chromosome marker; genetic disorder; contig.
 XX
 OS Unidentified.
 XX
 PN WO2003054152-A2.
 XX
 PD 03-JUL-2003.
 XX
 PF 10-DEC-2002; 2002WO-US039555.
 XX
 PR 10-DEC-2001; 2001US-0339739P.
 PR 11-DEC-2001; 2001US-0339453P.
 PR 14-MAR-2002; 2002US-0365091P.
 PR 14-MAR-2002; 2002US-0365384P.
 PR 12-APR-2002; 2002US-0372381P.
 PR 12-APR-2002; 2002US-0372615P.
 PR 22-APR-2002; 2002US-00128558.
 PR 24-APR-2002; 2002US-0376045P.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 XX Tang YT, Asundi V, Goodrich RW, Ren F, Zhang J, Zhao QA, Wang J;
 PI Chosh M, Xue AJ, Wehrman T, Weng G, Zhou P, Drmanac RT, Wang Z;
 PI Ma Y, Wang D, Chen R, Xu C, Boyle BJ;
 XX
 DR WPI: 2003-569235/53.
 XX
 DR New polynucleotides, useful for expressing recombinant proteins for
 PT analysis, characterization or therapeutic use, or as markers for tissues
 PT in which the corresponding protein is preferentially expressed.
 XX
 PS Disclosure; SEQ ID NO 2584; 1177pp; English.
 XX
 CC The invention comprises the amino acid and coding sequences of novel
 CC proteins. The DNA and protein sequences of the invention are useful as:
 CC markers for tissues in which the corresponding protein is preferentially
 CC expressed; as molecular weight markers on gels; as chromosome markers or
 CC tags; to identify chromosomes or to map related gene positions; and to
 CC compare with endogenous DNA sequences in patients to identify potential
 CC genetic disorders. The present amino acid sequence was used in the
 CC exemplification of the invention.
 XX
 SQ Sequence 399 AA;
 Query Match 100.0%; Score 1864; DB 7; Length 399;
 Best Local Similarity 100.0%; Pred. No. 9.3e-187;
 Matches 359; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MKSPFYRCQNTTSVEKGNQAVMGVLFSTGLGNLLALGLLARSGLGWCSSRRRLPLPSV 60
 DB 41 MKSPFYRCQNTTSVEKGNQAVMGVLFSTGLGNLLALGLLARSGLGWCSSRRRLPLPSV 100
 QY 61 FYMLVCGLTVDLLGKCLLSPVLAAYAQNRSLRVLAAPALDNLSCQAFAPFMSFFGLSST 120
 DB 101 FYMLVCGLTVDLLGKCLLSPVLAAYAQNRSLRVLAAPALDNLSCQAFAPFMSFFGLSST 160
 QY 121 LQLLMALECWLSLGHGHPFFYRRHITLRLGALVAPVVSFAFLAFALPFMGFGKVFQYCPG 180
 DB 161 LQLLMALECWLSLGHGHPFFYRRHITLRLGALVAPVVSFAFLAFALPFMGFGKVFQYCPG 220
 QY 181 TWCFIQWVHEEGSLVGLSVLYSSLMALLVATVLCNLAGMRLYAMHRRRLQHRPSCT 240
 DB 221 TWCFIQWVHEEGSLVGLSVLYSSLMALLVATVLCNLAGMRLYAMHRRRLQHRPSCT 280
 QY 241 RDCAEPRADGRASPOPLELDHLLALMTVLFTWCSLPVIYRAYGAFKQVKEKNRTS 300
 DB 281 RDCAEPRADGRASPOPLELDHLLALMTVLFTWCSLPVIYRAYGAFKQVKEKNRTS 340
 QY 301 EEAEEDLRALRFLSVISIVDPWIFIRPSVPFRIFFFHKKIFIRPLRYRSCSNSTNMESSL 359


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|||||
341 EAEDRALRPLSVISIVDPWIFIRFSPVFRIFRPHKIFIRPLRYRSCNSNSTMESSL 399

Db 121 LQLLAWALECWSLGLHPPFFRRHITLRLGALVAPVVSFAFLAFCALPFMGFGKVPQYCPG 180
181 TWCFIQWVHEEGSLSVLGYSVLYSSLMALLVATVLCNLGAMENLYAMHRRRLQHRPRSC 240
181 TWCFIQWVHEEGSLSVLGYSVLYSSLMALLVATVLCNLGAMENLYAMHRRRLQHRPRSC 240
241 RDCAEPRADGREASPOPLELDHLLALLMTVLFTWCSLPVI----- 282
241 RDCAEPRADGREASPOPLELDHLLALLMTVLFTWCSLPVI----- 300
283 -----YRAYGAFKDVKEKNTSEAEEDLRLRFLSVISIVD 319
301 RGKGGADRDGRCARRAAPWARKYRAYYGAFKDVKEKNTSEAEEDLRLRFLSVISIVD 360
320 PMIFIFRSPVFRIFRPHKIFIRPLRY 345
361 PMIFIFRSPVFRIFRPHKIFIRPLSY 386

RESULT 10
AAY94346
ID AAY94346 standard; protein; 369 AA.
XX
AC AAY94346;
XX
DT 22-AUG-2000 (first entry)
XX
DE Human cell surface receptor protein #13.
XX
KW Human; HCSR; cytostatic; antiarthritic; antirheumatic; antiasthmatic;
KW immunosuppressive; antiarteriosclerotic; antibacterial; antiparasitic;
KW neuroprotective; nootropic; anticonvulsant; cancer; leukaemia; melanoma;
KW rheumatoid arthritis; asthma; atherosclerosis; akathesia;
KW Alzheimer's diseases; multiple sclerosis; epilepsy.
XX
OS Homo sapiens.
XX
FH Key
FT Peptide 1..47
FT Region 6..20 /label= Signal_peptide
FT /note= "Prostaglandin D receptor"
FT Region 10..57
FT /note= "2 Poly-Immunoglobulin receptor"
FT Region 10
FT /note= "potential glycosylation site"
FT Region 11..58
FT /note= "2 Poly-Immunoglobulin receptor"
FT Region 12
FT /note= "potential phosphorylation site"
FT Region 33..280
FT /note= "7 Transmembrane receptor"
FT Region 41..58
FT /note= "Prostaglandin D receptor"
FT Protein 48..369
FT /label= HCSR-13
FT Region 50
FT /note= "potential phosphorylation site"
FT Region 52..99
FT /note= "2 Poly-Immunoglobulin receptor"
FT Region 69
FT /note= "potential phosphorylation site"
FT Region 90
FT /note= "potential glycosylation site"
FT Region 92
FT /note= "potential phosphorylation site"
FT Region 93..104
FT /note= "Prostaglandin D receptor"
FT Domain 144..161
FT /label= Transmembrane_domain
FT Region 145
FT /note= "potential phosphorylation site"
```

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|||||
341 EAEDRALRPLSVISIVDPWIFIRFSPVFRIFRPHKIFIRPLRYRSCNSNSTMESSL 399

Db 121 LQLLAWALECWSLGLHPPFFRRHITLRLGALVAPVVSFAFLAFCALPFMGFGKVPQYCPG 180
181 TWCFIQWVHEEGSLSVLGYSVLYSSLMALLVATVLCNLGAMENLYAMHRRRLQHRPRSC 240
181 TWCFIQWVHEEGSLSVLGYSVLYSSLMALLVATVLCNLGAMENLYAMHRRRLQHRPRSC 240
241 RDCAEPRADGREASPOPLELDHLLALLMTVLFTWCSLPVI----- 282
241 RDCAEPRADGREASPOPLELDHLLALLMTVLFTWCSLPVI----- 300
283 -----YRAYGAFKDVKEKNTSEAEEDLRLRFLSVISIVD 319
301 RGKGGADRDGRCARRAAPWARKYRAYYGAFKDVKEKNTSEAEEDLRLRFLSVISIVD 360
320 PMIFIFRSPVFRIFRPHKIFIRPLRY 345
361 PMIFIFRSPVFRIFRPHKIFIRPLSY 386

RESULT 9
ADE07993
ID ADE07993 standard; protein; 424 AA.
XX
AC ADE07993;
XX
DT 29-JAN-2004 (first entry)
XX
DE Novel protein (useful for identifying genetic disorders) #148.
XX
KW novel gene; novel protein; tissue marker; molecular weight marker;
KW chromosome marker; genetic disorder.
XX
OS Unidentified.
XX
PN WO2003054152-A2.
XX
PD 03-JUL-2003.
XX
PF 10-DEC-2002; 2002WO-US039555.
XX
PR 10-DEC-2001; 2001US-0339739P.
PR 11-DEC-2001; 2001US-0339453P.
PR 14-MAR-2002; 2002US-0365091P.
PR 14-MAR-2002; 2002US-0365384P.
PR 12-APR-2002; 2002US-0372381P.
PR 12-APR-2002; 2002US-0372615P.
PR 22-APR-2002; 2002US-00128558.
PR 24-APR-2002; 2002US-0376045P.
XX
PA (HYSB-) HYSEQ INC.
XX
PI Tang YT, Aeundi V, Goodrich RW, Ren F, Zhang J, Zhao QA, Wang J;
PI Ghosh M, Xue AJ, Wehrman T, Weng G, Zhou P, Drmanac RT, Wang Z;
PI Ma Y, Wang D, Chen R, Xu C, Boyle BJ;
XX
DR WPI: 2003-569235/53.
DR N-PSDB; ADE07082.
XX
PT New polynucleotides, useful for expressing recombinant proteins for
PT analysis, characterization or therapeutic use, or as markers for tissues
PT in which the corresponding protein is preferentially expressed.
XX
PS Claim 20; SEQ ID NO 1059; 1177pp; English.
XX
CC The invention comprises the amino acid and coding sequences of novel
CC proteins. The DNA and protein sequences of the invention are useful as:
CC markers for tissues in which the corresponding protein is preferentially
CC expressed; as molecular weight markers on gels; as chromosome markers or
CC tags; to identify chromosomes or to map related gene positions; and to
CC compare with endogenous DNA sequences in patients to identify potential
CC genetic disorders. The present amino acid sequence represents a protein
CC of the invention.
XX
SQ Sequence 424 AA;

Query Match 94.3%; Score 1757.5; DB 7; Length 424;
Best Local Similarity 89.1%; Pred. No. 1.6e-175;
Matches 344; Conservative 0; Mismatches 1; Indels 41; Gaps 1;

QY 1 MKSPFYRCNTTSVEKNSAVMGVLFSTGLGNLALGLLARSGLGWCRRRLPLPSV 60
Db 1 MKSPFYRCNTTSVEKNSAVMGVLFSTGLGNLALGLLARSGLGWCRRRLPLPSV 60
QY 61 FYMLVGLTVDLLGKCLSPVLAAYQNRSLRVLAPALDNLSCQAFAMFFSFGLSST 120
Db 61 FYMLVGLTVDLLGKCLSPVLAAYQNRSLRVLAPALDNLSCQAFAMFFSFGLSST 120
QY 121 LQLLAWALECWSLGLHPPFFRRHITLRLGALVAPVVSFAFLAFCALPFMGFGKVPQYCPG 180
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CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung)), chronic constriction
CC injury (CCI) and spared nerve injury (SNI) in an animal (e.g. Gene
CC therapy). The sequence presented is a rat protein (described in Table 3
CC of the specification) which is differentially expressed during pain.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 357 AA;

Query Match 74.4%; Score 1386.5; DB 7; Length 357;
Best Local Similarity 76.1%; Pred. No. 1.2e-136;
Matches 271; Conservative 30; Mismatches 50; Indels 5; Gaps 2;
QY 6 YRCQNTTSVEKGSNAVMGVGFSTGLGNLLALGLLARSGLGWCRRPLRPLPSVFYMLV 65
DB 5 YRCQATWVERGSSATMGVLFAGLLGNLLALLVLLARSGLGSCRPGPLHPPSPVFYVLV 64
QY 66 CGLTVTDLGKCLLSPVLAAYQNRSLRVLAPALDNLSCQAFPMSPFGLSSTQLLA 125
DB 65 CGLTVTDLGKCLLSPVLAAYQNRSLRVLAPALDNLSCQAFPMSPFGLSSTQLLA 124
QY 126 MALECWLSLGHPPFYRRHITRLGALVAPVVSFAFLAFALCPMPGFGKFVQYCPGTWCPI 185
DB 125 MALECWLSLGHPPFYRRHITARGVLVAPVAGFSLAFALCPMPGFGKFVQYCPGTWCPI 184
QY 186 QMVHEGSLVGLVSYLSSMALLVLATVLCNGLAMRNLYAMHRLQRHPRSCTRDCAE 245
DB 185 QMTHKRSFVIGFVLSYSSMALLVLATVLCNGLAMRNLYAMHRRQHRHPRCSRDRQAQ 244
QY 246 PRADGERSQPLELDHLLLMVTFMCSLPVIYRAYYCAFVDKVKNTSEAEAD 305
DB 245 SGSDYRHGSPNLELDHFLVLLATVTFMCSLPVIYRAYYCAFVLLV--DRADGDESD 301
QY 306 LRALRFLSVISVDPMFIFRSPVFRIPPHKIPRPLRVSRCSNS--TNMESSL 359
DB 302 LQALRFLSVISVDPMFIFRSPVFRIPPHKIPRPLRVSRCSNS--TNMESSL 357

RESULT 12

AD029615

ID AD029615 standard; protein; 357 AA.

XX AC AD029615;

DT 29-JUL-2004 (first entry)

DE Mouse GPCR PTGDR, SEQ ID NO:717.

XX G protein-coupled receptor; GPCR; drug screening; diagnosis;
KW transgenic mouse; neurological disorder; adrenal gland disorder;
KW colon disorder; intestinal disorder; cardiovascular disorder;
KW muscular disorder; blood disorder; immune disorder; bone disorder;
KW joint disorder; metabolic disorder; nutritive disorder; cancer;
KW kidney disorder; liver disorder; lung disorder; breast disorder;
KW ovary disorder; uterus disorder; prostate disorder; testis disorder;
KW skin disorder; stomach disorder; pancreas disorder; spleen disorder;
KW thymus disorder; thyroid disorder; antiparkinsonian; antianemic;
KW cytostatic; antiinflammatory; vasotropic; antianginal; antiarrhythmic;
KW CNS; central nervous system; respiratory; antidiarrhoeic; antidiabetic;
KW virucide; hepatotropic; antibacterial; antinaemic; antiseborrhoeic;

KW dermatological; antiulcer; antithyroid; antiallergic; anorectic;
KW immunosuppressive; nephrotropic; gene therapy; GPCR modulator; mouse;
XX murine; receptor.
OS Mus musculus.
XX WO2004040000-A2.
XX 13-MAY-2004.
XX 09-SEP-2003; 2003WO-US028226.
XX 09-SEP-2002; 2002US-0409303P.
XX 09-APR-2003; 2003US-0461329P.
XX (PRIM-) PRIMAL INC.
XX Gaitanaris GA, Bergmann JE, Gragerov A, Hohmann J, Li F;
XX Madisen L, McIlwain KL, Pavlova MN, Vassiliadis D, Zeng H;
XX WPI; 2004-390329/36.
XX N-PSDB; ADO30316.
XX Novel mammalian G protein coupled receptors, useful for identifying
XX compounds that modulates diagnosing and treating disease condition
XX associated with GPCR dysfunction e.g. autoimmune diseases, angina
XX pectoris, Parkinson's disease.
XX Claim 151; SEQ ID NO 717; 542pp; English.

CC The invention relates to human and mouse G protein-coupled receptors
CC (GPCRs) and nucleic acids encoding them. The invention also relates to
CC sequences at least 90% identical to the GPCR proteins and nucleic acids
CC of the invention; methods of treating, preventing or diagnosing diseases
CC associated with GPCRs of the invention; methods of screening for
CC compounds useful in the treatment of GPCR-related diseases; a transgenic
CC mouse comprising a GPCR gene of the invention; a mouse comprising a
CC mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived
CC from the transgenic mice; kits comprising several mice, each of which has
CC a mutation in a different GPCR gene of the invention; and kits comprising
CC probes which hybridise to GPCR polynucleotides of the invention. The
CC invention further discloses variants of the GPCR polypeptides and vectors
CC comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may
CC be used in the diagnosis, treatment or prevention of a wide variety of
CC diseases including neurological disorders (e.g., Alzheimer's disease,
CC depression, diabetic neuropathy, Parkinson's disease or schizophrenia);
CC disorders of the adrenal gland; disorders of the colon or intestine
CC (e.g., Crohn's disease, diarrhoea, food poisoning or irritable bowel
CC syndrome); cardiovascular disorders (e.g., angina, cardiac arrhythmia or
CC myocardial infarction); muscular disorders; blood disorders (e.g.,
CC anaemia or leukaemia); immune disorders (e.g., autoimmune disorders or
CC AIDS); bone and joint disorders (e.g., osteoarthritis, rheumatoid
CC arthritis, gout or osteoporosis); metabolic or nutritive disorders (e.g.,
CC obesity, enzyme deficiency-related diseases or vitamin deficiency-related
CC diseases); and disorders of the kidney, liver, lung, breast, ovary,
CC uterus, prostate, testis, skin, stomach, pancreas, spleen, thymus and
CC thyroid (e.g., cancers). The present sequence represents a GPCR of the
CC invention. Note: The full sequence data for this patent did not form part
CC of the printed specification; those sequences not shown were obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 357 AA;

Query Match 72.3%; Score 1347.5; DB 8; Length 357;
Best Local Similarity 73.3%; Pred. No. 1.5e-132;
Matches 261; Conservative 39; Mismatches 51; Indels 5; Gaps 2;

QY 6 YRCQNTTSVEKGSNAVMGVGFSTGLGNLLALGLLARSGLGWCRRPLRPLPSVFYMLV 65

DB 5 YRCQSTWVERGSSATMGAVLFGAGLLGNLLALLVLLARSGLGSCRPGPLHPPSPVFYVLV 64

QY 66 CGLTVTDLGKCLLSPVLAAYQNRSLRVLAPALDNLSCQAFPMSPFGLSSTQLLA 125

Db 65 CGLTVTDLGKCLISPNVLAAYAQNSLKELLFASGNQLCETAFILMSFGLASTLQLLA 124
QY 126 MALECWLSLGHPPFFRRHITLRGALVAPVVSFAFALPMFGKFGKVOYCPGTWCFFI 185
Db 125 MAVECWLSLGHPPFFRRHITLRGALVAPVVSFAFALPMFGKFGKVOYCPGTWCFFI 184
QY 186 QMVHEGSLVGLSVLYSSIMALLVLAIVLVCNIGAMRNLYAMHRRLOHPRSCRTDCAE 245
Db 185 QMTHKERSFSVIGFSVLYSSIMALLVLAIVLVCNIGAMRNLYAMHRRLOHPRSCRTDCAE 244
QY 246 PRADGREASPOPLEELDHLLALMTVLTMCSLPLVIRAYYGAFAKDVKEKNTSBEAD 305
Db 245 SGSDYRHGSLHLELDHFVLLALMTVLTMCSLPLVIRAYYGAFAFAKDVKEKNTSBEAD 301
QY 306 LRALRFLSVISIDPWFIFIRFSPVPRIFRPFHFIKIFIRPLRYRSCNS--TNMESSL 359
Db 302 LQALRFLSVISIDPWFIFIRFSPVPRIFRPFHFIKIFIRPLRYRSCNS--TNMESSL 357

RESULT 13

AAR84708
ID AAR84708 standard; protein; 357 AA.

XX AC AAR84708;

XX DT 06-JUN-1996 (first entry)

XX DE Prostaglandin D receptor.

XX KW Prostaglandin D receptor; mouse; PGD-2; therapy; immune activator.

XX OS Mus musculus.

XX PN JP07258295-A.

XX PD 09-OCT-1995.

XX PF 22-MAR-1994; 94JP-00075382.

XX PR 22-MAR-1994; 94JP-00075382.

XX PA (ONONY) ONO PHARM CO LTD.

XX DR WPI; 1995-380075/49.

XX DR N-PSDB; AAT05171, AAT05172.

XX PT Novel murine prostaglandin D receptor - used for the treatment and prevention of diseases caused by PGD-2.

XX PS Claim 3; Page 6-7; 11pp; Japanese.

XX CC This sequence represents the murine prostaglandin D receptor. The encoding sequence was obtained through reverse transcription PCR (using the primers represented by AAT05173-T05176). The full length DNA sequence can be used in a vector to transform cells to produce this sequence. This sequence can be used as an agent for the prevention and treatment of diseases caused by excessive production of PGD-2, such as an immune activator and an inhibitor of bleeding

XX SQ Sequence 357 AA;

Query Match 72.2%; Score 1346.5; DB 2; Length 357;
Best Local Similarity 73.3%; Pred. No. 2e-132;
Matches 261; Conservative 39; Mismatches 51; Indels 5; Gaps 2;

QY 6 YRCQNTTSVSKGSAYVGGVLFSTGLIGNLLALGLLARSGLGWCRRRLPLRPLSVFVMLV 65

Db 5 YRCQNTTSVSKGSAYVGGVLFSTGLIGNLLALGLLARSGLGWCRRRLPLRPLSVFVMLV 64

QY 66 CGLTVTDLGKCLISPNVLAAYAQNSLKELLFASGNQLCETAFILMSFGLASTLQLLA 125

Db 65 CGLTVTDLGKCLISPNVLAAYAQNSLKELLFASGNQLCETAFILMSFGLASTLQLLA 124

QY 126 MALECWLSLGHPPFFRRHITLRGALVAPVVSFAFALPMFGKFGKVOYCPGTWCFFI 185
Db 125 MAVECWLSLGHPPFFRRHITLRGALVAPVVSFAFALPMFGKFGKVOYCPGTWCFFI 184
QY 186 QMVHEGSLVGLSVLYSSIMALLVLAIVLVCNIGAMRNLYAMHRRLOHPRSCRTDCAE 245
Db 185 QMTHKERSFSVIGFSVLYSSIMALLVLAIVLVCNIGAMRNLYAMHRRLOHPRSCRTDCAE 244
QY 246 PRADGREASPOPLEELDHLLALMTVLTMCSLPLVIRAYYGAFAKDVKEKNTSBEAD 305
Db 245 SGSDYRHGSLHLELDHFVLLALMTVLTMCSLPLVIRAYYGAFAFAKDVKEKNTSBEAD 301
QY 306 LRALRFLSVISIDPWFIFIRFSPVPRIFRPFHFIKIFIRPLRYRSCNS--TNMESSL 359
Db 302 LQALRFLSVISIDPWFIFIRFSPVPRIFRPFHFIKIFIRPLRYRSCNS--TNMESSL 357

RESULT 14

ADP55149
ID ADP55149 standard; protein; 144 AA.

XX AC ADP55149;

XX DT 18-NOV-2004 (first entry)

XX DE Human PRO protein sequence SEQ ID NO:1125.

XX KW human; PRO; immune related disease; inflammatory immune response; immune response stimulation; anti-allergic; antianemic; antiarthritic; antidiabetic; antidiabetic; anti-inflammatory; antipsoriatic; antirheumatic; antithyroid; CNS; dermatological; gastrointestinal; haemostatic; hepatotropic; immunostimulant; immunosuppressive; muscular; nephrotropic; neuroprotective; osteopathic; respiratory; vasotropic; virucide; gene therapy.

XX OS Homo sapiens.

XX PN WO2004039956-A2.

XX PD 13-MAY-2004.

XX PF 28-OCT-2003; 2003WO-US034381.

XX PR 29-OCT-2002; 2002US-0422472P.

XX PA (GETH) GENENTECH INC.

XX PI Aggarwal S, Clark H, Gurney AL, Schoenfeld J, Williams PM; Wood WI, Wu TD;

XX DR WPI; 2004-376182/35.

XX DR N-PSDB; ADP55148.

XX PT New PRO polynucleotides and polypeptides, useful in diagnosing and treating an immune related disease, e.g. systemic lupus erythematosus, rheumatoid arthritis, diabetes mellitus or asthma and in stimulating an immune response.

XX PS Claim 1; SEQ ID NO 1125; 3009pp; English.

XX CC The present invention describes an isolated PRO nucleic acid (I). Also described: (1) a vector comprising (I); (2) a host cell comprising the vector of (1); (3) a process for producing a PRO polypeptide; (4) an isolated PRO polypeptide; (5) a chimeric molecule comprising the polypeptide of (4) fused to a heterologous amino acid sequence; (6) an antibody which specifically binds to a polypeptide of (4); (7) a composition of matter comprising a polypeptide of (4), an agonist or antagonist of the polypeptide or an antibody that binds to the polypeptide in combination with a carrier; (8) an article of manufacture comprising a container, a label on the container and a composition of matter of (7); (9) a method of treating an immune related disease in a mammal; (10) a method for determining the presence of a PRO polypeptide

CC in a sample suspected of having the polypeptide; (11) a method of
 CC diagnosing an immune related disease or an inflammatory immune response
 CC in mammal; (12) a method of identifying a compound that inhibits or
 CC mimics the activity of or expression of a gene encoding a PRO polypeptide
 CC ; and (13) a method of stimulating the immune response in a mammal. The
 CC PRO sequences have anti-allergic, antianemic, antiarthritic,
 CC antiachmatic, antidiabetic, antiinflammatory, antiporiatic,
 CC antirheumatic, antithyroid, CNS, dermatological, gastrointestinal,
 CC haemostatic, hepatotropic, immunostimulant, immunosuppressive, muscular,
 CC nephrotropic, neuroprotective, osteopathic, respiratory, vasotropic and
 CC virucide activities, and can be used in gene therapy. The nucleic acid
 CC (I) and the encoded polypeptides, compositions, kits and methods are
 CC useful in diagnosing and treating an immune related disease and in
 CC stimulating an immune response. The present sequence represents a human
 CC PRO protein from the present invention.

XX SQ Sequence 144 AA;

Query Match 40.3%; Score 752; DB 8; Length 144;
 Best Local Similarity 100.0%; Pred. No. 1.8e-70;
 Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 216 LCNLGAMRNLYAMHRRLLQHRPSTCTDCAEPADGREGASPOPLELHLLALLMTVLFT 275
 Db 1 LCNLGAMRNLYAMHRRLLQHRPSTCTDCAEPADGREGASPOPLELHLLALLMTVLFT 60

Qy 276 MCSLPVIYRAYYGAFKDVKEKNTSEAEIDLRLALFLSVISIDVPWIFIRSPVPRIF 335
 Db 61 MCSLPVIYRAYYGAFKDVKEKNTSEAEIDLRLALFLSVISIDVPWIFIRSPVPRIF 120

Qy 336 HKIPRLPLVRSRCSNSTNMESL 359
 Db 121 HKIPRLPLVRSRCSNSTNMESL 144

RESULT 15

ADO29619
 ID ADO29619 standard; protein; 362 AA.

AC ADO29619;

DT 29-JUL-2004 (first entry)

DE Mouse GPCR PTGER2, SEQ ID NO:721.

XX G protein-coupled receptor; GPCR; drug screening; diagnosis;
 KW transgenic mouse; neurological disorder; adrenal gland disorder;
 KW colon disorder; intestinal disorder; cardiovascular disorder;
 KW muscular disorder; blood disorder; immune disorder; bone disorder;
 KW joint disorder; metabolic disorder; nutritive disorder; cancer;
 KW kidney disorder; liver disorder; lung disorder; breast disorder;
 KW ovary disorder; uterus disorder; prostate disorder; testis disorder;
 KW skin disorder; stomach disorder; pancreas disorder; spleen disorder;
 KW thymus disorder; thyroid disorder; antiparkinsonian; antimanic;
 KW cytosatic; antinflammatory; vasotropic; antianginal; antiarrhythmic;
 KW CNS; central nervous system; respiratory; antidiarrhoeic; antidiabetic;
 KW virucide; hepatotropic; antibacterial; antianemic; antiseborrhoeic;
 KW dermatological; antitumor; antithyroid; antiallergic; anorectic;
 KW immunosuppressive; nephrotropic; gene therapy; GPCR modulator; mouse;
 KW murine; receptor.

XX Mus musculus.

XX WO2004040000-A2.

XX 13-MAY-2004.

XX 09-SEP-2003; 2003WO-US028226.

XX 09-SEP-2002; 2002US-0409303P.

XX 09-APR-2003; 2003US-0461329P.

XX (PRIM-) PRIMAL INC.

XX

PI Gaitanaris GA, Bergmann JE, Gragerov A, Hohmann J, Li F;
 PI Madisen L, McIlwain KL, Pavlova MN, Vassilatis D, Zeng H;

XX WPI: 2004-390329/36.

DR N-PSDB; ADO30318.

XX Novel mammalian G protein coupled receptors, useful for identifying
 PT compounds that modulates diagnosing and treating disease condition
 PT associated with GPCR dysfunction e.g. autoimmune diseases, angina
 PT pectoris, Parkinson's disease.

XX Claim 151; SEQ ID NO 721; 542pp; English.

XX The invention relates to human and mouse G protein-coupled receptors
 CC (GPCRs) and nucleic acids encoding them. The invention also relates to
 CC sequences at least 90% identical to the GPCR proteins and nucleic acids
 CC of the invention; methods of treating, preventing or diagnosing diseases
 CC associated with GPCRs of the invention; methods of screening for
 CC compounds useful in the treatment of GPCR-related diseases; a transgenic
 CC mouse comprising a GPCR gene of the invention; a mouse comprising a
 CC mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived
 CC from the transgenic mice; kits comprising several mice, each of which has
 CC a mutation in a different GPCR gene of the invention; and kits comprising
 CC probes which hybridise to GPCR polynucleotides of the invention. The
 CC invention further discloses variants of the GPCR polypeptides and vectors
 CC comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may
 CC be used in the diagnosis, treatment or prevention of a wide variety of
 CC diseases including neurological disorders (e.g., Alzheimer's disease,
 CC depression, diabetic neuropathy, Parkinson's disease or schizophrenia);
 CC disorders of the adrenal gland; disorders of the colon or intestine
 CC (e.g., Crohn's disease, diarrhoea, food poisoning or irritable bowel
 CC syndrome); cardiovascular disorders (e.g., angina, cardiac arrhythmia or
 CC myocardial infarction); muscular disorders; blood disorders (e.g.,
 CC anaemia or leukaemia); immune disorders (e.g., autoimmune disorders or
 CC AIDS); bone and joint disorders (e.g., osteoarthritis, rheumatoid
 CC arthritis, gout or osteoporosis); metabolic or nutritive disorders (e.g.,
 CC obesity, enzyme deficiency-related diseases or vitamin deficiency-related
 CC diseases); and disorders of the kidney, liver, lung, breast, ovary,
 CC uterus, prostate, testis, skin, stomach, pancreas, spleen, thymus and
 CC thyroid (e.g., cancers). The present sequence represents a GPCR of the
 CC invention. Note: The full sequence data for this patent did not form part
 CC of the printed specification; those sequences not shown were obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 362 AA;

Query Match 38.0%; Score 707.5; DB 8; Length 362;
 Best Local Similarity 44.5%; Pred. No. 2.9e-65;
 Matches 159; Conservative 58; Mismatches 115; Indels 25; Gaps 9;

Qy 8 CQNTTSVEKGN SAVMGVLPSTGLLGNLLALGALLARSLG--WCSRRPLPLPSVFYMLV 65

Db 14 CKSRQWLGGESPAISSVMFSAGVLGNLIALALLARRWRGDTGCSAGS-RTSLSLFHLV 72

Qy 66 CGLTVDLLKCLLSPVLLAAVAQNLSRLVAPALDNLSCQAFPMFSFGLSSTQLLA 125

Db 73 TELVLDTDLGTCLISPVLLASYSRNTLVALAP-ESHACTYFAFTWTFSLATMLMFA 130

Qy 126 MALECWLSLGHPPFYRRHITLRLGALVAPVVSFAFLAFALPMFGFKVOYCPGTWCPI 185

Db 131 MALERYLSIGYPFYRRHLSRRGLAVLPVIYGASLLFCSLLPNLYGEYVOYCPGTWCPI 190

Qy 186 QMVEEGSLSVLGYSLYSSLMALLVLTATVLCNLGAMRNLYAMHRRLLQHRPSTCTDCAE 245

Db 191 R--HGR-----TAYLQYATMTLLLIIVAVLACNISVLNLIRHRRSR--SRCGLSGSS 241

Qy 246 PRADG---REASQPLEDLHLLALLMTVLTWLTWLTWLTWLTWLTWLTWLTWLTWLTW 302

Db 242 LRPGSGRRGERTSMAEETDHLILLAIMITFAICSLPFTTFPAYMETSLKKE----- 295

Qy 303 AEDLRALFLSVISIDVPWIFIRSPVFRIFPHKIFIR-PLRYRSCNSSTNMESS 358

Db 296 -WDLRALRFLSVNSIIDPWVFAILRPPVLFRLMESVLCRCRTSLRTOEAAQOTSCSTQSS 351

Search completed: April 22, 2005, 21:27:24
Job time : 66.771 secs

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OM protein - protein search, using sw model

Run on: April 22, 2005, 20:46:09 ; Search time 17.5399 Seconds
(without alignments)
1969.437 Million cell updates/sec

Title: US-10-689-861-4
Perfect score: 1864
Sequence: 1 MKSPFFRCQNTTSVEKNSA.....IRPLVRSRCSNTNMESL 359
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1864	100.0	359	2 I39153	prostanoid DP rece
2	943	50.6	231	2 I59269	prostaglandin D re
3	707.5	38.0	362	2 S66674	prostaglandin E re
4	689	37.0	358	2 I38920	prostaglandin E2 r
5	688	36.9	358	2 S51312	EP2 prostaglandin
6	597	32.0	386	2 A57066	prostacyclin recep
7	596.5	32.0	417	2 A54416	prostacyclin recep
8	585.5	31.4	416	2 S52078	prostacyclin - rat
9	458.5	24.6	513	2 A46638	prostaglandin E re
10	452.5	24.3	488	2 JC2241	prostaglandin E re
11	443	23.8	488	2 A53572	prostaglandin E2 r
12	314	16.8	362	2 S48689	prostaglandin E(2)
13	313.5	16.8	366	2 S51280	EP3-alpha receptor
14	308	16.5	365	2 A42414	prostaglandin E re
15	308	16.5	365	2 JN0593	prostaglandin E2 r
16	307.5	16.5	361	2 A45211	prostaglandin E re
17	307.5	16.5	364	2 JC2115	prostaglandin E re
18	307.5	16.5	364	2 S65009	prostaglandin E re
19	298.5	16.0	361	2 A53216	prostaglandin E2 r
20	298.5	16.0	393	2 S51318	prostaglandin E re
21	297.5	16.0	390	2 S43175	prostaglandin E re
22	297.5	16.0	390	2 S51313	prostaglandin E re
23	296.5	15.9	411	2 B53216	prostaglandin E2 r
24	294	15.8	388	2 S51316	prostaglandin E re
25	294	15.8	388	2 I38750	prostaglandin recep
26	293.5	15.7	365	2 I38748	prostaglandin recep
27	293.5	15.7	365	2 S51315	prostaglandin E re
28	292.5	15.7	367	2 JC2056	prostaglandin E2 r
29	292.5	15.7	369	2 A25359	thromboxane A-2 re

30	292.5	15.7	407	2 T02670	probable thromboxa
31	291.5	15.6	374	2 I38747	prostaglandin recep
32	291.5	15.6	374	2 S51317	prostaglandin E re
33	291.5	15.6	425	2 S51319	prostaglandin E re
34	289.5	15.5	343	2 A49117	thromboxane A2 rec
35	286.5	15.4	385	2 S36765	prostaglandin E re
36	284.5	15.3	362	2 S36766	prostaglandin E re
37	284.5	15.3	387	2 S36767	prostaglandin E re
38	284.5	15.3	417	2 S36764	prostaglandin E re
39	266	14.3	341	2 I55623	thromboxane A2 rec
40	257	13.8	341	2 JH0606	thromboxane A2 rec
41	255.5	13.7	402	1 A49690	prostaglandin E re
42	247.5	13.3	76	2 I80042	prostaglandin D re
43	246	13.2	405	2 S66525	prostanoid recepto
44	241	12.9	366	2 A49877	prostaglandin F re
45	238	12.8	366	2 I53488	prostaglandin F2 a

ALIGNMENTS

RESULT 1

I39153
prostanoid DP receptor - human
N;Alternate names: prostaglandin D2 receptor
C;Species: Homo sapiens (man)
C;Date: 09-Mar-1996 #sequence_revision 03-May-1996 #text_change 09-Jul-2004
R;Accession: I39153; I39150; I39149
R;Boile, Y.; Sawyer, N.; Slipetz, D.M.; Metters, K.M.; Abramovitz, M.
J. Biol. Chem. 270, 18910-18916, 1995
A;Title: Molecular cloning and characterization of the human prostanoid DP receptor.
A;Reference number: I39149; MUID:95370201; PMID:7642548
A;Accession: I39153
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-282 <RES>
A;Cross-references: UNIPROT:Q13258; EMBL:U31332; NID:g940378; PIDN:AAC50178.1; PID:g9403
A;Accession: I39150
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 216-359 <RES2>
A;Cross-references: EMBL:U31099; NID:g940376; PIDN:AAC50177.1; PID:g940377
A;Accession: I39149
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 283-328 <RES3>
A;Cross-references: EMBL:U31098; NID:g940374; PIDN:AAC50176.1; PID:g940375
C;Genetics:
A;Gene: GDB:PTGDR
A;Cross-references: GDB:681159
A;Map position: 10q23-10q23
C;Superfamily: prostaglandin E receptor EP1
C;Keywords: G protein-coupled receptor

Query Match	100.0%;	Score 1864;	DB 2;	Length 359;
Best Local Similarity	100.0%;	Pred. No. 4.1e-153;		
Matches	359;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;
Qy	1	MKSPFFRCQNTTSVEKNSAVMGVLFSTGLGNLALGLLAEBSGLGWCSSRRPLRPLPSV	60	
Db	1	MKSPFFRCQNTTSVEKNSAVMGVLFSTGLGNLALGLLAEBSGLGWCSSRRPLRPLPSV	60	
Qy	61	FYMLVGLTVTDLGKCLLSPVVLAAYAQNRSLRVLPALDNLSCQAFAFMFSGFLSST	120	
Db	61	FYMLVGLTVTDLGKCLLSPVVLAAYAQNRSLRVLPALDNLSCQAFAFMFSGFLSST	120	
Qy	121	LQLLAMALECWLGLSHGHPFFRRHITLRLGALVAPVVSFAFSLAFALPFMGFGFVQYCPG	180	
Db	121	LQLLAMALECWLGLSHGHPFFRRHITLRLGALVAPVVSFAFSLAFALPFMGFGFVQYCPG	180	
Qy	181	TWCFIQMVHEGSLSVLGYSLVSLMALVTLVLCNIGAMNLYAMHRRLLQRHRSCT	240	
Db	181	TWCFIQMVHEGSLSVLGYSLVSLMALVTLVLCNIGAMNLYAMHRRLLQRHRSCT	240	

QY 241 RDCAEPRADGASPOPLELHLLALLMTVLTWCSPVIYRAYGAFKDVKEKNRTS 300
Db 241 RDCAEPRADGASPOPLELHLLALLMTVLTWCSPVIYRAYGAFKDVKEKNRTS 300
QY 301 EEAEDLRALFLSVISIVDPWIFIRSPVFRIFHHKIFIRPLRYRSCSNSTNMESSL 359
Db 301 EEAEDLRALFLSVISIVDPWIFIRSPVFRIFHHKIFIRPLRYRSCSNSTNMESSL 359
RESULT 2
159269
prostaglandin D receptor (prostanoid DP receptor) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 04-Sep-1998
C:Accession: I59269
R:Hirata, M.; Kakizuka, A.; Aizawa, M.; Ushikubi, F.; Narumiya, S.
Proc. Natl. Acad. Sci. U.S.A. 91, 11192-11196, 1994
A:Title: Molecular characterization of a mouse prostaglandin D receptor and functional e
A:Reference number: I59269; MUID:95062232; PMID:7972033
A:Accession: I59269
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-231 <RES>
A:Cross-references: GB:D29764; NID:9577718; PID:9577719
C:Superfamily: prostaglandin E receptor EP1
Query Match 50.6%; Score 943; DB 2; Length 231;
Best Local Similarity 79.2%; Pred. No. 6.4e-74;
Matches 179; Conservative 19; Mismatches 28; Indels 0; Gaps 0;
QY 6 YRCQNTTSVEKNSAVMGVLFSTGLGNLLALGLLARSGLWCRRPLPLPSVFVMLV 65
Db 5 YRCQNTTSVEKNSAVMGVLFSTGLGNLLALGLLARSGLWCRRPLPLPSVFVMLV 64
QY 66 CGLTVTDLGKLLSPVLAAYQAQRSLRVLPALDNLSCQAFAPFMSFGLSSTLQLLA 125
Db 65 CGLTVTDLGKLLSPVLAAYQAQRSLRVLPALDNLSCQAFAPFMSFGLSSTLQLLA 124
QY 126 MALECWLSLGHPPFYRRHITLRGALVAPVVSFAFALCPALPMGFGKFVQYCPGTWCFI 185
Db 125 MAVECWLSLGHPPFYRRHITLRGALVAPVVSFAFALCPALPMGFGKFVQYCPGTWCFI 184
QY 186 QMVHEGSLSVLGYSVLYSSLMALLVLTVCNLGAMRNLYAMHRLQHRPRCTRDCAE 245
Db 185 QMIIKERSFSGVLSYSSLMALLVLTVCNLGAMRNLYAMHRLQHRPRCTRDCAE 230
RESULT 3
S66674
prostaglandin E receptor EP2 subtype - mouse
C:Species: Mus musculus (house mouse)
C:Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C:Accession: S66674
R:Katsuyama, M.; Nishigaki, N.; Sugimoto, Y.; Morimoto, K.; Negishi, M.; Narumiya, S.; I
FEBS Lett. 372, 151-156, 1995
A:Title: The mouse prostaglandin E receptor EP(2) subtype: cloning, expression, and Nor
A:Reference number: S66674; MUID:96000196; PMID:7556658
A:Accession: S66674
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-362 <KAT>
A:Cross-references: UNIPROT:Q62053; EMBL:D50589; NID:g829048; PID:g8290
C:Superfamily: prostaglandin E receptor EP1
Query Match 38.0%; Score 707.5; DB 2; Length 362;
Best Local Similarity 44.5%; Pred. No. 2e-53;
Matches 159; Conservative 58; Mismatches 115; Indels 25; Gaps 9;
QY 8 CQNTTSVEKNSAVMGVLFSTGLGNLLALGLLARSGLG--WCRRPLPLPSVFVMLV 65
Db 14 CKSQWLLSGSPAISSVMFSGVLSYSSLMALLVLTVCNLGAMRNLYAMHRLQHRPRCTRDCAE 72

QY 66 CGLTVTDLGKLLSPVLAAYQAQRSLRVLPALDNLSCQAFAPFMSFGLSSTLQLLA 125
Db 73 TELVTDLLGKLLSPVLAAYQAQRSLRVLPALDNLSCQAFAPFMSFGLSSTLQLLA 130
QY 126 MALECWLSLGHPPFYRRHITLRGALVAPVVSFAFALCPALPMGFGKFVQYCPGTWCFI 185
Db 131 MALERYLSLGHPPFYRRHITLRGALVAPVVSFAFALCPALPMGFGKFVQYCPGTWCFI 190
QY 186 QMVHEGSLSVLGYSVLYSSLMALLVLTVCNLGAMRNLYAMHRLQHRPRCTRDCAE 245
Db 191 R--HGR-----TAYLQYATMLLLLVAVLACNISVILNLRHRRSR--SRCGLSGSS 241
QY 246 PRADG---REASQPUELDHLLALLMTVLTWCSPVIYRAYGAFKDVKEKNRTS 302
Db 242 LRGPGRRGERTSMAEETDHLILLAIMITITFAICSLPFTIFAYMDETSLSLKEK----- 295
QY 303 AEDLRALFLSVISIVDPWIFIRSPVFRIFHHKIFIRPLRYRSCSNSTNMESS 358
Db 296 -WDLRALFLSVISIVDPWIFIRSPVFRIFHHKIFIRPLRYRSCSNSTNMESS 351
RESULT 4
I38920
prostaglandin E2 receptor - human
C:Species: Homo sapiens (man)
C:Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 09-Jul-2004
C:Accession: I38920
R:Regan, J.W.; Bailey, T.J.; Pepperl, D.J.; Pierce, K.L.; Bogardus, A.M.; Donello, J.E.;
Mol. Pharmacol. 46, 213-220, 1994
A:Title: Cloning of a novel human prostaglandin receptor with characteristics of the pha
A:Reference number: I38920; MUID:94359483; PMID:8078484
A:Accession: I38920
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-358 <RES>
A:Cross-references: UNIPROT:P43116; EMBL:U9487; NID:g639719; PID:AAA61681.1; PID:g6326
C:Superfamily: prostaglandin E receptor EP1
Query Match 37.0%; Score 689; DB 2; Length 358;
Best Local Similarity 43.7%; Pred. No. 7.8e-52;
Matches 157; Conservative 54; Mismatches 118; Indels 30; Gaps 10;
QY 8 CQNTTSVEKNSAVMGVLFSTGLGNLLALGLLARSGLG--WCRRPLPLPSVFVMLV 65
Db 13 CETROWLPGESPAISSVMFSGVLSYSSLMALLVLTVCNLGAMRNLYAMHRLQHRPRCTRDCAE 71
QY 66 CGLTVTDLGKLLSPVLAAYQAQRSLRVLPALDNLSCQAFAPFMSFGLSSTLQLLA 125
Db 72 TELVTDLLGKLLSPVLAAYQAQRSLRVLPALDNLSCQAFAPFMSFGLSSTLQLLA 129
QY 126 MALECWLSLGHPPFYRRHITLRGALVAPVVSFAFALCPALPMGFGKFVQYCPGTWCFI 185
Db 130 MALERYLSLGHPPFYRRHITLRGALVAPVVSFAFALCPALPMGFGKFVQYCPGTWCFI 189
QY 186 QMVHEGSLSVLGYSVLYSSLMALLVLTVCNLGAMRNLYAMHRLQHRPRCTRDCAE 245
Db 190 R--HGR-----TAYLQYATMLLLLVAVLACNISVILNLRHRRSR--SRCGLSGSS 240
QY 246 ----PRADGASPOPLELHLLALLMTVLTWCSPVIYRAYGAFKDVKEKNRTS 301
Db 241 GRGPGARRRGERTSMAEETDHLILLAIMITITFAICSLPFTIFAYMDETSLSLKEK----- 291
QY 302 EAE--DLRALFLSVISIVDPWIFIRSPVFRIFHHKIFIRPLRYRSCSNSTNMESS 357
Db 292 RKEKWDQLALFLSVISIVDPWIFIRSPVFRIFHHKIFIRPLRYRSCSNSTNMESS 350
RESULT 5
S51312
EP2 prostaglandin receptor - human
C:Species: Homo sapiens (man)
C:Date: 07-May-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004
C:Accession: S51312

Circulation 90, 1643-1647, 1994
A:Title: Molecular cloning of human prostacyclin receptor cDNA and its gene expression
A:Reference number: 152867; MUID:95008086; PMID:7923647
A:Accession: 152867
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-386 <RES>
A:Cross-references: GB:D29634; NID:G577629; PID:BAA06110.1; PID:G577630
A:Genetics:

A: Gene: GDB:191316
A: Cross-references: GDB:373439; OMIM:600022
A: Map position: 19q13.3-19q13.3
C: Superfamily: prostaglandin E receptor EPI

C;keywords: transmembrane protein

Query Match	32.0%	Score 597;	DB 2;	Length 386;
Best Local Similarity	42.3%;	Pred. NO. 7.1e-44;		

Qy 8 CQTTTSVEKGSANVGGVLFTSTGLNLLALGLLARSGLGWCRRRPLPSVFYMLVCG 67
:
:
:: :: : : : : : :

Qy 68 LTVTDLKCKLLSPVLVLAAYQNRSLVLA---PALDNSICQAFAPFMSFGLSLTQLL 124

56 LRAIDLUGLSTFUSFAVVAIAKNSLUGLARGGFA-----LCLDAFAFAWIFGSLMSMLLUF 111

125 AMALECWLSGLGHPFFRRHITLRLGALVAPVWSAFSLAFCALPFMGFGKFFVQYCFGTWCF 184

DB	112	AMAVEKCRUWHFYTAQDGGDFRCRKAUFAITAFVCLFCAFLPGLSGRQROUJLPGSNCF	171
Qy	185	IQM--VHEEGSLVGVSYLSMALLVLATVLCNLGMRLNYAMHRRLRQHPRCSTRD	242

00	QY	243	CAEPRADGREASPOQL----	EELDHLLLLALMTLFTMCSLPVIYRAYYGAFKDKVKCKNRT	299
172	DEKWAQPGGA-----	AFSUAIRAGLWALLWALFELCNSVILDSUCTIRAQKQRQOS	---	223	

DD
QY

424 -----LGFPRKUEDEVDHLLRLMIVWMAVCSDFLIIRCTQAVAP-----DS 288

300 SEEADLRALRFLSVISIVDPWFIFIRFSPVR 332

DD 269 SSEMGDLEAFRFIAFNFIUUPWVFIFERNVVFQ 301

RESULT 7

A54416

prostacyclin receptor - mouse

C;Species: Mus musculus (house mouse)

C:\Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 20-Jun-2000

C;Accession: A54416

R;Namba, T.; Oida, H.; Sugimoto, Y.; Kakizuka, A.; Negishi, M.; Ichikawa, A.; Narumiya, Y.

J. Biol. Chem. 269, 9986-9992, 1994

A;Title: cDNA cloning of a mouse prostacyclin receptor. Multiple signaling pathways and

A;Reference number: A54416; MUID:94193694; PMID:7511597

A;Accession: A54416

A;Status: preliminary
M.Molecule type: TPNA

A;Molecule type: mRNA
A.Positions: 1-417 -NAM-

A;Residues: 1-417 <NAM>
 X-Cross-References: CB:026157. NID:0403687. PIDN:BA005144 1. PID:0493688

A;Cross-references: GB:D26157; NID:g493687; PIDN:BAA05144.1; PID:g493688
C.Superfamily: prostaglandin E receptor EP1

C;Superfamily: prostaglandin E receptor EPI

Query Match 32.0%: Score 596.5: DB 2: Length 417:

Query Match 32.0%; Score 596.5; DB 2; Length 417;
Best Local Similarity 42.8%; Pred. No. 8.5e-44;

BEST LOCAL SIMILARITY	42.8%;	PRED. NO. 8.5E-44;
MATCHES 139:	CONSERVATIVE	43: MISMATCHES 114:
		INDELS 29: GAPS 7:

Matches 139; conservative 43; mismatches 114; under 23; gaps 7;

QY 8 QNTTSVEKGN SAVMGGVLFSTGTLGNLLALGLLARSGLGWCRRRLRPLPSVFYMLVCG 67

[illegible]

Db 35 CWNITYVQDSVGPATSTLMFVAGVWGNGLALGILG-----ARR--RSHPSAFAVLVTG 85

[illegible]

Qy 68 LTVTDLLGKCLLSPVVLAAAYAQNRSRLVLPALDNSLCQAFAFMFSSFFGLSSTLQLLAMA 127

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Db 86 LAVTDLLGTCFLSPAVFVAYARNSSLLGLAHG-GTMLCDTFAFAMTFFGLASTLILFAMA 144

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QY 128 LECWLSLGHGPFYRRHITLRLGALVAPVVSFAFSLAFALCFPMGFGKFVQYCPGTWCFIOM 187
Db 145 VERCLALSHPLYAQDGGPCARFALPSIYAFCLFCSPLLLGLGHEHQYCPGSCWCFIRM 204
QY 188 VHEEGSLVGLGYSLVYSSLMALLVTLATVLCNLGAMRNLYAMHRRLQHRPRSCSTRDCAEP 247
Db 205 --RSAQPGGCAFAFSLAYASLWALLVTSIFFCNGSVTLISLHYMYRQRRHGSFV-----PT 257
QY 248 ADGREGASPOPLELDLHLLALMTVLFMTCSLPVIYRAYGAFKDVKEKRTSEBAEDLR 307
Db 258 SRARE-----DEVYHLILLALMTVMVAVCSLPMIRGTQAIAP-----DSREMGDLL 305
QY 308 ALRFLSVISIVDPWFIFIRSPVFR 332
Db 306 AFRFNAFNILDPWFILFRKAVFQ 330

RESULT 8
S52078
prostaglandin - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 14-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
C;Accession: S52078
R;Sasaki, Y.; Usui, T.; Tanaka, I.; Nakagawa, O.; Sando, T.; Takahashi, T.; Namba, T.; N
Biochim. Biophys. Acta 1224, 601-605, 1994
A;Title: Cloning and expression of a cDNA for rat prostacyclin receptor.
A;Reference number: S52078; MUID:95101758; PMID:7803522
A;Accession: S52078
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-416 <SAS>
A;Cross-references: UNIPROT:P43253; GB:D28966; NID:G602775; PIDN:BA06091.1; PID:G602776
C;Superfamily: prostaglandin E receptor EPI

Query Match 31.4%; Score 585.5; DB 2; Length 416;
Best Local Similarity 42.6%; Pred. No. 7.5e-43;
Matches 139; Conservative 44; Mismatches 112; Indels 31; Gaps 8;

QY 8 QNNTSVKGNKSAVMGVLFTSLGLLGNLLALGALLARSLGLWCGRRLPLPSVFMVLCG 67
Db 34 CWNITVQDSVGPATSTLMTFVAGVGNLGLILG-----ARR--RSHPSAFALVTG 84
QY 68 LTVTDLGLKLLSPVLAAYQNRSLRVLAPALDNLSCQAFAPFMSFFGLSSTLQLLAWA 127
Db 85 LAVTDLGTCTSPAVFAYVARNSSLLGLANG--GTMCDCTFAFAMIFFGLASTLILFAMA 143
QY 128 LECWLSLGHGPFYRRHITLRLGALVAPVVSFAFSLAFALCFPMGFGKFVQYCPGTWCFIOM 187
Db 144 VERCLALSHPLYAQDGGPCARLALPAIYAFCLFCSPLLLGLGHEHQYCPGSCWCFIRM 203
QY 188 -VHEEGSLVGLGYSLVYSSLMALLVTLATVLCNLGAMRNLYAMHRRLQHRPRSCSTRDCAEP 246
Db 204 RSPQPGGCA---FSLAYASLWALLVTSIFFCNGSVTLISLCHMYRQRRHGSFV-----P 255
QY 247 ADGREGASPOPLELDLHLLALMTVLFMTCSLPVIYRAYGAFKDVKEKRTSEBAEDL 306
Db 256 TSARE-----DEVYHLILLALMTGMVAVCSLPLIRGTQAIAP-----DSREMGDLL 303
QY 307 RALRFLSVISIVDPWFIFIRSPVFR 332
Db 304 HAFRFNAFNILDPWFILFRKAVFQ 329

RESULT 9
A46638
prostaglandin E receptor EP2 subtype - mouse
C;Species: Mus musculus (house mouse)
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A46638
R;Honda, A.; Sugimoto, Y.; Namba, T.; Watabe, A.; Irie, A.; Negishi, M.; Narumiya, S.; I
J. Biol. Chem. 268, 7759-7762, 1993
A;Title: Cloning and expression of a cDNA for mouse prostaglandin E receptor EP2 subtype
A;Reference number: A46638; MUID:93216741; PMID:8385118
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A;Accession: A46638
A;Status: preliminary
A;Molecule type: nucleic acid
A;Residues: 1-513 <HON>
A;Cross-references: UNIPROT:P32240; GB:D13458; NID:G303699; PIDN:BA02714.1; PID:G303700
A;Experimental source: mastocytoma P-815 cells
A;Note: sequence extracted from NCBI backbone (NCBIN:128997, NCBIP:128998)
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; transmembrane protein

Query Match 24.6%; Score 458.5; DB 2; Length 513;
Best Local Similarity 31.9%; Pred. No. 8.2e-32;
Matches 118; Conservative 65; Mismatches 132; Indels 55; Gaps 11;

QY 1 MKSPFYRCNTTSVEKGN SAV-MGGVLFSTGLLGNLLALGALLARSLGLWCGRRLPLPS 59
Db 26 MSIPGVNASFSSTPERLNSPVTIPAVMFIFGVVGNLVAIVLCK-----SRKEQK--ET 77
QY 60 VFYMLVCGLTVDLLGKLLSPVLAAYQNRSLRVLAPALDNLSCQAFAPFMSFFGLSS 119
Db 78 TFYTLVCGLAVTDLLGTLVSPVTIATYMKGQ-----WFG-DOALCDYSTFILLFFGLSG 131
QY 120 TLQLLAWALECWLSLGHGPFYRRHITLRLGALVAPVVSFAFSLAFALCFPMGFGKFVQYCP 179
Db 132 LSIICAMSIERYLAINHAFYSHYVDKRLAGLTIFAIVASNVLFALPNNMGLGRSEROYP 191
QY 180 GTWCFTQMVHEGSLVLCY---SVLYSSLMALLVTLATVLCNLGAMRNLYAMHRRLQ-- 234
Db 192 GTWCFTI-----DWTNTVTAAYAFSYNYAGFSFLILATVLCNVLVCGALLMRHQFMRRT 246
QY 235 -----HPRSTRCDCAEPDRGASPPQLE-----ELDHLLLLALMT 271
Db 247 SLGTEQHAAAAAASVACRGHAGASPALQRLSDFRFRSFPRIAGAEIQWILLIATS 306
QY 272 VLFTMCSLPVIYRAYYGA FKD---VKEKRTSEEAEDLRALRFLSVISIVDPWFIFIRS 328
Db 307 LVVLICSIPLVVRVFNQLYQPNVVKD1SRN-----PDQAIRIASVNPILDPWIYILLRK 362
QY 329 PVFPIFFHKI 338
Db 363 TVLSKAIEKI 372

RESULT 10
JC2241
prostaglandin E receptor EP2 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 28-Aug-1985 #sequence_revision 07-Oct-1994 #text_change 09-Jul-2004
C;Accession: JC2241
R;Sando, T.; Usui, T.; Tanaka, I.; Mori, K.; Sasaki, Y.; Fukuda, Y.; Namba, T.; Sugimoto,
Biochem. Biophys. Res. Commun. 200, 1329-1333, 1994
A;Title: Molecular cloning and expression of rat prostaglandin E receptor EP2 subtype.
A;Reference number: JC2241; MUID:94241990; PMID:8185583
A;Accession: JC2241
A;Molecule type: mRNA
A;Residues: 1-488 <SAS>
A;Cross-references: UNIPROT:P43114; DBJ:D28860; NID:G516827; PIDN:BA06011.1; PID:G51682
C;Superfamily: vertebrate rhodopsin
C;Keywords: glycoprotein; phosphoprotein; receptor; transmembrane protein
F;20-44/Domain: transmembrane #status predicted <TM1>
F;56-79/Domain: transmembrane #status predicted <TM2>
F;97-116/Domain: transmembrane #status predicted <TM3>
F;136-160/Domain: transmembrane #status predicted <TM4>
F;185-211/Domain: transmembrane #status predicted <TM5>
F;271-298/Domain: transmembrane #status predicted <TM6>
F;316-335/Domain: transmembrane #status predicted <TM7>
F;7,177/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;222,262,373,374/Binding site: phosphate (Ser) (covalent) (by CAMP-dependent kinase) #st
Query Match 24.3%; Score 452.5; DB 2; Length 488;
Best Local Similarity 32.7%; Pred. No. 2.6e-31;
Matches 121; Conservative 66; Mismatches 128; Indels 55; Gaps 13;
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EP3-alpha receptor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 07-May-1995 #sequence_revision 01-Sep-1995 #text_change 23-Jul-1999
C:Accession: S51280
R:Neuschaefer-Rube, F.; de Vries, C.; Haenecke, K.; Jungermann, K.; Poeschel, G.P.
submitted to the EMBL Data Library, January 1995
A:Reference number: S51280
A:Accession: S51280
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-366 <NEU>
A:Cross-references: EMBL:X83855; NID:g633623; PIDN:CAA58735.1; PID:g633624
C:Superfamily: prostaglandin E receptor EP1

Query Match 16.8%; Score 313.5; DB 2; Length 366;
Best Local Similarity 28.8%; Pred. No. 1.9e-19;
Matches 105; Conservative 61; Mismatches 148; Indels 53; Gaps 13;

QY 10 NTTSEKGNVAVGG---VLFSTGLGNLALGLLARSGLGWCRRPLRLPLPSVFMVLC 66
Db 16 NQSSAADGCGSVSVAFPIITMTVTGFGNALMLLVRS-----YRRRESKRKKSFLLCIG 70

QY 67 GLTVDLLGKLLSPVLAAYQNRSRLVLAAPALDNLSCQAFAPFMSFFGLSSTLQLLAM 126
Db 71 WLALTDLVGQLTSPVILVLSQRWEQLDPS--GRLCTFFGLTMTVFGLSLLVASAM 128

QY 127 ALECWLSLGHPPFFYRRHITRLGALVAPVVSASFALFALCFALPFMGFKGVQVCPGTWCFI- 185
Db 129 AVERALAIRAPHWYASHMKTRATRAVLVGLVWLSVLAFLPVLGVSRYVQWPGTWCFTS 188

QY 186 -----QMVHEGSLVGLSVYSSLMALLVLATVLCNLGAMRNLYAMHRRLQHRP 237
Db 189 TGPAGNETDSAREPGSVA---FASAFACGLGALLVVTFACTNLATIKALVS----- 235

QY 238 SCTRDCAEPRAD---GREASPOPLELDHLLALMTVLTMCSPVIVRYAYGAFKDV 294
Db 236 RCRAKAAASQSAQWGRITTTETAIQ-----LMGIMCVL-SVCWSPLLIMLMKMFNQMS 288

QY 295 E---KNRTSEAE---DLRALRFLSVISIVDPWIFIRSPVFRIFPHKIFIRPLRYRSR 348
Db 289 VEQCKTQMGKEKCNFSFLIAVRLASNLQILDPPWVYLLLRKILLRKFCQ---IRD--HTNY 343

QY 349 CSNSTNM 355
Db 344 ASSSTSL 350

RESULT 14
A42414
Prostaglandin E receptor EP3 subtype - mouse
C:Species: Mus musculus (house mouse)
C:Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
R: Sugimoto, Y.; Namba, T.; Honda, A.; Hayashi, Y.; Negishi, M.; Ichikawa, A.; Narumiya, J. Biol. Chem. 267, 6463-6466, 1992
A:Title: Cloning and expression of a cDNA for mouse prostaglandin E receptor EP3 subtype
A:Reference number: A42414; MUID:92202182; PMID:1372606
A:Accession: A42414
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-365 <SUG>
A:Cross-references: UNIPROT:P30557; GB:D10204; NID:g220571; PIDN:BAA01051.1; PID:g220572
A>Note: sequence extracted from NCBI backbone (NCBIN:89525, NCBI:P:89530)
C:Superfamily: prostaglandin E receptor EP1
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 16.5%; Score 308; DB 2; Length 365;
Best Local Similarity 28.5%; Pred. No. 5.5e-19;
Matches 105; Conservative 66; Mismatches 139; Indels 58; Gaps 15;

QY 10 NTTSEKGNVAVGGV-LFSTGLGNLALGLLARSGLGWCRRPLRLPLPSVFMVLC 68
Db 18 SSTDDCGSVSVAFPIITMTVTGFGNALMLLVRS-----YRRRESKRKKSFLLCIG 72

QY 69 TVTDLGKLLSPVLAAYQNRSRLVLAAPALDNLSCQAFAPFMSFFGLSSTLQLLAMAL 128
Db 73 ALTDLVGQLTSPVILVLSQRWEQLDPS--GRLCTFFGLTMTVFGLSLLVASAMAV 130

QY 129 ECLWLSLGHPPFFYRRHITRLGALVAPV---VSASFALFALCFALPFMGFKGVQVCPGTWCFI 185
Db 131 ERALAIRAPHWYASHMKTR---ATFVLLGVWLSVLAFLPVLGVSRYVQWPGTWCFT 186

QY 186 QM-----VHEGSLVGLSVYSSLMALLVLATVLCNLGAMRNLYAMHRRLQHRP 236
Db 187 STGPAGNETDPAEPGSVA---FASAFACGLGALLVVTFACTNLATIKALVS----- 234

QY 237 RSCTRDCAEPRAD---GREASPOPLELDHLLALMTVLTMCSPVIVRYAYGAFKDV 293
Db 235 -RCRAKAAVSQSAQWGRITTTETAIQ-----LMGIMCVL-SVCWSPLLIMLMKMFNQM 286

QY 294 KE---KNRTSEAE---DLRALRFLSVISIVDPWIFIRSPVFRIFPHKIFIRPLRYRS 347
Db 287 SVEQCKTQMGKEKCNFSFLIAVRLASNLQILDPPWVYLLLRKILLRKFCQ---IRD--HTN 341

QY 348 RCSNSTNM 355
Db 342 YASSSTSL 349

RESULT 15
JN0693
Prostaglandin E2 receptor EP3 chain - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 09-Jul-2004
C:Accession: JN0693; PN0551; S40683
R:Takeuchi, K.; Abe, T.; Takahashi, N.; Abe, K.
Biochem. Biophys. Res. Commun. 194, 885-891, 1993
A:Title: Molecular cloning and intrarenal localization of rat prostaglandin E2 receptor
A:Reference number: S40683; MUID:93343951; PMID:8393672
A:Accession: JN0693
A:Molecule type: mRNA
A:Residues: 1-365 <TAK>
A:Cross-references: UNIPROT:P34980; GB:D14869; NID:g467530; PIDN:BAA03585.1; PID:g467531
A:Accession: PN0551
A:Molecule type: protein
A:Residues: 336-365 <TAK>
C:Comment: This protein exerts an inhibitory effect on water and sodium reabsorption by
C:Superfamily: prostaglandin E receptor EP1
C:Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane protein

F:31-55/Domain: transmembrane #status predicted <TM1>
F:69-89/Domain: transmembrane #status predicted <TM2>
F:109-130/Domain: transmembrane #status predicted <TM3>
F:152-173/Domain: transmembrane #status predicted <TM4>
F:204-229/Domain: transmembrane #status predicted <TM5>
F:260-283/Domain: transmembrane #status predicted <TM6>
F:304-325/Domain: transmembrane #status predicted <TM7>
F:16,193/Binding site: carboxylate (Asn) (covalent) #status predicted
F:59,64/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 16.5%; Score 308; DB 2; Length 365;
Best Local Similarity 28.6%; Pred. No. 5.5e-19;
Matches 106; Conservative 60; Mismatches 144; Indels 60; Gaps 15;

QY 10 NTTSEKGNVAVGG---VLFSTGLGNLALGLLARSGLGWCRRPLRLPLPSVFMVLC 66
Db 16 NQSSAADGCGSVSVAFPIITMTVTGFGNALMLLVRS-----YRRRESKRKKSFLLCIG 70

QY 67 GLTVDLLGKLLSPVLAAYQNRSRLVLAAPALDNLSCQAFAPFMSFFGLSSTLQLLAM 126
Db 71 WLALTDLVGQLTSPVILVLSQRWEQLDPS--GRLCTFFGLTMTVFGLSLLVASAM 128

QY 127 ALECWLSLGHPPFFYRRHITRLGALVAPV---VSASFALFALCFALPFMGFKGVQVCPGTWTC 183
Db 129 AVERALAIRAPHWYASHMKTR-----ATFVLLGVWLSVLAFLPVLGVSRYVQWPGTWC 184

QY 184 FI-----QMVHEGSLVGLSVYSSLMALLVLATVLCNLGAMRNLYAMHRRLQ 234

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Db 185 FISTGPAGNETDSAREPGSVA---FASAFACLGGLLALVVTTFACNLATIKALVS----- 234
Qy 235 HPRSCTRDCAEPRAD---GREASQPLEELDLHLLALMTVLTMCSLPVIYRAYYGAFK 291
Db 235 ---RCRAKAAASQSSAQWGRITTETAIQ-----LMGIMCVL-SVCWSPLLIWMLKMFN 284
Qy 292 DVKE---KNRTSEAE---DLRALRFLSVISIVDPWIFIIFRSPVFRIFPHKIFIRPLRY 345
Db 285 QMSVEQCKTQMGKEKCNCSFLIAVRLASLNQILDPPWYLLLRKILLRKFQ---IRD--H 339
Qy 346 RSRCNSNTNM 355
Db 340 TNYASSTSL 349

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Search completed: April 22, 2005, 21:30:02
 Job time : 17.5389 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 22, 2005, 18:00:17 ; Search time 63.5786 Seconds

(without alignments)
2891.482 Million cell updates/sec

Title: US-10-689-861-4

Perfect score: 1864
Sequence: 1 MKSPFRCQNTTSVEKNSA.....IRPLRYSRCSNTMSSL 359

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03:.*
1: uniprot_sprot:.*
2: uniprot_trembl:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1864	100.0	359	1 P22R_HUMAN	Q13258 homo sapien
2	1388.5	74.5	357	2 O9R261	O9R261 rattus norv
3	1386.5	74.4	357	2 O35932	O35932 rattus norv
4	1347.5	72.3	357	1 P22R_MOUSE	P70263 rattus norv
5	1342.5	72.0	357	2 O8CQK3	O8CQK3 mus musculu
6	714	38.3	361	1 P222_CANFA	O9XCH2 canis famli
7	707.5	38.0	362	1 P222_MOUSE	O62053 mus musculu
8	688	36.9	358	1 P222_HUMAN	O63928 rattus norv
9	674	36.2	357	1 P222_MOUSE	O8H157
10	665	35.7	361	2 O8H157	O8H157 oryctolagus
11	662	35.5	352	2 O8M009	O8M009 bos taurus
12	658.5	35.3	371	2 O6N215	O6N215 xenopus lae
13	628.5	33.7	385	1 P12R_BOVIN	P79393 bos taurus
14	597	32.0	386	1 P12R_HUMAN	P43119 homo sapien
15	592.5	32.0	415	1 P12R_MOUSE	P43252 mus musculu
16	585.5	31.8	408	2 O8B275	O8B275 mus musculu
17	585.5	31.4	416	1 P12R_RAT	P43253 rattus norv
18	497.5	26.7	481	2 O6PFT8	O6PFT8 brachydanto
19	458.5	24.6	488	2 O91VE4	O91VE4 mus musculu
20	458.5	24.6	513	1 P224_MOUSE	P33240 mus musculu
21	452.5	24.3	488	1 P224_RAT	P43114 rattus norv
22	446.5	24.0	492	2 O8M008	O8M008 bos taurus
23	445	23.9	492	2 O9T016	O9T016 canis famli
24	443	23.8	488	1 P224_HUMAN	P34008 homo sapien
25	442	23.7	490	2 O95J39	O95J39 macaca fasc
26	442	23.7	490	2 O7JGJ7	O7JGJ7 papio hamae
27	440	23.6	490	1 P224_PANTR	O95K10 pan troglod
28	436.5	23.4	488	1 P224_RABIT	O28691 oryctolagus
29	393	21.1	488	2 O7TSX4	O7TSX4 rattus norv
30	316.5	17.0	154	2 O7TSX3	O7TSX3 mus musculu
31	312	16.7	362	2 O6P2F2	O6P2F2 mus musculu

32	310	16.6	360	2 O99PG3	O99PG3 rattus norv
33	308	16.5	365	1 P223_MOUSE	P30557 mus musculu
34	308	16.5	365	1 P223_RAT	P34980 rattus norv
35	302.5	16.2	416	2 O6VPS5	O6VPS5 canis famli
36	300.5	16.1	168	2 O95M50	O95M50 bos taurus
37	300.5	16.1	370	2 O6VPS4	O6VPS4 canis famli
38	297.5	16.0	390	1 P223_HUMAN	P43115 homo sapien
39	296.5	15.9	411	1 P223_RABIT	P46069 oryctolagus
40	292.5	15.7	369	1 P223_HUMAN	P21731 homo sapien
41	292.5	15.7	407	2 O75228	O75228 homo sapien
42	291.5	15.6	366	2 O6TTN3	O6TTN3 homo sapien
43	291.5	15.6	393	2 O00326	O00326 homo sapien
44	291.5	15.6	402	2 O00325	O00325 homo sapien
45	284.5	15.3	417	1 P223_BOVIN	P34979 bos taurus

ALIGNMENTS

RESULT 1
PD2R_HUMAN STANDARD; PRT; 359 AA.
ID PD2R_HUMAN Q13258; Q13250; Q13251;
AC Q13258; Q13250; Q13251;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Prostaglandin D2 receptor (Prostanoid DP receptor) (P2D receptor).
GN Name=PTGDR;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=55370201; PubMed=7642548; DOI=10.1074/jbc.270.32.18910;
RA Bole Y., Sawyer N., Slipeck D.M., Metters K.M., Abramovitz M.;
RT "Molecular cloning and characterization of the human prostanoid DP
receptor.";
RL J. Biol. Chem. 270:18910-18916(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Straube R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toibiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loggiano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunnarsson P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Buttefield Y.S.N., Krzywicki M.I., Skalek U., Smalins D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
proc. Natl. Acad. Sci. U.S.A. 99:16999-16903(2002).
-!- FUNCTION: Receptor for prostaglandin D2 (PGD2). The activity of
this receptor is mainly mediated by G(i)s proteins that stimulate
adenylate cyclase, resulting in an elevation of intracellular
cAMP. A mobilization of calcium is also observed, but without
formation of inositol 1,4,5-trisphosphate.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- TISSUE SPECIFICITY: Expressed in retina and small intestine.
-!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
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CC or send an email to license@isb-sib.ch).

DR EMBL: U31332; AAC50178.1; -;
DR EMBL: U31098; AAC50176.1; -;
DR EMBL: U31099; AAC50177.1; -;
DR EMBL: BC040968; AAC40968.1; -;
DR PIR: I39153; I39153.
DR Genem: HGNC:9591; PTGDR.
DR MIM: 604687; -;
DR GO: GO:0016021; C:integral to membrane; NAS.
DR GO: GO:0004956; F:prostaglandin D receptor activity; NAS.
DR GO: GO:0007186; F:G-protein coupled receptor protein signalin. . .; NAS.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR InterPro: IPR000376; Pglndnd_receptor.
DR InterPro: IPR008365; Prostanoidrecept.
DR InterPro: IPR001105; Thbox_receptor.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PRO1788; PROSTANOIDR.
DR PRINTS: PRO0429; THROMBOXANER.
DR PROSITE: PS00237; G_PROTEIN_RECP_F1_1; FALSE_NEG.
DR PROSITE: PS50262; G_PROTEIN_RECP_F1_2; 1.
KW G-protein coupled receptor; Glycoprotein; Transmembrane.
FT DOMAIN 1 21
FT TRANSMEM 22 42
FT TRANSMEM 43 59
FT TRANSMEM 60 80
FT TRANSMEM 81 107
FT TRANSMEM 108 128
FT TRANSMEM 129 150
FT TRANSMEM 151 171
FT TRANSMEM 172 195
FT TRANSMEM 196 216
FT TRANSMEM 217 262
FT TRANSMEM 263 283
FT DOMAIN 284 310
FT TRANSMEM 311 331
FT TRANSMEM 332 359
FT DISULFID 105 183
FT CARBOHYD 10 10
FT CARBOHYD 90 90
FT CARBOHYD 297 297
SQ SEQUENCE 359 AA; 40270 MW; 098F89F38D0BE12A CRC64;

Query Match 100.0%; Score 1854; DB 1; Length 359;
Best Local Similarity 100.0%; Pred. No. 4.1e-137;
Matches 359; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKSPFYRCNTTSYVEKNSAVMGVLFSTGLGNLALGLARSGLGMSRRPLRPLPSV 60
DB 1 MKSPFYRCNTTSYVEKNSAVMGVLFSTGLGNLALGLARSGLGMSRRPLRPLPSV 60
QY 61 FYMLVCGITVTDLIGKCLISPVLAAYVONRSRLVAPALDNLCOAFAPFMSFGSLST 120
DB 61 FYMLVCGITVTDLIGKCLISPVLAAYVONRSRLVAPALDNLCOAFAPFMSFGSLST 120
QY 121 LQLLAMLECWLSLGHFFRYRHITRLGALVAPVSAFSLAFCLPFMGFKFVQYCPG 180
DB 121 LQLLAMLECWLSLGHFFRYRHITRLGALVAPVSAFSLAFCLPFMGFKFVQYCPG 180
QY 181 TWCFIQWHEBGSLSVLGYSSLMALVLAIVLCNLGAMRNLYAMHRRLOQRHPSCT 240
DB 181 TWCFIQWHEBGSLSVLGYSSLMALVLAIVLCNLGAMRNLYAMHRRLOQRHPSCT 240
QY 241 RDCGAPRADGSAPOPLEEIDHLLALMTVLFMCSLPVYRAYYGAFFDVKEKRTS 300
DB 241 RDCGAPRADGSAPOPLEEIDHLLALMTVLFMCSLPVYRAYYGAFFDVKEKRTS 300
QY 301 EEAEDLRALRFLSVISIVDPWFIIFRSVPFRIFPHKIFIRPLRYRRCNSNTMESTL 359

DB 301 EEAEDLRALRFLSVISIVDPWFIIFRSVPFRIFPHKIFIRPLRYRRCNSNTMESTL 359

RESULT 2
Q9R261 ID PRELIMINARY; PRT; 357 AA.
AC Q9R261;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Prostaglandin D2 receptor.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STEAIN=Sprague-Dawley;
RX MEDLINE=99376163; PubMed=10448933; DOI=10.1016/S0014-2999(99)00358-1;
RA Wright D.H., Nantel F., Metters K.M., Ford-Hutchinson A.W.;
RT "A novel biological role for prostaglandin D2 is suggested by
RT distribution studies of the rat Dp prostanoid receptor.";
RL Eur. J. Pharmacol. 377:101-115 (1999).
DR EMBL: AF120101; AAD23564.1; -;
DR GO: GO:0016021; C:integral to membrane; IEA.
DR GO: GO:0004956; F:prostaglandin D receptor activity; IEA.
DR GO: GO:0004972; F:receptor activity; IEA.
DR GO: GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO: GO:0004960; F:chromoblastane receptor activity; IEA.
DR GO: GO:0007186; F:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR InterPro: IPR000376; Pglndnd_receptor.
DR InterPro: IPR008365; Prostanoidrecept.
DR InterPro: IPR001105; Thbox_receptor.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PRO1788; PROSTANOIDR.
DR PRINTS: PRO0854; PRSTNOIDPR.
DR PRINTS: PRO0429; THROMBOXANER.
DR PROSITE: PS50262; G_PROTEIN_RECP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 357 AA; 39768 MW; A65E1355E52B8286 CRC64;

Query Match 74.5%; Score 1388.5; DB 2; Length 357;
Best Local Similarity 76.1%; Pred. No. 4.4e-100;
Matches 271; Conservative 30; Mismatches 50; Indels 5; Gaps 2;

QY 6 YRCQNTTSYVEKNSAVMGVLFSTGLGNLALGLARSGLGMSRRPLRPLPSVFMV 65
DB 5 YRCQNTTSYVEKNSAVMGVLFSTGLGNLALGLARSGLGMSRRPLRPLPSVFMV 65
QY 66 CGLTVTDLIGKCLISPVLAAYVONRSRLVAPALDNLCOAFAPFMSFGSLSTLQLLA 125
DB 66 CGLTVTDLIGKCLISPVLAAYVONRSRLVAPALDNLCOAFAPFMSFGSLSTLQLLA 125
QY 126 MALECWLSLGHFFRYRHITRLGALVAPVSAFSLAFCLPFMGFKFVQYCPGTCFI 185
DB 126 MALECWLSLGHFFRYRHITRLGALVAPVSAFSLAFCLPFMGFKFVQYCPGTCFI 185
QY 185 QMIHKRSFSVIGFSVLYSSLMALVLAIVLCNLGAMRNLYAMHRRLOQRHPSCT 244
DB 185 QMIHKRSFSVIGFSVLYSSLMALVLAIVLCNLGAMRNLYAMHRRLOQRHPSCT 244
QY 246 PRADGSAPOPLEEIDHLLALMTVLFMCSLPVYRAYYGAFFDVKEKRTSEAD 305
DB 246 PRADGSAPOPLEEIDHLLALMTVLFMCSLPVYRAYYGAFFDVKEKRTSEAD 305
QY 306 LRALRFLSVISIVDPWFIIFRSVPFRIFPHKIFIRPLRYRRCNSNTMESTL 359
DB 306 LRALRFLSVISIVDPWFIIFRSVPFRIFPHKIFIRPLRYRRCNSNTMESTL 359

035932 ID 035932 PRELIMINARY; PRT; 357 AA.
 AC 035932;
 DT 01-JAN-1998 (TREMBLrel. 05, Created)
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Prostaglandin D2 receptor.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxId=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Retina;
 RX MEDLINE=98387174; PubMed=9721719;
 RA Geraschenko D., Beuckmann C.T., Kanaoka Y., Eguchi N., Gordon W.C.,
 RA "Uradu Y., Baaran N.G., Hayashi O.,
 RT "Dominant expression of rat prostanoic acid D receptor mRNA in
 RT leptomeninges, inner segments of photoreceptor cells, iris epithelium,
 RT and ciliary processes.";
 RL J. Neurochem. 71:937-945(1998).
 DR EMBL: U92289; AAB71762.1; -
 DR GO: GO:0016021; C: integral to membrane, IEA.
 DR GO: GO:0004956; F: prostaglandin D receptor activity, IEA.
 DR GO: GO:0004872; F: receptor activity, IEA.
 DR GO: GO:0001584; F: rhodopsin-like receptor activity, IEA.
 DR GO: GO:0004960; F: rhodopsin-like receptor activity, IEA.
 DR GO: GO:0007186; P: G-protein coupled receptor protein signalin. . .; IEA.
 DR Interpro: IPR000276; GPCR_Rhodopsn.
 DR Interpro: IPR000376; Gplndnd_receptor.
 DR Interpro: IPR008365; Prostanoidrecept.
 DR Interpro: IPR001105; Thbox_receptor.
 DR Pfam: PF00001; 7tm.1.1.
 DR PRINTS: PRO1786; PROSTANOIDR.
 DR PRINTS: PRO0854; PROSTNOIDDR.
 DR PRINTS: PRO0429; THROMBOXANR.
 DR PROSITE: PSS0262; G_PROTEIN_RECPT_FL_2; 1.
 KM RECEPTOR.
 SQ SEQUENCE 357 AA; 39802 MW; DB966276DD68184C CRC64;
 Query Match 74.4%; Score 1386.5; DB 2; Length 357;
 Best Local Similarity 76.1%; Pred. No. 6.3e-100;
 Matches 271; Conservative 30; Mismatches 50; Indels 5; Gaps 2;
 QY 6 YRCNTSVKSGKSAVWGVLFTSGTLGNLTAAGLARSIGKGRRLPLRLPVEFMV 65
 DB 5 YRCQAAWVERGSSATNGVLFSAGLGNLTAAGLARSIGKGRRLPRLPVEFMV 64
 QY 66 CGLTVDLLGKCLSPVLAAYQNRSLRYLAPALDNSLCOAFAPFMSFGLSTTQLLA 125
 DB 65 CGLTIVHLGKCLSPVLAAYQNRSLRYLAPALDNSLCOAFAPFMSFGLSTTQLLA 124
 QY 126 MALECWLSLGHPPFYRRHITLRLGALVAPVSAFSLAFCALPFMGFGKPVQYCGTWCFT 185
 DB 125 MALECWLSLGHPPFYRRHITLRLGALVAPVSAFSLAFCALPFMGFGKPVQYCGTWCFT 184
 QY 186 QMHEGSGSLVAGSYVYSSIMLVATVLCNLGAMRNRYAMRRLOQRPRSTPCAE 245
 DB 185 QMHEGSGSLVAGSYVYSSIMLVATVLCNLGAMRNRYAMRRLOQRPRSTPCAE 244
 QY 246 PRADGSEASPOPEEDLHLLALMTVLFTMCSLPVYRAYVYGAFOVKEKNTSEAD 305
 DB 245 SGSDYRHGSPNPEEDLHLLALMTVLFTMCSLPVYRAYVYGAFOVKEKNTSEAD 304
 QY 306 LRAARLPLSVISIVDPWFIIFRSPVFRIFPHKIFIRPLARYSRCSNS--TNMESL 359
 DB 302 LQALRPLSVISIVDPWFIIFRSPVFRIFPHKIFIRPLARYSRCSNS--TNMESL 357
 RESULT 4
 PDR_MOUSE STANDARD; PRT; 357 AA.
 ID PD2R_MOUSE
 AC P70263;

DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Prostaglandin D2 receptor (Prostanoid DP receptor) (PGD receptor).
 GN Name=Pgdrt;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/Sv; TISSUE=Lung;
 RX MEDLINE=95062232; PubMed=7972033;
 RA Hirata M., Kakizuka A., Aizawa M., Ushikubi F., Narumiya S.,
 RT "Molecular characterization of a mouse prostaglandin D receptor and
 RT functional expression of the cloned gene.";
 RL Proc. Natl. Acad. Sci. U.S.A. 91:11192-11196(1994).
 CC -1- FUNCTION: Receptor for prostaglandin D2 (PGD2). The activity of
 CC this receptor is mainly mediated by G(s) proteins that stimulate
 CC adenylyl cyclase, resulting in an elevation of intracellular
 CC cAMP. A mobilization of calcium is also observed, but without
 CC formation of inositol 1,4,5-trisphosphate.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- TISSUE SPECIFICITY: Most abundantly expressed in the ileum,
 CC followed by lung, stomach and uterus.
 CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
 CC -----
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 CC -----
 DR EMBL: D29765; BAA06168.1; -
 DR EMBL: D29764; BAA06168.1; JOINED.
 DR MGI: M102966; Pgdrt.
 DR GO: GO:0004856; F: prostaglandin D receptor activity, IDA.
 DR GO: GO:0001785; F: prostaglandin J receptor activity, IDA.
 DR Interpro: IPR000276; GPCR_Rhodopsn.
 DR Interpro: IPR000376; Gplndnd_receptor.
 DR Interpro: IPR008365; Prostanoidrecept.
 DR Interpro: IPR001105; Thbox_receptor.
 DR Pfam: PF00001; 7tm.1.1.
 DR PRINTS: PRO1786; PROSTANOIDR.
 DR PRINTS: PRO0854; PROSTNOIDDR.
 DR PROSITE: PSS0237; G_PROTEIN_RECPT_FL_1; FALSE_NEG.
 DR PROSITE: PSS0262; G_PROTEIN_RECPT_FL_2; 1.
 DR G-protein coupled receptor; Glycoprotein; Transmembrane.
 KW DOMAIN 1
 FT TRANSSEM 1 20
 FT TRANSSEM 21 41
 FT DOMAIN 42 58
 FT TRANSSEM 59 79
 FT DOMAIN 80 106
 FT TRANSSEM 107 127
 FT DOMAIN 128 149
 FT TRANSSEM 150 170
 FT DOMAIN 171 194
 FT TRANSSEM 195 215
 FT DOMAIN 216 261
 FT TRANSSEM 262 282
 FT DOMAIN 283 306
 FT TRANSSEM 307 327
 FT DOMAIN 328 357
 FT DISULFID 104 182
 FT CARBOHYD 2 2
 FT TRANSSEM 89 89
 SQ SEQUENCE 357 AA; 40005 MW; 91CBFF7A5396B505 CRC64;
 Query Match 72.3%; Score 1347.5; DB 1; Length 357;
 Best Local Similarity 73.3%; Pred. No. 6.9e-97;
 Matches 261; Conservative 39; Mismatches 51; Indels 5; Gaps 2;

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QY 6 YRCNTTSVEKGNASVWGVLFSTGILLGNLLALGLARSGLGWCSRRRLPLPSVFMV
DB 5 YRCQTSIHWBERGSATATGAVLFGAGLLGNLLALVILARSGLGCRPPLPSPSVFVLV
QY 66 CGLTVDLLKCLISPVVLAAYANONSLRYLAPALDNLSCQAFAPFMSFFGLSSTQLLA
DB 65 CGLTVDLLKCLISPVVLAAYANONSLKELLPASGNQCEBFAFLMSFFGLASTQLLA
QY 126 MALECMWLSLGHPPFYRRHITRLGALVAPVVSASFALCPALPFMGPKFPQYCGTWCFFI
DB 125 MAVECMWLSLGHPPFYRRHITRLRGVLAAPVVAACFLAFCALPFAFGKFPQYCGTWCFFI
QY 186 QMVEBESLSLVGVSVYSSIMALLVATVLCNIGAMRNLYAMHRLQRRHPRSCTRDCAE
DB 185 QMHIKERSFSVIGSVYSSIMALLVATVLCNIGAMRNLYDMHRRQRRHPRHCRSDBAQ
QY 246 PRADGRASPOPBEEDHLLALMTVLFPMCSLPVITYRAYGAFKDKVKNRTSEBAED
DB 245 SGSDYRHSGLHPBEEDHFLVLAALMTVLFPMCSLPITYRAYGAF--KLENKAEGDSED
QY 306 LRAIRFLSVISYDPMWIFIFRSPVFRIFPHKIFIRPLRARSRCNS--TMMESL 359
DB 302 LQALRFLSVISYDPMWIFIFRISVFPMFLPHKVFTRPLIYRNMSSHQSQSVSESTL 357

RESULT 5
ID Q8CCM3 PRELIMINARY; PRT; 357 AA.
AC Q8CCM3;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Mus musculus adult male olfactory brain cDNA, RIKEN full-length
DE enriched library, clone:6430566C09 product:prostaglandin D receptor,
DE full insert sequence.
DE Name=Ptdgr;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Olfactory brain;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Mech. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Olfactory brain;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Olfactory brain;
RA The FANTOM Consortium;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Olfactory brain;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayashizaki Y., Sugahara Y., Shibata K., Itoh M.,
RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and substructure of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]

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RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Olfactory brain;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagata S., Sasaki N., Carninci P.,
RA Kono H., Akiyama U., Nishi K., Kitesuna T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanabe M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsunaga S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Olfactory brain;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hata A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Kono H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL, AK032488; BAC27895.1; -.
DR MGI, MGI:102966; Pegdr.
DR GO, GO:0016021; C:integral to membrane; TMS.
DR GO, GO:0004956; F:prostaglandin D receptor activity; IDA.
DR GO, GO:0001785; F:prostaglandin J receptor activity; IDA.
DR InterPro: IPR000276; GPCR_Rhodopsin.
DR InterPro: IPR000376; Glnand_receptor.
DR InterPro: IPR008365; Prostanoidrecept.
DR InterPro: IPR001105; Thbox_receptor.
DR Pfam: PF00001; 7tm.1; 1.
DR PRINTS: PR01786; PROSTANOIDR.
DR PRINTS: PR00854; PRSTNOIDPR.
DR PRINTS: PR00429; THROMBOXANR.
DR PROSITE, PS50262; G_PROTEIN_RECCEP_F1_2, 1.
DR KME Receptor.
SQ SEQUENCE 357 AA; 39990 MW; A0FAFE3E5D77E952 CRC64;

Query Match 72.0%; Score 1342.5; DB 2; Length 357;
Best Local Similarity 73.0%; Pred. No. 1.7e-96;
Matches 260; Conservative 39; Mismatches 52; Indels 5; Gaps 2;

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RESULT 6
PE22_CANFA STANDARD: PRT; 361 AA.

AC 09XT82;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Prostaglandin E2 receptor, EP2 subtype (Prostanoid EP2 receptor) (PGE receptor, EP2 subtype).
GN Name=PTGER2;
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99338573; PubMed=10410384; DOI=10.1016/S0090-6980(98)00081-1;
RA Hibbs T.A., Lu B., Smock S.L., Vestergaard P., Pan L.C., Owen T.A.;
RT "Molecular cloning and characterization of the canine prostaglandin E receptor EP2 subtype."
RL Prostaglandins Other Lipid Mediat. 57:133-147(1999).
CC -1- FUNCTION: Receptor for prostaglandin E2 (PGE2). The activity of this receptor is mediated by G(s) proteins that stimulate adenylyate cyclase. The subsequent raise in intracellular cAMP is responsible for the relaxing effect of this receptor on smooth muscle (by similarity).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC -----
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CC -----
DR EMBL: AF075602; AAD43140.1; -
DR InterPro: IPR001923; EP2_receptor.
DR InterPro: IPR00276; GPCR_Rhodpsn.
DR InterPro: IPR008365; Prostanoidrecept.
DR InterPro: IPR01105; Tbox_receptor.
DR Pfam: PF00001; 7tm.1; 1.
DR PRINTS: PRO0237; GPCRHOPODSN.
DR PRINTS: PRO1788; PROSTANOIDR.
DR PRINTS: PRO0581; PROSTOIDEPR2.
DR PRINTS: PRO0429; THROMBOXANER.
DR PROSITE: PS00237; G_PROTEIN_RECPT_FL_1; 1.
DR PROSITE: PS50262; G_PROTEIN_RECPT_FL_2; 1.
KM G-protein coupled receptor; Glycoprotein; Transmembrane.
FT DOMAIN 1 23
FT TRANSSEM 24 47
FT DOMAIN 48 65
FT TRANSSEM 66 91
FT DOMAIN 92 111
FT TRANSSEM 112 132
FT DOMAIN 133 151
FT TRANSSEM 152 176
FT DOMAIN 177 198
FT TRANSSEM 199 223
FT DOMAIN 224 262
FT TRANSSEM 263 286
FT DOMAIN 287 299
FT TRANSSEM 300 323
FT DOMAIN 324 361
FT DISULFID 109 187
FT CARBOHYD 6 6
FT CARBOHYD 96 96
FT CARBOHYD 287 287
SQ SEQUENCE 361 AA; 40274 MW; BC997FC8BD4FBDDB CBC64;

Query Match 38.3%; Score 714; DB 1; Length 361;

Best Local Similarity 44.7%; Pred. No. 1.5e-47;
Matches 161; Conservative 54; Mismatches 115; Indels 30; Gaps 10;

RESULT 7
PE22_MOUSE STANDARD: PRT; 362 AA.

AC 062053;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Prostaglandin E2 receptor, EP2 subtype (Prostanoid EP2 receptor) (PGE receptor, EP2 subtype).
GN Name=PTGER2; Synonyms=Ptger2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=ddY; TISSUE=Lung;
RX MEDLINE=96000196; PubMed=7556658; DOI=10.1016/0014-5793(95)00966-D;
RA Katsuyama M., Nishigaki N., Sugimoto Y., Morimoto K., Negishi M.,
RA Narumiya S., Ichikawa A.;
RT "The mouse prostaglandin E receptor EP2 subtype: cloning, expression, RT and northern blot analysis.";
RL PNAS Lett. 372:151-156(1995).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6J; TISSUE=Mammary gland;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Straubeberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Huleh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Tohiyuki S., Carninci P., Prange C.J.,
RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huliy S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Heiton B., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Buterfield Y.S.N., Krzywinski M.I., Skalek U., Smalhus D.E.,
RA Scherch A., Schein J.B., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human

QY 8 COUNTSVKKNQSAWGVLFSTGLGNLALGLARSLGKMSRRPLRP-SVYPMVC 66
DB 13 CESREMLPSGSPALSSAMFAGVIGNILALLARRRGGAGRGAGGNSISLHVLT 72
QY 67 GLTVLDLKGKLLSPVLAAYAKNSLRLVLPALDNSLCQAFAPFSPFGSLSTQLAM 126
DB 73 ELVFTDLGCTGISIVVLAASARNOTLALBP--BRACITFAFAMTFSLATMLMFLAM 130
QY 127 ALECMVLSGHPFFYRRHTTLRLGALVAVPSAFSLAFCALPFGKFGVQCPGWCEIQ 186
DB 131 ALERLYISGRVYFGVHTRRGGLAVLPITYVSLFCSPLDGLGVQVQCPGWCFIR 190
QY 187 MHEBGSLSVLGYSVLSMALVLTATVLCNLGAMRLYMHRRLOHP-----RSCIR 241
DB 191 --HGR-----YAVYQLVATLTLILLIVAVLACNFSVILNLMHRRSGRSCGPSLGGC-R 242
QY 242 DCAEPRADGRASPPQPELEHLHLLALMTVLFTMCSLPVYRAYGAFKQVKEKGRTRSE 301
DB 243 DSGSTRRGGRVSV--VAETHLLILAIINTTFAICSLPFTTFAY-----MNEISS 291
QY 302 EAE--DLRALRPLSVISIVDPWIFIPSPVFRIFFKIFIR-PLVYRSRCSNSTMSS 358
DB 292 RREKMDQLALRFLINSIIDPWFAIRPVLRLMRSLCCRVSLRAQDATQTSISQSN 351

RT and mouse cDNA sequences.",
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -1- FUNCTION: Receptor for prostaglandin E2 (PGE2). The activity of
 CC this receptor is mediated by G(s) proteins that stimulate
 CC adenylylate cyclase. The subsequent raise in intracellular cAMP is
 CC responsible for the relaxing effect of this receptor on smooth
 CC muscle.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; D50589; BAA09137.1; -.
 DR EMBL; BC005440; AAH05440.1; -.
 DR PIR; S66674; S66674.
 DR MGI; MGI:97794; Ptger2.
 DR InterPro; IPR001923; EP2_receptor.
 DR InterPro; IPR00276; GPCR_Rhodopsn.
 DR InterPro; IPR008365; Prostanoidrecept.
 DR InterPro; IPR001105; Tbox_receptor.
 DR Pfam; PF00001; 7tm.1; 1.
 DR PRINTS; PR00237; GPCRHHODOPS.
 DR PRINTS; PR01788; PROSTANOIDR.
 DR PRINTS; PR00581; PRSTNOIDEP2R.
 DR PRINTS; PR00429; THROMBOXANER.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
 KM G-protein coupled receptor; Glycoprotein; Transmembrane.
 FT DOMAIN 1 24
 FT TRANSMEM 25 48
 FT DOMAIN 49 66
 FT TRANSMEM 67 92
 FT DOMAIN 93 112
 FT TRANSMEM 113 133
 FT DOMAIN 134 152
 FT TRANSMEM 153 177
 FT DOMAIN 178 199
 FT TRANSMEM 200 224
 FT DOMAIN 225 262
 FT TRANSMEM 263 286
 FT DOMAIN 287 299
 FT TRANSMEM 300 323
 FT DOMAIN 324 362
 FT DISULFID 110 188
 FT CARBOHYD 6
 SQ SEQUENCE 362 AA; 40478 MW; A79FCEB86771F44 CRC64;
 Query Match 38.0%; Score 707.5; DB 1; Length 362;
 Best Local Similarity 44.5%; Pred. No. 4.9e-47;
 Matches 159; Conservative 58; Mismatches 115; Indels 25; Gaps 9;
 Oy 8 CONTTSVEKNSAWGVLFSTGLGNLALGLLARSGLG--WCSRRRLPLPSVFWLV 65
 Db 14 CKSQWMLSGSPAISSVWFSAGVGNIALALARRKRGTCGSAAG--RTSISLFWLV 72
 Oy 66 CGLTVDLGLKCLSPVLAAYAQNRSRLVLAAPALDNLCOAFAPFMSFGLSTLQLLA 125
 Db 73 TELVITDLGLTCLSPVLAAYSRNQLTVALAP--ESHACTYPAFTMTFFSLATMLMFA 130
 Oy 126 MALCEWLSLGHPPFRRRIITRLGALVAPVVSASLACALPMGFGFVQYCGRTWCFI 185
 Db 131 MALRRYSLIGPYPRRHLSRRGLAVLPVYGSALFLPCSLPLNYGYYVQYCGRTWCFI 190
 Oy 186 QMVEEBSLSTLVGSVYSMALVLAIVTCNIGAMNKLAMRRRLORHRRSCTRDCAE 245
 Db 191 R-HGR-----TAYLQYATMLLITVAIVACNISVIITLIRHRRSR--SRGLSGSS 241

Oy 246 PRADG--REASPOPLEDHLILLALMTVLFMCSLPIVTRYAYGAFKDKVKENRTSEE 302
 Db 242 LRGGSRRRRGERTSMAEETHLILLIMITTFACISLPFTFYMETSTLSKER----- 295
 Oy 303 AEDLRARFLSVISYDVPWFIFFRSPVPRIFPHKIFIR-PLVYRSRCSNSTWESS 358
 Db 296 -WDLRRLFLSVNSIIDPWFALRPVLRMSVLCRISLRTOEQNQTSCSTQSS 351
 RESULT 8
 PE22_HUMAN STANDARD; PRT; 358 AA.
 AC P4316;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 29-MAR-2004 (Rel. 43, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Prostaglandin E2 receptor, EP2 subtype (Prostanoid EP2 receptor) (PGE
 DE receptor, EP2 subtype).
 GN Name=PTGER2;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RX MEDLINE=94359483; PubMed=8076484;
 RA Regan J.W., Bailey T.J., Pepperl D.J., Pierce K.L., Bogardus A.M.,
 RA Donello J.E., Fairbairn C.E., Kedzie K.M., Woodward D.F., Gil D.W.;
 RT "Cloning of a novel human prostaglandin receptor with characteristics
 RT Mol. Pharmacol. 46:213-220(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Oakley C.J.;
 RL Submitted (JAN-1995) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9455330; PubMed=10521663; DOI=10.1016/S0378-1119(99)00323-6;
 RA Smock S.L., Pan L.C., Castleden T.A., Lu B., Mather R.J., Owen T.A.;
 RT "Cloning, structural characterization, and chromosomal localization of
 RT the gene encoding the human prostaglandin E2 receptor EP2 subtype.";
 RL Gene 237:393-402(1999).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RA Warren C.N., Aronstam R.S., Sharma S.V.;
 RT "cDNA clones of human proteins involved in signal transduction
 RT sequenced by the Guthrie cDNA resource center (www.cdna.org).";
 RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Receptor for prostaglandin E2 (PGE2). The activity of
 CC this receptor is mediated by G(s) proteins that stimulate
 CC adenylylate cyclase. The subsequent raise in intracellular cAMP is
 CC responsible for the relaxing effect of this receptor on smooth
 CC muscle.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- TISSUE SPECIFICITY: Placenta and lung.
 CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; U19487; AAA61681.1; -.
 DR EMBL; X83868; CAA58749.1; -.
 DR EMBL; AF134202; AAD44177.1; -.
 DR EMBL; AF134201; AAD44177.1; JOINED.
 DR EMBL; AY275471; AAB92303.1; -.
 DR PIR; I38920; I38920.

DR PIR; S51312; S51312.
 DR Genew; HGNC:9594; PTGER2.
 DR MIM; 176804; -
 DR CO; GO:0005887; C: integral to plasma membrane; TAS.
 DR CO; GO:0004957; F: prostaglandin E receptor activity; TAS.
 DR CO; GO:0007186; P: G-protein coupled receptor protein signalin. . . ; TAS.
 DR InterPro; IPR001923; E2 receptor.
 DR InterPro; IPR000276; GPCR_Rhodopsn.
 DR InterPro; IPR008365; Prostanoidrecept.
 DR InterPro; IPR001105; Thbox_receptor.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCRHHODPSN.
 DR PRINTS; PR01788; PROSTANOIDR.
 DR PRINTS; PR00581; PRSTNOIDEP2R.
 DR PRINTS; PR00429; THROMBOXANR.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
 DR G-protein coupled receptor; Glycoprotein; Transmembrane.
 FT DOMAIN 1 23
 FT TRANSSEM 24 47
 FT TRANSSEM 48 65
 FT TRANSSEM 66 91
 FT TRANSSEM 92 111
 FT TRANSSEM 112 132
 FT TRANSSEM 133 151
 FT TRANSSEM 152 176
 FT TRANSSEM 177 198
 FT TRANSSEM 199 223
 FT TRANSSEM 224 262
 FT TRANSSEM 263 299
 FT TRANSSEM 300 323
 FT TRANSSEM 324 358
 FT DISUPFID 109 187
 FT CARBOHYD 3 3
 FT CARBOHYD 6 6
 FT CARBOHYD 96 96
 FT CARBOHYD 287 287
 FT CONFICT 150 150
 SQ SEQUENCE 358 AA; 39760 MW; B3B0E2A3CFE2E363 CRC64;
 Query Match 36.9%; Score 688; DB 1; Length 358;
 Best Local Similarity 43.7%; Pred. No. 1.6e-45;
 Matches 157; Conservative 54; Mismatches 118; Indels 30; Gaps 10;
 QY 8 CQNTTSVEKNSAVMGVLTSTGLGKULALGLARSGLG--WCSRRLPLRPSPVPMV 65
 DB 13 CETRQWLPGEPSPAISSVMSFAGVNLIALALARRMRGVCSSAGRSSL-SLFVTV 71
 QY 66 CGLTVTDLKGKCLISPVVLAAYANRSLVAPALDLSLOAFPMSPFGLSTQLLA 125
 DB 72 TELVFTDLSTCLISPVVLAAYANRSLVAPALDLSLOAFPMSPFGLSTQLLA 129
 QY 126 MALECWLSLGHPEFYRRHITLRLGALVAPVSAFSAFCALEPMFGPKFYQCPGTWCFI 185
 DB 130 MALEERYISIHPIFYQGRVRSGLAVLPVIVANSLLFCSPLIDYQVYQCGTWCFI 189
 QY 186 QMVEHSGSLVGLSVLYSSIMALLVATVLCNIGAMRNLYAMHRIQHRHRSCTRDCAE 245
 DB 190 R--HGR-----TAVLQLYATLLLLIIVSVLACNPSVILNIRHRRSRR--SRGSPSLGS 240
 QY 246 -----PRADGRASQPLEEDHLLALMTVLPFMCSLPVIVRYAFAFDVKNKNTSE 301
 DB 241 GGGPGARRRGERSVMAEETDHLTLALMTITTFVCSLPPTIFAY-----WNETSS 291
 QY 302 EAE--DLRALRFLSVISIVDPWIFIRSPVFRIFFFKIFIR-PLRYRSRCSNSTNMES 357
 DB 292 RKKEKMDQALRFLSINIIIDPWFAIRPVLRLMRVLCRISLRQDATQISCTQS 350
 RESULT 9
 PE22 RAT
 ID _PE22_RAT STANDARD; PRT; 357 AA.

AC Q62928;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Prostaglandin E2 receptor, EP2 subtype (Prostanoid EP2 receptor) (PGE
 DE receptor, EP2 subtype).
 OS Name=Ptger2;
 GN Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 CX NCBI_TaxId=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung;
 RC MEDLINE=98141044; PubMed=937820; DOI=10.1016/S0014-2999(97)01383-6;
 RA Boile Y., Stocco R., Sawyer N., Slipetz D.M., Unglin M.D.,
 RA Neuschaefer-Rube F., Puschel G.P., Metters K.M., Abramovitz M.;
 RT "Molecular cloning and expression of a rat prostaglandin E2 receptor
 RT of the EP2 subtype.";
 RL Prostaglandins 54:713-725(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley, TISSUE=Spleen;
 RC MEDLINE=98141044; PubMed=937820; DOI=10.1016/S0014-2999(97)01383-6;
 RA Boile Y., Stocco R., Sawyer N., Slipetz D.M., Unglin M.D.,
 RA Neuschaefer-Rube F., Puschel G.P., Metters K.M., Abramovitz M.;
 RT "Molecular cloning and characterization of the four rat prostaglandin
 RT E2 prostanoind receptor subtypes.";
 RL Eur. J. Pharmacol. 340:227-241(1997).
 CC -1- FUNCTION: Receptor for prostaglandin E2 (PGE2). The activity of
 CC this receptor is mediated by G(s) proteins that stimulate
 CC adenylyl cyclase. The subsequent raise in intracellular cAMP is
 CC responsible for the relaxing effect of this receptor on smooth
 CC muscle (By similarity).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
 CC
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 CC
 CC EMBL; U48858; AAA97889.1; -
 CC EMBL; U94708; AAB53325.1; -
 DR RGD; 620020; Ptger2.
 DR InterPro; IPR001923; EP2_receptor.
 DR InterPro; IPR000276; GPCR_Rhodopsn.
 DR InterPro; IPR008365; Prostanoidrecept.
 DR InterPro; IPR001105; Thbox_receptor.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCRHHODPSN.
 DR PRINTS; PR01788; PROSTANOIDR.
 DR PRINTS; PR00581; PRSTNOIDEP2R.
 DR PRINTS; PR00429; THROMBOXANR.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
 DR G-protein coupled receptor; Glycoprotein; Transmembrane.
 FT DOMAIN 1 24
 FT TRANSSEM 25 48
 FT TRANSSEM 49 66
 FT TRANSSEM 67 92
 FT TRANSSEM 93 112
 FT TRANSSEM 113 133
 FT TRANSSEM 134 152
 FT TRANSSEM 153 177
 FT TRANSSEM 178 199
 FT TRANSSEM 200 224
 FT TRANSSEM 225 262
 FT TRANSSEM 263 286
 FT TRANSSEM 287 299
 FT TRANSSEM 300 323
 FT TRANSSEM 324 358

FT DOMAIN 324 357 Cytoplasmic (Potential).
 FT DSUFID 110 188 By similarity.
 FT CARBOHYD 6 N-linked (GlcNAc...) (Potential).
 SQ SEQUENCE 357 AA; 39771 MW; AAB22AE280AEFF80 CRC64;
 Query Match 36.2%; Score 674; DB 1; Length 357;
 Best Local Similarity 44.7%; Pred. No. 2e-44;
 Matches 148; Conservative 54; Mismatches 105; Indels 24; Gaps 8;

QY 8 COUNTSVEKNSAVMGVLFSTGLNLALGLARSGGLG--WGRRLPLPSPVFTMLV 65
 DB 14 CESRQVLLSDSPASSVFTAGVGLNMLALARRMRGDTGCSAGS-RTSISLFFHLV 72
 QY 66 CGLTVDLKGKCLSPVLLAAYAONRSLRVLPALDLSLCOAFPFMSFGLSSTLQLLA 125
 DB 73 TELVTDLGLTCLISPVLLASYSRQNTLVALLP--EERACTYFAFTMTFSLATMLMFLA 130
 QY 126 MALECMWLSLGHPPFYRRHITRLGALVAPVVSASFALFCAIPFMGFGKFGVYCGTWCFT 185
 DB 131 MALERYLAIGHFYRRVRVSRGGLAVLPAYGVSLFCSLPILNYGEVYQCGTWCFT 190
 QY 186 QMHEBSLSVLGVSIVYSSIMALLVATVLCNIGAMRNLYAMHRLQHRPSCTRCAE 245
 DB 191 Q-HGR-----TAYLQYATVLLLLIVAVLGCNISVILNLRMQLRKR--SRGLSGSS 241
 QY 246 PRADG---REASPOLEELDLHLALMTVLFMTCSLPVIRAYYGAFKDVKERNRTSEE 302
 DB 242 LRGGSRRRRGERTMAETDHLILALMTITFAVCSLPFTTFAIMDETSSKKE----- 295
 QY 303 AEDLRALRFLSVISIVDPWIFIFRSPVFR 333
 DB 296 -WDLRALRFLSVNSIIDPWVFLIRPVLRL 325

RESULT 10
 Q8HY57 PRELIMINARY; PRT; 361 AA.

AC Q8HY57;
 DT 01-MAR-2003 (Tremblrel. 23, Created)
 DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
 DE Prostaglandin E2 receptor EP2.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OC NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Guan Y., Stillman B.A., Zhang Y., Schneider A., Saito O., Davis L.S.,
 RA Breyer M.D.;
 RT "Cloning of rabbit prostaglandin E2 receptor EP2.";
 RL J. Am. Soc. Nephrol. 7:1646-1646(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Pubmed=12097143; DOI=10.1186/1471-2210-2-14;
 RA Guan Y., Stillman B.A., Zhang Y., Schneider A., Saito O., Davis L.S.,
 RA Redha R., Breyer R.M., Breyer M.D.;
 RT "Cloning and expression of the rabbit prostaglandin EP2 receptor.";
 RL BMC Pharmacol. 2:14-14(2002).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
 CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 DR EMBL: AY166779; AAO13013.1; -;
 DR GO: GO:0016021; C:integral to membrane; IEA.
 DR GO: GO:0004957; F:prostaglandin E receptor activity; IEA.
 DR GO: GO:0004872; F:receptor activity; IEA.
 DR GO: GO:0004960; F:rhodopsin-like receptor activity; IEA.
 DR GO: GO:0007186; P:G-protein coupled receptor protein signalin...; IEA.
 DR InterPro: IPR001923; EP2_receptor.
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR InterPro: IPR008365; Prostanoidrecept.
 DR InterPro: IPR001105; Thox_receptor.
 DR Pfam: PF00001; 7tm_1; 1.

DR PRINTS; PR00237; GECRRHODPSN.
 DR PRINTS; PR01788; PROSTANOIDR.
 DR PRINTS; PR00581; PRSTOIDEPR.
 DR PRINTS; PR00429; THROMBOXANR.
 DR PROSITE; PR00237; G_PROTEIN_RECP_F1_1; 1.
 DR PROSITE; PS50262; G_PROTEIN_RECP_F1_2; 1.
 DR G-protein coupled receptor; Receptor; Transmembrane.
 SQ SEQUENCE 361 AA; 39945 MW; E735BC61F60B19D CRC64;
 Query Match 35.7%; Score 665; DB 2; Length 361;
 Best Local Similarity 42.6%; Pred. No. 1e-43;
 Matches 155; Conservative 50; Mismatches 117; Indels 42; Gaps 11;

QY 8 COUNTSVEKNSAVMGVLFSTGLNLALGLARSGGLG--WGRRLPLPSPVFTMLV 65
 DB 13 CEROMLPSESPALISAVMSAGVLTGLNLALALARRMRADAGRSAGRTSLFLFHLVLT 72
 QY 67 GLTVDLKGKCLSPVLLAAYAONRSLRVLPALDLSLCOAFPFMSFGLSSTLQLLA 126
 DB 73 ELVFTDLGTCFISPVLLASYSRQNTLVALLP--DGRACTYFAFAMTFSLATMLMFLA 130
 QY 127 ALSCWLSLGHPPFYRRHITRLGALVAPVVSASFALFCAIPFMGFGKFGVYCGTWCFT 186
 DB 131 ALERYLSIGHFYRRYQCRITRGGGLAVLPAYTSLSLFCSLPLDYGERYVYQCGTWCFT 190
 QY 187 MVHEBSLSVLGVSIVYSSIMALLVATVLCNIGAMRNLYAMHRLQHRPSCTRCAE 246
 DB 191 -HGR-----TAYLQYATVLLLLIVAVLGCNISVILNLMQLRKR--SRGLSGSS 241
 QY 247 RADGREASP-----QPLELDHLALMTVLFMTCSLPVIRAYYGAFKDVKERN 297
 DB 238 SGSGR--GGPRTRRRGERSVAEBTDHLILALMTITFAVCSLPFTTFAIMDETSSKKE-----MN 287
 QY 298 RTSEBAE--DLRALRFLSVISIVDPWIFIFRSPVFRIFRKFIR-PLR-----YRSRCS 350
 DB 288 ETSRREKMDLQALRFLSVNSIIDPWVFLIRPVLRL 325

RESULT 11
 Q8MJ09 PRELIMINARY; PRT; 352 AA.

AC Q8MJ09;
 DT 01-OCT-2002 (Tremblrel. 22, Created)
 DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
 DE EP2 receptor.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovinae; Bos.
 OC NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=22694625; Pubmed=12810564; DOI=10.1210/en.2002-0088;
 RA Arosh J.A., Bann S.K., Chapdelaine P., Emond V., Kim J.J.,
 RA MacLaren L.A., Fortier M.A.;
 RT "Molecular Cloning and Characterization of Bovine Prostaglandin E(2) Receptor EP2 and EP4: Expression and Regulation in Endometrium and Myometrium during the Estrous Cycle and Early Pregnancy.";
 RT Endocrinology 144:3076-3091(2003).
 RL -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
 CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 DR EMBL: AF339402; AA001234.1; -;
 DR GO: GO:0016021; C:integral to membrane; IEA.
 DR GO: GO:0004957; F:prostaglandin E receptor activity; IEA.
 DR GO: GO:0004872; F:receptor activity; IEA.
 DR GO: GO:0001584; F:rhodopsin-like receptor activity; IEA.
 DR GO: GO:0007186; P:G-protein coupled receptor protein signalin...; IEA.
 DR InterPro: IPR001923; EP2_receptor.

DR InterPro; IPR000276; GPCR_Rhodopsn.
 DR InterPro; IPR008365; Prostanoidrecept.
 DR Pfam; PF00001; 7tm 1; 1.
 DR PRINTS; PRO0237; GPCR_RHODOPSIN.
 DR PRINTS; PRO1788; PROSTANOIDR.
 DR PRINTS; PRO0581; PRSTNOIDEP2R.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
 DR G-protein coupled receptor; Receptor; Transmembrane.
 SO SEQUENCE 352 AA; 39726 MW; 9EB8F8F45B37287 CRC64;

Query Match 35.5%; Score 662; DB 2; Length 352;
 Best Local Similarity 42.7%; Pred. No. 1.7e-43;
 Matches 149; Conservative 59; Mismatches 115; Indels 26; Gaps 8;

QY 17 GNSAVMGVLFSTGLGNTLALGLLARSGLGWCGRRLPLP-SVFYMLVCGLVTTDLG 75
 DB 22 GESPAISSVMTAGVNLALALVLRMRDSSGRSEGRNSISLFFVLVTELVTTDLG 81
 QY 76 KCLLSPVVLAAYANRSRLRVAPALDNLCOAFAPFNSFGLSSTLOLALBQMLSLG 135
 DB 82 TCLISPVVLAAYANRSRLRVAPALDNLCOAFAPFNSFGLSSTLOLALBQMLSLG 139
 QY 136 HPEFRRHITLRLGALVAPVVASFALFALFPMGFGKFGVYCPGTWCFIQWHEBGLS 195
 DB 140 HPVYGRVTRRSGLAVLPITYISLFLCSPLLDHMKVQYNGTWCFFIG--HKQT-- 195
 QY 196 VLGSVSYSSLMALLVATVLCNIGAMRNLYAMRRLQORHRSCTRDCAERADGREASP 255
 DB 196 ---VLRVATLILLLIIVLACNFSVYVNLIMHRGRSRGSPSLSSHRARVSWA- 251
 QY 256 QPLELHLLALMTVLTFTWCSLPVYRAYGAFKVKENRTSEAEDELRLPLSVI 315
 DB 252 ---EETHLLILALMTTTFVACSPLPTIFAY-----MENSRSKEMDLQALRFLSIN 301
 QY 316 SIYDPMIFIFRSFVRIFFPKIFIR-PLR---YRSRCSNSTMESGL 359
 DB 302 SIIDPMVFAILRPVLRMRSVLCCRVSLFTQEAOTQSCSTQSNASKOI 350

RESULT 12
 Q6NZ15 PRELIMINARY; PRT; 371 AA.

AC 06NZ15; 05-JUL-2004 (Tremblrel, 27, Created)
 DT 05-JUL-2004 (Tremblrel, 27, Last sequence update)
 DE MCC69060 protein.
 GN Name=MCC69060;
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN 1] SEQUENCE FROM N.A.
 RP TISSUE=Spleen;
 RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner K.H., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marinsina K., Farmer A.A., Rubin G.W., Hong L.,
 RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udell T.B., Toshlyuk S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman W., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Krzyzinski M.I., Skalska U., Smalue D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Spleen;
 RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
 RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
 RA Richardson P.;
 RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
 RT initiative.";
 RL Dev. Dyn. 225:384-391 (2002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Spleen;
 RA Klein S., Strausberg R.;
 RL Submitted (FEB-2004) to the EMBL/Genbank/DBJ databases.
 DR EMBL; BC066120; AAH66120.1; -;
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0004957; F:prostaglandin H receptor activity; IEA.
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
 DR GO; GO:0004960; F:chromoboxane receptor activity; IEA.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. ; IEA.
 DR InterPro; IPR001923; EP2_receptor.
 DR InterPro; IPR000276; GPCR_Rhodopsn.
 DR InterPro; IPR008365; Prostanoidrecept.
 DR InterPro; IPR001105; Thbox_receptor.
 DR Pfam; PF00001; 7tm 1; 1.
 DR PRINTS; PRO0237; GPCR_RHODOPSIN.
 DR PRINTS; PRO1788; PROSTANOIDR.
 DR PRINTS; PRO0581; PRSTNOIDEP2R.
 DR PRINTS; PRO0429; THROMBOXANER.
 DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
 SO SEQUENCE 371 AA; 41896 MW; 76B83A03B5E5B0AD CRC64;

Query Match 35.3%; Score 658.5; DB 2; Length 371;
 Best Local Similarity 39.5%; Pred. No. 3.3e-43;
 Matches 141; Conservative 71; Mismatches 110; Indels 35; Gaps 9;

QY 8 CONTTSVEKNSAVMGVLFSTGLGNTLALGLLARSGLGWCGRRLPLP-SVFYMLVCG 67
 DB 9 CESNCHANGSESPAVASVAGVNLALVLEN-----RRRAVKGMSLPHILVTG 62
 QY 68 LVTVDLIGKCLSPVLAAYANRSRLRVAPALDNLCOAFAPFNSFGLSSTLOLALMA 127
 DB 63 LVITDLMGTGMSIPVLAAYANRSRLRVAPALDNLCOAFAPFNSFGLSSTLOLALMA 122
 QY 128 LECMLSIGHFFRRHITLRLGALVAPVVASFALFALFPMGFGKFGVYCPGTWCFIQW 187
 DB 123 LERMAIGHVYVEKFSKRCGLVTPFPVYSFCIFCLFPAKMGVGEIYQCPGTWCFTNM 182
 QY 188 ---VHEGSLSVLGSVLYSSLMALLVATVLCNIGAMRNLYAMRRLQORHRSCTRDCAE 245
 DB 183 RCGHNGSTGNT-YSTLYATLILLLIIVLTCNFIYIVSLVRNKR-QKARLVTK----- 236
 QY 246 PRADGEASPOPLEEDHLLILALMTVLTFTWCSLPVYRAYGAFKVKENRTSEAEAD 305
 DB 237 -----BERMSMS-EEDHLLILALMTTTFVACSPLPTIFAY-----RD 265
 QY 306 LALRLSVSYSDPMIFIFRSFVRIFFPKIFIR-PLRKYR-----SRCNS 352
 DB 286 LALRLSVSYSDPMIFIFRSFVRIFFPKIFIR-PLRKYR-----SRCNS 352

RESULT 13
 P1ZR BOVIN STANDARD; PRT; 385 AA.

AC P79393; 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 25-JAN-2005 (Rel. 46, Last annotation update)

DE Prostacyclin receptor (Prostanoid IP receptor) (PGI receptor)
 DE (Prostaglandin 12 receptor).
 GN Name=PTGIR;
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Kunitantia; Pecora; Bovidae;
 OC Bovinae; Bos.
 NCBI_TaxId=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Hasse A., Schroer K.;
 RT "Cloning and sequencing of the bovine prostacyclin receptor gene."
 RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Receptor for prostacyclin (prostaglandin 12 or PGI2).
 CC The activity of this receptor is mediated by G(s) proteins which
 CC activate adenylate cyclase.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; Z93039; CAB07510.1; -;
 DR EMBL; Z93040; CAB07510.1; JOINED.
 DR InterPro; IPR000276; GPCR_Rhodopsn.
 DR InterPro; IPR000370; IP_receptor.
 DR InterPro; IPR008365; Prostanoidrecept.
 DR InterPro; IPR001105; Thbox_receptor.
 DR Pfam; PF00001; 7tm.1; 1.
 DR PRINTS; PRO1786; PROSTANOIR.
 DR PRINTS; PRO0429; THROMBOXANR.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
 KM G-protein coupled receptor; Glycoprotein; Lipoprotein; Palmitate;
 KM Transmembrane.
 FT DOMAIN 1 16 Extracellular (Potential).
 FT TRANSSEM 17 38 1 (Potential).
 FT DOMAIN 39 51 Cytoplasmic (Potential).
 FT TRANSSEM 52 76 2 (Potential).
 FT DOMAIN 77 94 Extracellular (Potential).
 FT TRANSSEM 95 115 3 (Potential).
 FT DOMAIN 116 134 Cytoplasmic (Potential).
 FT TRANSSEM 135 158 4 (Potential).
 FT DOMAIN 159 181 Extracellular (Potential).
 FT TRANSSEM 182 208 5 (Potential).
 FT DOMAIN 209 234 Cytoplasmic (Potential).
 FT TRANSSEM 235 259 6 (Potential).
 FT DOMAIN 260 273 Extracellular (Potential).
 FT TRANSSEM 274 294 7 (Potential).
 FT DOMAIN 295 385 Cytoplasmic (Potential).
 FT DISULFID 5 165 By similarity.
 FT DISULFID 92 170 By similarity.
 FT LIPID 308 308 S-palmitoyl cysteine (By similarity).
 FT CARBOHYD 7 N-linked (GlcNAc...) (Potential).
 SQ SEQUENCE 385 AA; 41247 MW; 0CDAS44D18E035C7 CRC64;
 Query Match 33.7%; Score 628.5; DB 1; Length 385;
 Best Local Similarity 44.1%; Pred. No. 7.4e-41;
 Matches 156; Conservative 46; Mismatches 109; Indels 43; Gaps 11;
 QY 8 CONTTSVEKNSAVMGVLFSTGLIGLILGLIARSLGKSRPLPLPVSFVYMLVCG 67
 DB 5 CRNLTLYRDSVGPATSTLTFVAGVNGALGIIG-----ARRHSR--PSAPAVLVATG 55
 QY 68 LTVYDLGKLLSVVLAAYNONSLRVL---PALDNLCOAFAPFSPFGSSTLQL 124
 DB 56 LGVTDLGTCLSPAVFAVARNSSLGLAAGRPA---LCDARPAFTTFGLASTLILF 111

QY 125 AMALBECMLSGHPFFRRHITLRLGALVAVVSASFSLAFALPFGPKFVQYCPGTWCF 184
 DB 112 AMASVERCLASHPYLAQDLGPRRRLALPAIYAFCTIFCSLPFLIGHQYCPGSMCF 171
 QY 185 IOM-VHEEGSLVIGSVYSSIMALLVATVLCNIGAMENLYAMRRRLORHRSCTRDG 243
 DB 172 IRRRSABPGGCAFL---LAVASLVALLVAIVLCNCSVTLSLRMTROQRHQRCPR-- 226
 QY 244 AEPRADGREASPOPLEBDHLILALMTVLFETWCSLPVI--YRAYGAFKDYKERTSE 301
 DB 227 --FRAG-----DEVHDLILALMTGIMAVCSPLPFGIRGFOALAP-----DSS 270
 QY 302 EADDLARLRLSVISYIDPFIIFRSPV--RIFRHKIFRPLRYRSCNS 352
 DB 271 EMDLILAFRENAENPILDPVWFIIFRKSVRQLKLFCCLSRPAQDSRTSL 324
 RESULT 14
 P12R HUMAN STANDARD; PRT; 386 AA.
 ID P12R_HUMAN
 AC P43119;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 25-JAN-2005 (Rel. 46, Last annotation update)
 DE Prostacyclin receptor (Prostanoid IP receptor) (PGI receptor)
 DE (Prostaglandin 12 receptor).
 GN Name=PTGIR; Synonyms=PRIPR;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung;
 RX MEDLINE=94216334; PubMed=7512962;
 RA Bole Y., Rushmore T.H., Darmon-Goodwin A., Grygorczyk R.,
 RA Sliet D.M., Metters K.M., Abramovitz M.,
 RT "Cloning and expression of a cDNA for the human prostanoid IP
 RT receptor."
 RL J. Biol. Chem. 269:12173-12178 (1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94237286; PubMed=7514139; DOI=10.1016/0014-5793(94)00355-6;
 RA Katsuyama M., Sugimoto Y., Namba T., Irie A., Negishi M., Narumiya S.,
 RA Ichikawa A.;
 RT "Cloning and expression of a cDNA for the human prostacyclin
 RT receptor."
 RL FEBS Lett. 344:74-78 (1994).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung;
 RX MEDLINE=95008086; PubMed=7923647;
 RA Nakagawa O., Tanaka I., Ueki T., Harada M., Sasaki Y., Itoh H.,
 RA Yoshimasa T., Namba T., Narumiya S., Nakao K.;
 RT "Molecular cloning of human prostacyclin receptor cDNA and its gene
 RT expression in the cardiovascular system."
 RL Circulation 90:1643-1647 (1994).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95394450; PubMed=7665161;
 RA Ogawa Y., Tanaka I., Inoue M., Yoshitake Y., Ise N., Nakagawa O.,
 RA Ueki T., Itoh H., Yoshimasa T., Narumiya S.;
 RT "Structural organization and chromosomal assignment of the human
 RT prostacyclin receptor gene."
 RL Genomics 27:142-148 (1995).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RA Warren C.N., Aronstam R.S., Sharma S.V.;
 RT "cDNA clones of human proteins involved in signal transduction
 RT sequenced by the Guthrie cDNA resource center (www.cdna.org).";
 RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
 RN [6]

RP PALMITOYLATION.
 RX MEDLINE=22486644; PubMed=12488443; DOI=10.1074/jbc.M210637200;
 RA Miggin S.M., Lawler O.A., Kinsella B.T.;
 RT "Palmitoylation of the human prostacyclin receptor. Functional
 RL implications of palmitoylation and isoprenylation.";
 RN J. Biol. Chem. 278:6947-6958(2003).
 RP DISULFIDE BONDS.
 RX PubMed=15194446; DOI=10.1016/j.ejphar.2004.04.041;
 RA Giguere V., Gallant M.A., de Brum-Fernandes A.J., Parent J.-L.;
 RT "Role of extracellular cysteine residues in
 RL dimerization/oligomerization of the human prostacyclin receptor.";
 CC Eur. J. Pharmacol. 494:11-22(2004).
 CC -1- FUNCTION: Receptor for prostacyclin (prostaglandin I2 or PGi2).
 CC The activity of this receptor is mediated by G(s) proteins which
 CC activate adenylate cyclase.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
 CC -----
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 CC -----
 DR EMBL: L29016; AAA36448.1; -;
 DR EMBL: D25418; BAA05008.1; -;
 DR EMBL: D29634; BAA06110.1; -;
 DR EMBL: D38127; BAA07325.1; -;
 DR EMBL: D38128; BAA07325.1; JOINED.
 DR EMBL: AY242134; AAO92301.1; -;
 DR PIR: A57066; A57066;
 DR Genew; HGNC:9602; PTGIR.
 DR MM; 600022; -;
 DR GO: GO:0005887; C: integral to plasma membrane; TAS.
 DR GO: GO:0004959; F: prostaglandin I receptor activity; TAS.
 DR GO: GO:0007267; P: cell-cell signaling; TAS.
 DR GO: GO:0007187; P: G-protein signaling, coupled to cyclic nucl. . .; TAS.
 DR Interpro: IPR000276; GPCR_Rhodopsn.
 DR Interpro: IPR000370; IP_receptor.
 DR Interpro: IPR008365; Prostanoidrecept.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PRINTS: PRO0237; GPCRHOPOPSN.
 DR PRINTS: PRO1788; PROSTANOIDR.
 DR PRINTS: PRO0429; THROMBOXANR.
 DR PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE: PS50264; G_PROTEIN_RECEP_F1_2; 1.
 KM G-protein coupled receptor; Glycoprotein; Lipoprotein; Palmitate;
 KM Transmembrane.
 FT DOMAIN 1 16
 FT TRANSSEM 17 38
 FT TRANSSEM 39 51
 FT TRANSSEM 52 76
 FT TRANSSEM 77 94
 FT TRANSSEM 95 115
 FT TRANSSEM 116 134
 FT TRANSSEM 135 158
 FT TRANSSEM 159 181
 FT TRANSSEM 182 208
 FT TRANSSEM 209 235
 FT TRANSSEM 236 260
 FT TRANSSEM 261 274
 FT TRANSSEM 275 295
 FT TRANSSEM 296 386
 FT DISULFID 5 165
 FT DISULFID 92 170
 FT LIPID 308 308
 FT LIPID 311 311
 FT CARBOHYD 7
 SQ SEQUENCE 386 AA; 40955 MW; 2B6B0CDBACE1608 CRC64;

Query Match 32.0%; Score 597; DB 1; Length 386;
 Best Local Similarity 42.3%; Pred. No. 2,1e-38;
 Matches 141; Conservative 46; Mismatches 102; Indels 44; Gaps 9;
 QY 8 CONTSVKGNASAVMGVLFSTGLGNLALGLIARSGLGWCSRRRLPLSPSVFMYLVC 67
 DB CRNLTYVRGSGVATSTLTFMFAVGAVNGALGLIS-----ARRPAR--PSAFAVLVTG 55
 QY 68 LTVYDILGKLLSVVLAARQNSLFLVA---PALNSICQAFAPFMSPGLSSTYQL 124
 DB LAAVDLLGTSFLSPAVVAARNSLLGLARGPA---LCDAPAFMTFFGLASMLIF 111
 QY 125 AMALECWLISGHPFFRYRHTLRGALVAPVASFAPCALPPMGKGFQYCPGTWCF 184
 DB AMAVERTLASHPLVYQDQPRCARLALPAIYAFVFLPGLGQHQYCPGSMCF 171
 QY 185 IQM--VHEGSLSVLGYSVYSIMALLVATVLCNIGAMRNLYAMHRLQRHRSCTRD 242
 DB LRMRWAPGGA---AFSLAVAGLVALLVAIFLCNGSVTLSCRMVROQRHGS---- 223
 QY 243 CAERADGRASQPL---EEDHLLALMTYVLFMCSPVYIYRAYGAFKDYKERT 299
 DB LGRPRRTGEVDHLLILALMTVMVAVCSPLTTRCTQAVAP-----DS 268
 QY 300 SEAEDELALRFLSVISIVDPPIRSPVFR 332
 DB SSEMGDLARFYAFNPILDPWFILFRKAVFQ 301
 RESULT 15
 P12R MOUSE STANDARD; PRT; 415 AA.
 AC P43252;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 25-JAN-2005 (Rel. 46, Last annotation update)
 DE Prostacyclin receptor (Prostanoid IP receptor) (PGI receptor)
 GN Name=Ptgir;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94193694; PubMed=7511597;
 RA Namba T., Oida H., Sugimoto Y., Negishi M., Kakizuka A., Ichikawa A.,
 RA Narumiya S.;
 RT "cDNA cloning of a mouse prostacyclin receptor. Multiple signaling
 RT pathways and expression in thymic medulla.";
 RL J. Biol. Chem. 269:9986-9992(1994).
 CC -1- FUNCTION: Receptor for prostacyclin (prostaglandin I2 or PGi2).
 CC The activity of this receptor is mediated by G(s) proteins which
 CC activate adenylate cyclase.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
 CC -----
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 CC -----
 DR EMBL: D26157; BAA05144.1; ALT_INIT.
 DR MGD; MGI:99535; Ptgir.
 DR Interpro: IPR000276; GPCR_Rhodopsn.
 DR Interpro: IPR000370; IP_receptor.
 DR Interpro: IPR008365; Prostanoidrecept.
 DR Interpro: IPR001105; Thbox_receptor.
 DR Pfam; PF00001; 7tm_1; 1.

DR PRINTS; PR00237; GPCR RHODOPSIN.
 DR PRINTS; PR01788; PROSTANOIDS.
 DR PRINTS; PR00429; THROMBOXANER.
 DR PROSITE; PS00237; G_PROTEIN_RECP_F1_1.
 DR PROSITE; PS50262; G_PROTEIN_RECP_F2_1.
 DR G-protein coupled receptor; Lipoprotein; Palmitate;
 Transmembrane.
 KW DOMAIN 1 44 Extracellular (Potential).
 FT TRANSMEM 45 66 1 (Potential).
 FT DOMAIN 67 79 Cytoplasmic (Potential).
 FT TRANSMEM 80 104 2 (Potential).
 FT DOMAIN 105 122 Extracellular (Potential).
 FT TRANSMEM 123 143 3 (Potential).
 FT DOMAIN 144 162 Cytoplasmic (Potential).
 FT TRANSMEM 163 186 4 (Potential).
 FT DOMAIN 187 215 Extracellular (Potential).
 FT TRANSMEM 216 236 5 (Potential).
 FT DOMAIN 237 263 Cytoplasmic (Potential).
 FT TRANSMEM 264 288 6 (Potential).
 FT DOMAIN 289 301 Extracellular (Potential).
 FT TRANSMEM 302 322 7 (Potential).
 FT DOMAIN 323 415 Cytoplasmic (Potential).
 FT DISULFID 33 193 By similarity.
 FT DISULFID 120 198 By similarity.
 FT LIPID 335 335 S-palmitoyl cysteine (By similarity).
 FT LIPID 338 338 S-palmitoyl cysteine (By similarity).
 FT CARBOHYD 35 35 N-linked (GlcNAc...) (Potential).
 SQ SEQUENCE 415 AA; 44462 MW; 306929582DDDD24C CRC64;

Query Match 32.0%; Score 596.5; DB 1; Length 415;
 Best Local Similarity 42.8%; Pred. No. 2.5e-38;
 Matches 139; Conservative 43; Mismatches 114; Indels 29; Gaps 7;

QY 8 COUNTSVKNSAVMGVLFSTGLGNLALGLARSGLCSSRRPLRPLSVFYMLVCG 67
 DB 33 CWNITVQDSVGPATSTLTFVAGVNGALGILG-----ARR--RSHPSAPAVLVGT 83
 QY 68 LTVTDLGKCLSPVLAAYVQNRSLRVLAAPALDNSLQAFAPFMSFGLSTQLLAMA 127
 DB 84 LAVTDLGTCTCLSPAVFAVARNSSILGLANG-GTMLCDTFAPAMTFGLASTLILFAMA 142
 QY 128 LECWLSLGHPEFFRRHITLRLGALVAPVSAFSLAFQALPFGKGVQCPGTWCTIQM 187
 DB 143 VERCLALSHPLYAQLDGPRCARPALPSIYAFCCLPGLGHEHQYCPGSMCFIRM 202
 QY 188 VHEGSLSVLGYSVLSIMALLVLAIVLCSLGMARNLYAMHRLQHPHSCTRDCAEP 247
 DB 203 --RSAQPGGCAFSLAIVSLMLVTSIFPCNGSVTLSDYHMYRQORRHGSEFV-----PT 255
 QY 248 ADGREASPOPLEEDHLLALLMTVLFTWCSPVIYRAYYGAFKDYKKNRTSEAEADLR 307
 DB 256 SRARE-----DEVYHLLALLMTVIMAVCSLPLMIRGFTQAIAP-----DSREMGDLL 303
 QY 308 ALRFLSVISIVDPWIFIIIFRSPFR 332
 DB 304 AFRNAPNPIIDPWVFILFRKAVFQ 328

Search completed: April 22, 2005, 21:29:25
 Job time : 64.5786 secs

Db 121 LQLLAMLECWLSIGHPFFRRHTTLRLGALVAPVSAFSLAFALPFGMGKGVQCPG 180
QY 181 TWCFIQWHEGSGSVGYSLVSSLMALLVLAIVLCNLGAMRLYAMHRLQHPHSC 240
Db 181 TWCFIQWHEGSGSVGYSLVSSLMALLVLAIVLCNLGAMRLYAMHRLQHPHSC 240
QY 241 RDCAEPRADREASPOPLEEDHLLALLMTVLFTMCSLPVIYRAYYGAFFDVKEKRTS 300
Db 241 RDCAEPRADREASPOPLEEDHLLALLMTVLFTMCSLPVIYRAYYGAFFDVKEKRTS 300
QY 301 EEAEDLALRFLSVISIVDPWIFIFRSVPVRIFFHKIFIRPLRYRSCNSTMSSL 359
Db 301 EEAEDLALRFLSVISIVDPWIFIFRSVPVRIFFHKIFIRPLRYRSCNSTMSSL 359

RESULT 2

US-10-276-774-2370
; Sequence 2370, Application US/10276774
; Publication No. US20040053245A1
; GENERAL INFORMATION:
; APPLICANT: Hyeag, Y, Tom et al
; APPLICANT: Yang, Y, Tom et al
; TITLE OF INVENTION: No. US20040053245A1el Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-030
; CURRENT APPLICATION NUMBER: US/10/276,774
; PRIOR APPLICATION NUMBER: 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 09/496,914
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 2700
; SOFTWARE: Custom
; SEQ ID NO 2370
; LENGTH: 399
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-276-774-2370

Query Match 100.0%; Score 1864; DB 15; Length 399;
Best Local Similarity 100.0%; Pred. No. 2.8e-173;
Matches 359; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKSPFYRCNTTSYKGNASVAMGVLFSTGLGNLALGLARSGLCMSRRPLRPV 60
Db 41 MKSPFYRCNTTSYKGNASVAMGVLFSTGLGNLALGLARSGLCMSRRPLRPV 100
QY 61 FYMLVCGLTVDLLGKCLSPVLAAYANQNSLRVLAALDNLCOAFAPFMSFGLSST 120
Db 101 FYMLVCGLTVDLLGKCLSPVLAAYANQNSLRVLAALDNLCOAFAPFMSFGLSST 160
QY 121 LQLLAMLECWLSIGHPFFRRHTTLRLGALVAPVSAFSLAFALPFGMGKGVQCPG 180
Db 161 LQLLAMLECWLSIGHPFFRRHTTLRLGALVAPVSAFSLAFALPFGMGKGVQCPG 220
QY 181 TWCFIQWHEGSGSVGYSLVSSLMALLVLAIVLCNLGAMRLYAMHRLQHPHSC 240
Db 221 TWCFIQWHEGSGSVGYSLVSSLMALLVLAIVLCNLGAMRLYAMHRLQHPHSC 280
QY 241 RDCAEPRADREASPOPLEEDHLLALLMTVLFTMCSLPVIYRAYYGAFFDVKEKRTS 300
Db 281 RDCAEPRADREASPOPLEEDHLLALLMTVLFTMCSLPVIYRAYYGAFFDVKEKRTS 340
QY 301 EEAEDLALRFLSVISIVDPWIFIFRSVPVRIFFHKIFIRPLRYRSCNSTMSSL 359
Db 341 EEAEDLALRFLSVISIVDPWIFIFRSVPVRIFFHKIFIRPLRYRSCNSTMSSL 399

RESULT 3

US-10-225-567A-291
; Sequence 291, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:

; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burner, Glenn C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 291
; LENGTH: 358
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-291

Query Match 37.0%; Score 689; DB 14; Length 358;
Best Local Similarity 43.7%; Pred. No. 1.3e-58;
Matches 157; Conservative 54; Mismatches 118; Indels 30; Gaps 10;

QY 8 CQNTTSYKGNASVAMGVLFSTGLGNLALGLARSG--WCSRRPLRPVFMV 65
Db 13 CQNTTSYKGNASVAMGVLFSTGLGNLALGLARSG--WCSRRPLRPVFMV 71
QY 66 CGLTVDLLGKCLSPVLAAYANQNSLRVLAALDNLCOAFAPFMSFGLSSTIQLLA 125
Db 72 TELVFTDLGTCILSPVLAAYANQNSLRVLAALDNLCOAFAPFMSFGLSSTIQLLA 129
QY 126 MALECWLSIGHPFFRRHTTLRLGALVAPVSAFSLAFALPFGMGKGVQCPGTCFI 185
Db 130 MALECWLSIGHPFFRRHTTLRLGALVAPVSAFSLAFALPFGMGKGVQCPGTCFI 189
QY 186 QWHEGSGSVGYSLVSSLMALLVLAIVLCNLGAMRLYAMHRLQHPHSC 245
Db 190 R--HGR---TAYLQVATLLLVSVLACNFSVILNIRHRSR--SRGSGSLGS 240
QY 246 ---PRADREASPOPLEEDHLLALLMTVLFTMCSLPVIYRAYYGAFFDVKEKRTS 301
Db 241 GRGPGARRGERVSAEFTDHLILALMTITRACVSLPTIRAY-----METSS 291
QY 302 EAE--DIRALRFLSVISIVDPWIFIFRSVPVRIFFHKIFIR-PLRYRSCNSTMSSL 357
Db 292 RKEKMDLQALRFLSVISIVDPWIFIFRSVPVRIFFHKIFIR-PLRYRSCNSTMSSL 350

RESULT 4

US-10-352-684A-36
; Sequence 36, Application US/10352684A
; Publication No. US20030215452A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals Inc.
; APPLICANT: Carroll, Joseph M.
; APPLICANT: Healy, Aileen
; APPLICANT: Welch, Nadine S.
; APPLICANT: Kelly, Louise M.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: HEMATOLOGICAL DISORDERS USING 131, 148, 199, 12303, 13906,
; TITLE OF INVENTION: 15513, 17822, 302, 5677, 194, 14393, 28059, 7366, 12212,
; TITLE OF INVENTION: 1981, 261, 12416, 270, 1410, 137, 13051, 1847, 1849,
; FILE REFERENCE: MP102-019P1RNONMIM
; CURRENT APPLICATION NUMBER: US/10/352,684A
; CURRENT FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: US 60/354,333
; PRIOR FILING DATE: 2002-02-04
; PRIOR APPLICATION NUMBER: US 60/360,258
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/364,476
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: US 60/375,626
; PRIOR FILING DATE: 2002-04-26

Query Match	37.0%;	Score 689;	DB 15;	Length 358;
Best Local Similarity	43.7%;	Pred. No. 1.3e-58;		
Matches 157;	Conservative 54;	Mismatches 118;	Indels 30;	Gaps 10;

RESULT 5
US-10-366-288-36
Sequence 36, Application US/10366288
Publication No. US20030216288A1
GENERAL INFORMATION:
APPLICANT: Powell, Douglas
APPLICANT: Welch, Nadine S.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
TITLE OF INVENTION: AIDS AND HIV-RELATED DISORDERS USING
TITLE OF INVENTION: 340021, 1720, 1693, 1552, 1682, 1675, 12825, 9952, 5816,
TITLE OF INVENTION: 100021, 1611, 1371, 14324, 126, 270, 312, 167, 326, 18926,
TITLE OF INVENTION: 6747, 1793, 1784 OR 2045 MOLECULES
FILE REFERENCE: MP102-02551RNOMNTH
CURRENT APPLICATION NUMBER: US/10366, 288
CURRENT FILING DATE: 2003-02-13
PRIOR APPLICATION NUMBER: 60/357, 391
PRIOR FILING DATE: 2002-02-15
PRIOR APPLICATION NUMBER: 60/380, 249
PRIOR FILING DATE: 2002-05-13
PRIOR APPLICATION NUMBER: 60/391, 306
PRIOR FILING DATE: 2002-06-25
PRIOR APPLICATION NUMBER: 60/406, 297
PRIOR FILING DATE: 2002-08-27

Query Match	37.0%	Score 689;	DB 15;	Length 358;
Best Local Similarity	43.7%	Pred. No. 1.3e-58;		
Matches 157;	Conservative 54;	Mismatches 118;	Indels 30;	Gaps 10;

RESULT 6
US-10-755-889-92

Query Match	37.0%;	Score 689;	DB 16;	Length 358;
Best Local Similarity	43.7%;	Pred. No. 1.3e-58;		
Matches 157;	Conservative 54;	Mismatches 118;	Indels 30;	Gaps 10

Dy 8 CQNTTSVEKNSAVMGVLFTSTGLGNLALGILARSIG- WCSRRPLRLPSVPEMLV 65
| : | : | : | : | : | : | : | : | : | : | :
Db 13 CETRQWLPPESPAISSVMFAGVLGNLTALLARRRGDVGCSAGRSSL-SLEHLV 71

CURRENT FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: 60/195,747
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: 09/170,496
PRIOR FILING DATE: 1998-10-13
NUMBER OF SEQ ID NOS: 589
SOFTWARE: PatentIn Version 2.1
SEQ ID NO 559
LENGTH: 358
TYPE: PRT
ORGANISM: Homo sapiens
US-09-826-509-559

Query Match 36.6%; Score 683; DB 10; Length 358;
Best Local Similarity 43.5%; Pred. No. 5.2e-58;
Matches 156; Conservative 54; Mismatches 119; Indels 30; Gaps 10;

QY 8 CONTTSVEKNSAVMGVLESTGLGNLALGLIARSGLG--WCSRRPLRLPSVFTYLV 65
DB 13 CETRQWLPPEGSPAISSVMFSGVIGNLIALALARRRGDVGCSAGRSSL-SLFHVLV 71
QY 66 CGLVTDLGKCLISPVVLAAYANRSLRVAPALDNLSCQAFPFMSFGLSTLQLLA 125
DB 72 TELVFTDLGCLISPVVLAAYANRSLRVAPALDNLSCQAFPFMSFGLSTLQLLA 129
QY 126 MALECMWLSLGHPPFRHHTITRLGALVAPVVSASFALFALPFMGFGKVOYCPGTWCFI 185
DB 130 MALEKRVISLGHPPFRHHTITRLGALVAPVVSASFALFALPFMGFGKVOYCPGTWCFI 189
QY 186 QMVEBGLSVLGYSVLYSSLMALVLAIVLCNIGAMRNLYAMHRLQHRHSCSTRDCAE 245
DB 190 R--HGR-----TAVLQLYATLLILIVSVLACNFSVILNLRHRRSR--SRCGSLGS 240
QY 246 ----PRADGRBASQPLELDHLLALMTVLFTMCSLPVIYRYGAFKDYKERTSE 301
DB 241 GRCGPARRGERVSMABEEDHKLALMTITTFVAVCSLPTTFAY-----MNETSS 291
QY 302 EAE--DLRALRFLSVISIVDPWIFIFRSPVFRIFPKIFIR--PLAYRSRCSNSTMES 357
DB 292 RKEMDLQALRFLSINSIIDPWVFAILRPVLRMSVLCRISLRKQDQTQISCTQS 350

RESULT 10
US-10-925-095-559

Sequence 559, Application US/10925095
Publication No. US20050019840A1
GENERAL INFORMATION:
APPLICANT: Lehmann-Bruinsma, Karin
APPLICANT: Lian, I-Lian
TITLE OF INVENTION: Non-Endogenous, Constitutively Activated Known G
TITLE OF INVENTION: Protein-Coupled Receptors
FILE REFERENCE: AREN-207
CURRENT APPLICATION NUMBER: US/10/925,095
CURRENT FILING DATE: 2004-08-24
PRIOR APPLICATION NUMBER: US/09/826,509
PRIOR FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: 60/195,747
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: 09/170,496
PRIOR FILING DATE: 1998-10-13
NUMBER OF SEQ ID NOS: 589
SOFTWARE: PatentIn Version 2.1
SEQ ID NO 559
LENGTH: 358
TYPE: PRT
ORGANISM: Homo sapiens
US-10-925-095-559

Query Match 36.6%; Score 683; DB 17; Length 358;
Best Local Similarity 43.5%; Pred. No. 5.2e-58;
Matches 156; Conservative 54; Mismatches 119; Indels 30; Gaps 10;

QY 8 CONTTSVEKNSAVMGVLESTGLGNLALGLIARSGLG--WCSRRPLRLPSVFTYLV 65
DB 13 CETRQWLPPEGSPAISSVMFSGVIGNLIALALARRRGDVGCSAGRSSL-SLFHVLV 71
QY 66 CGLVTDLGKCLISPVVLAAYANRSLRVAPALDNLSCQAFPFMSFGLSTLQLLA 125
DB 72 TELVFTDLGCLISPVVLAAYANRSLRVAPALDNLSCQAFPFMSFGLSTLQLLA 129
QY 126 MALECMWLSLGHPPFRHHTITRLGALVAPVVSASFALFALPFMGFGKVOYCPGTWCFI 185
DB 130 MALEKRVISLGHPPFRHHTITRLGALVAPVVSASFALFALPFMGFGKVOYCPGTWCFI 189
QY 186 QMVEBGLSVLGYSVLYSSLMALVLAIVLCNIGAMRNLYAMHRLQHRHSCSTRDCAE 245
DB 190 R--HGR-----TAVLQLYATLLILIVSVLACNFSVILNLRHRRSR--SRCGSLGS 240
QY 246 ----PRADGRBASQPLELDHLLALMTVLFTMCSLPVIYRYGAFKDYKERTSE 301
DB 241 GRCGPARRGERVSMABEEDHKLALMTITTFVAVCSLPTTFAY-----MNETSS 291
QY 302 EAE--DLRALRFLSVISIVDPWIFIFRSPVFRIFPKIFIR--PLAYRSRCSNSTMES 357
DB 292 RKEMDLQALRFLSINSIIDPWVFAILRPVLRMSVLCRISLRKQDQTQISCTQS 350

RESULT 11
US-10-225-567A-285

Sequence 285, Application US/10225567A
Publication No. US20030113798A1
GENERAL INFORMATION:
APPLICANT: Lifespan Biosciences
APPLICANT: Brown, Joseph P.
APPLICANT: Butner, Glenna C.
TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
FILE REFERENCE: 1920-4-4
CURRENT APPLICATION NUMBER: US/10/225,567A
CURRENT FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 60/257,144
PRIOR FILING DATE: 2000-12-19
NUMBER OF SEQ ID NOS: 2292
SOFTWARE: PatentIn Version 3.1
SEQ ID NO 285
LENGTH: 386
TYPE: PRT
ORGANISM: Homo sapiens
US-10-225-567A-285

Query Match 32.0%; Score 597; DB 14; Length 386;
Best Local Similarity 42.3%; Pred. No. 1.4e-49;
Matches 141; Conservative 46; Mismatches 102; Indels 44; Gaps 9;

QY 8 CONTTSVEKNSAVMGVLESTGLGNLALGLIARSGLG--WCSRRPLRLPSVFTYLV 67
DB 5 CRMLTYVRSVGPATSTLMFVAGVNGGLALGILS-----ARRPAR--PSAFVAVLVG 55
QY 68 LYTVDLGLKCLISPVVLAAYANRSLRVLA---PALDNLSCQAFPFMSFGLSTLQLL 124
DB 56 LAATDLGTSFLSPAVFAVAAARSSSLGLARGPA---LCDAFAFAMTFEGLASMLILF 111
QY 125 AMALCWLISLGHPPFRHHTITRLGALVAPVVSASFALFALPFMGFGKVOYCPGTWCFI 184
DB 112 AMAVKCLASHPYVLAQDGRPCARLALPAITAFVLPALDLGLIGQHQYCPGSMCF 171
QY 185 IQN--VHEBGLSVLGYSVLYSSLMALVLAIVLCNIGAMRNLYAMHRLQHRHSCSTRD 242
DB 172 LRMRWQOPGGA---AFSLAYAGLVALLVAIFLCNGSVTLSCRMVROQKRHGS---- 223
QY 243 CAEPADGRBASQPLELDHLLALMTVLFTMCSLPVIYRYGAFKDYKERTSE 301
DB 224 -----LGRPRTGDEVDHLLILALMTVMAVCSLPTIRCFQAVAP-----DS 268
QY 300 SEAEADLALRFLSVISIVDPWIFIFRSPVFR 312

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      | | | | | : | : | : | : | : | :
269 S S E M G D L L A F R F Y A F N P I L D P W V F I L E R K A V F Q 301
Db

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RESULT 12
US-10-108-260A-3907
; Sequence 3907, Application US/10108260A
; Publication No. US20040005560A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20040005560A1el full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/10/108,260A
; CURRENT FILING DATE: 2002-03-27
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3907
; LENGTH: 289
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-108-260A-3907

```

Query Match	27.8%	Score 518.5	DB 15	length 289
Best Local Similarity	43.3%	Pred. No. 4.6e-42		
Matches 122	Conservative 39	Mismatches 82	Indels 39	Gaps 8

Qy	8	CONTTSVEKGNANVMGQVFTSGILGNLTALGILGASLGWCGRRRLRPLPSVAFYMLVCG	67
Db	5	CRNLTVYKGSVSPATSTLMFVAGVGVNGILATGLTS-----ARRAR--PSAFVAVLYTG	55
Qy	68	LTVTDLGKCLISPVVLLAAYAONRSRLVIA---PALDNSICQAFPMFMSFGISSTLQTL	124
Db	56	LAATLILGTSFLPSPAVFVAYARNSSLPGLARGSPA----LCDAFAFAMTFEFGASMLILF	111
Qy	125	AMALBCWLSLGHPPFRRIITRLIGLVAVPVVSASFSLAFCALDFPMGSGKVOYCPGTMCF	184
Db	112	ANAVERCIALSHPPVLYAQDLDPGCCALPAIATVFCVLFCALEPLGIGHQOYCPGSKCF	171
Qy	185	IQM--VHEGSLISVLGYSVLVSLSMALVLAIVLCNIGAMRNLYAMHRLIQRHRSCTRD	242
Db	172	LRMRAQPGCA---AFSLAYAGVLVALLVAAPFLGNGSVTLISLCRMVYQCKRQGS----	223
Qy	243	CAEPRADGKASFPQPL---EELDHLLLLALMTYLLFTMCSLPV	281
Db	224	-----LGRPRTEGDEVDHLLLLALMTVVMVCSLP	255

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RESULT 13
US-10-225-567A-296
; Sequence 296, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: Lifespan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burner, Glenna C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 296
; LENGTH: 488
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-296

```

Query Match	23.8%	Score 443	DB 14	Length 488
Best Local Similarity	31.9%	Pred. No. 2.1e-34		
Matches 126, Conservative	62	Mismatches 149	Indels 58	Gaps 13

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QY      1 MKSFYFCQNTLVSEVKGNAAV-MGCVFESTLGLNLALGLASGLCMGRRLPLRPLPS 59
        | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      1 MSTFGVNSSASLASPDRLNSPTTIAWMFI FGVGUNLVAIVLCK-----SRKEK--ET 52

QY      60 VFVMVLCSGLVTDTDLGKCLSPVVLAAYNQRSLRVLA PALDNSICQAFEFMSFEGLSS 119
        | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      53 TFFTLVCGSLATDLDLGLTVLSPVITATVMKGQ----WPG-GQPCXESTFLILFFLSISG 106

QY      120 TLQLMALMECWSLGHPEFFFRHHITLRIGALVAVVSASFSLAPFLPMFGRGKVQYCP 179
        | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      107 LSIICAMSVEVEYLAINHAYFYSHVDYKRKLAEITLFAYVAASVLFALPMMGGSSRLQYP 166

QY      180 GTMCFIQMVNHEGSLSVLGYSVLSSLMALLVLTVCNLGMARLYAMHRLOQHPRSSC 239
        | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      167 DTWCEDIDWT--TNVTAHAAYMYMAFGSSFLIATLVLCNVLCAGLLMHMQFPKRTSLG 224

QY      240 TRD-----CAERPADGREASPOPL-----EEDHLILLALMTVLFTMC 277
        | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      225 TEQHAAAAAASVASRGHPAASPALPRLSDFRRRSFRRIAGAEIQMVILLATSLVLVIC 284

QY      278 SLPVITYRAYGAFAFDVYEKNRTSEBAE-----DLRALFLSVLSIVDPWIFILPFSPVFR 332
        | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      285 SIPLVVRVF-----VNQLYOPSLEREYSKPNPDQAIRIASVPILDPWIYILLAKTVLS 338

QY      333 IFFHKI---FIR---PLRYRS-RCSNSTNNESSL 359
        | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      339 KAIEIKICLFCRIGSGRRERSGOHQSDORTSSAM 373

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RESULT 14
US-10-320-351-3
; Sequence 3, Application US/10320351
; Publication No. US20030134314A1
; GENERAL INFORMATION:
; APPLICANT: Healy, Aileen
; APPLICANT: Carroll, Joseph M.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: HEMATOLOGICAL DISORDERS USING 252, 304, 1980, 14717, 9941
; TITLE OF INVENTION: 19310 AND 17832
; FILE REFERENCE: MP101-292P1RM
; CURRENT APPLICATION NUMBER: US/10/320,351
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: 60/341,606
; PRIOR FILING DATE: 2001-12-17
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 488
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-320-351-3

```

Query Match	23.8%	Score 443;	DB 14;	Length 488;
Best Local Similarity	31.9%	Pred. No. 2.1e-34;		
Matches	126;	Conservative	62;	Mismatches 149; Indels 59; Gaps 13
QY	1	MKSPEYRCQNTSVKGNASAV-MGCVLESTGLGNLLALGLIARSGLCMSRRPLRPLDS	59	
DB	1	MSTPEVMSASISDPRLNSPVTIIPAMFIFGVGVGLVAIVLCK-----SEKEOK--ET	52	
QY	60	VFMYLVGGLATYTDILGKCLLSPVYLAATAAQNRSRLVLA PALDNLSCOAFAFMSDFGSS	119	
DB	53	TFYTLVCGLAATDLGTLIVSPVTIATIMKGO----WPG-GQPLCEKSTFLLFFSLSG	106	
QY	120	TLQLLALIECMLSIGHPFFYRRHITTLIGALVAVASAFSLAFCALPFGMGKGVQYCP	179	
DB	107	LSIICAMSEVERLIATNHAFYFYSHYVDKRLAGTLIPAVYASNVLFCAIPMVGSSRLQYP	166	
QY	180	GTWCICIQWHEEGSLSTLVGSLVSSLMALLVYLAIVLNLGAMRNLVYMMHRLQHPRSC	239	
DB	167	DTWCICIDMT--TNVTAHAAYSTMYAGSSFLIATVLCNVLCGALNRHROFMRRTISIG	224	

[illegible]

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RESULT 15
US-10-295-027-1326
: Publication 1326, Application US/10295027
: Publication No. US2003023350A1
GENERAL INFORMATION:
: APPLICANT: Afar, Daniel
: APPLICANT: Aziz, Natasha
: APPLICANT: Ginsberg, Wendy M.
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: APPLICANT: Mack, David H.
: APPLICANT: Murray, Richard
: APPLICANT: Watson, Susan R.
: APPLICANT: Eos Biotechnology, Inc.
: TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
: TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
: FILE REFERENCE: 018501-012500US
: CURRENT FILING DATE: 2002-11-13
: PRIOR APPLICATION NUMBER: US/10/295,027
: PRIOR FILING DATE: 2000-09-15
: PRIOR APPLICATION NUMBER: US 09/663,733
: PRIOR FILING DATE: 2001-11-13
: PRIOR APPLICATION NUMBER: US 60/335,666
: PRIOR FILING DATE: 2001-11-15
: PRIOR APPLICATION NUMBER: US 60/332,464
: PRIOR FILING DATE: 2001-11-21
: PRIOR APPLICATION NUMBER: US 60/334,393
: PRIOR FILING DATE: 2001-11-29
: PRIOR APPLICATION NUMBER: US 60/340,376
: PRIOR FILING DATE: 2001-12-14
: PRIOR APPLICATION NUMBER: US 60/347,211
: PRIOR FILING DATE: 2002-01-08
: PRIOR APPLICATION NUMBER: US 60/347,349
: PRIOR FILING DATE: 2002-01-10
: PRIOR APPLICATION NUMBER: US 60/355,250
: PRIOR FILING DATE: 2002-02-08
: PRIOR APPLICATION NUMBER: US 60/356,714
: PRIOR FILING DATE: 2002-02-13
: Remaining Prior Application data removed - See File Wrapper or PALM.
: NUMBER OF SEQ ID NOS: 186
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 1326
: LENGTH: 488
: TYPE: PRT
: ORGANISM: Homo sapiens
: US-10-295-027-1326

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Query Match	23.8%	Score 443	DB 15	Length 488
Similarity	31.9%	Pred. No. 2.1e-34		
Best Local	62	Conservative	149	Indels 58
Matches 126				Gaps 13

[illegible]

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Qy 120 TTGLLMALECWISLGHPEFYRRHTLLGALVAVPVVSAFSLACALPFGMGKFEVQCP 179
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Db 107 LSTICAMSVERTLIATINHAIFYSHYVDKRLAGLTLEFAYASVULFCALPNNGLSSRIQYP 166
      |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Qy 180 GTWCPIQWVHEGSLVIGSVLVSLSMALIVLATVLCNIGAMENLYAMHRRLODRHPRSC 239
      |||||
Db 167 DTWCPIQWVHEGSLVIGSVLVSLSMALIVLATVLCNVLGVCGALIRMHQFRRRPSLIG 224
      |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Qy 240 TRD-----CAEPRADGREGASPPQL-----EELDHLILLALMTVLPTWC 277
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Db 225 TEGHMAAAAASVASKGHPAASPALRLSDFFRRRSFRRIAGAEQWVILLIATLSVLVIC 284
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Qy 278 SLEVIYRAYYGAFKVKEKNRTSEBAE-----DLRALFTSVISIVDPFTIIFRSVFR 332
      |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 285 SIPLVAVRVE-----VNOLYQPSLTEREYSKNPDIQAIRIASVNPILDPWYIYLIRKTVLS 338
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Qy 333 IFPHKT---FIR---PLRYRS---RCSNNTWNESSL 359
      |||||
Db 339 KAIEKTKICLFCRIIGSRREKRSQGHLSDSQDORLSSAM 373

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Search completed: April 22, 2005, 21:43:06
Job time : 187.351 secs

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